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OM nucleic - nucleic search, using SW model

Run on: October 28, 2004, 03:10:13 ; Search time 11341 Seconds
(without alignments)
11275.139 Million cell updates/sec

Title: US-09-745-605-1
Perfect score: 2704
Sequence: 1 ggaagtgcgttcattccagcgtt.....aaaaaaaaaaaaaaaaaaaaa 2704

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues
Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
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9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2704	100.0	2704	6	AX180364	AX180364 Sequence
2	2617.2	96.8	2774	6	BD249810	BD249810 33 human
3	2604.6	96.3	2672	9	AB027233	AB027233 Homo sapi
4	2390.6	88.4	2658	9	BC027867	BC027867 Homo sapi
5	2229.4	82.4	2445	9	HSMB05512	AL834424 Homo sapi
6	2186.4	80.9	2780	6	BD249841	BD249841 33 human
7	1727.8	63.9	3532	9	HSMB03118	AL713801 Homo sapi
8	1654.2	61.2	166345	2	AC068728	AC068728 Homo sapi
9	1649.4	61.0	195976	9	HSAB04F10	AL121985 Human DNA
10	1369.4	50.6	1412	6	BD249842	BD249842 33 human
11	1369.4	50.6	1412	6	BD082372	BD082372 87 human
12	1326	49.0	1352	9	AF390894	AF390894 Homo sapi
13	1187.4	43.9	1250	9	HSMB04336	AL833025 Homo sapi
14	1076	39.8	1076	6	AR252549	AR252549 Sequence
15	1076	39.8	1076	6	AX092314	AX092314 Sequence
16	1076	39.8	1076	6	AX376124	AX376124 Sequence
17	1076	39.8	1076	6	AX403365	AX403365 Sequence
18	1076	39.8	1076	9	AY358512	AY358512 Homo sapi
19	1071	39.6	1083	9	AF291815	AF291815 Homo sapi

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24	879.8	32.5	1128	6	AX405882	AX405882 Sequence
25	851	31.5	1074	9	HSAB271869	AJ271869 Homo sapi
26	687	25.4	2334	6	CQ718717	CQ718717 Sequence
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37	331.6	12.3	344	6	AX884532	AX884532 Sequence
38	331.6	12.3	344	6	BD024142	BD024142 Sequence
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42	325.2	12.0	522	6	CQ140985	CQ140985 Sequence
43	325.2	12.0	522	6	CQ176644	CQ176644 Sequence
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45	325.2	12.0	522	6	CQ262264	CQ262264 Sequence

ALIGNMENTS

RESULT 1	AX180364	2704 bp	DNA	linear	PAT 06-AUG-2001
LOCUS	AX180364	Sequence 1 from Patent WO0146260.			
DEFINITION	AX180364				
ACCESSION	AX180364.1	GI:15132304			
VERSION					
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1	Scarling, G.C. and Finger, J.			
AUTHORS		Novel immunoglobulin superfamily members apex-1, apex-2 and apex-3			
TITLE		and uses thereof			
JOURNAL		Patent: WO 0146260-A 1 28-JUN-2001;			
		Bristol-Myers Squibb Co. (US)			
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Db	1	GGAAGTGGCTTCAATTCAGTGGCTGACCTCCAGAGCAATATAGCTGTTCCCAACAT	60		
QY	61	GCCTCACCCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTTGACCCCGTGA	120		
Db	61	GCCTCACCCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTTGACCCCGTGA	120		
QY	121	AAGAGCTGTCGCTTCGCTGCTGGTGGGGCCGTAATTCCCGCTGAAGTCCAAGTAAGC	180		
Db	121	AAGAGCTGTCGCTTCGCTGCTGGTGGGGCCGTAATTCCCGCTGAAGTCCAAGTAAGC	180		
QY	181	AAGTTGACTCTATTGTCTGACCTTCAACGCAACCCCTCTGTGACCATACAGCCAGAAG	240		

Db 181 AAGTTGACTTATTGTCTGGACCTTCAACACAAACCCCTTGTGTACCAATAACAGCCAGAAG 240
QY 241 GGGGCACTATCATAGTGACCCCAAAATCGTAATAGGAGAGAGATAGACTTCCAGATGGAG 300
Db 241 GGGGCACTATCATAGTGACCCCAAAATCGTAATAGGAGAGAGATAGACTTCCAGATGGAG 300
QY 301 GCTACTCCCTGAAGCTCAGCAAACTGAAGAATGACTCAGGAGTCTATGTGGGGA 360
Db 301 GCTACTCCCTGAAGCTCAGCAAACTGAAGAATGACTCAGGAGTCTATGTGGGGA 360
QY 361 TATACAGCTCATCACTCCAGCAGCCCTCCACCCAGAGTACGTGCTGATGTCTACGAGC 420
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Db 421 ACCGTGCAAGCCTAAAGTCAACCATGGGTCTGCAGAGCAATAAGATGGCACTGTGTGA 480
QY 481 CCAATCTGACATGCTGCATGGAACATGGGGAAGAGATGTGATTTATACCTGGAAGGCC 540
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QY 541 TGGGGCAAGCAGCCATGAGTCCCATTAATGGGTCCATCCTCCCATCTCTGGAGATGG 600
Db 541 TGGGGCAAGCAGCCATGAGTCCCATTAATGGGTCCATCCTCCCATCTCTGGAGATGG 600
QY 601 GAGAAAGTGATATGACCTTCATCTGCGTTCAGGAACCTGTGACAGAACTTCTCAA 660
Db 601 GAGAAAGTGATATGACCTTCATCTGCGTTCAGGAACCTGTGACAGAACTTCTCAA 660
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Db 661 GCCCCATCTTGCCAGGAAGCTCTGTGAAGTGTGCTGATGACCCAGATTCTCCATGG 720
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QY 781 TTTGGTTTCTGAAGAGAGAGAGACAAGAAGTACATTGAAAGAGAAGAAGAGTGGACA 840
Db 781 TTTGGTTTCTGAAGAGAGAGAGACAAGAAGTACATTGAAAGAGAAGAAGAGTGGACA 840
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Db 841 TTTGTGCGGAAACTCCTAACATATGCCCAATTCTGGAGAGAACACAGAGTACGACACAA 900
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Db 1801 AGGACAAAGACCTCCAGCCAGGCTTCATTTATGACACTTGTGCTGCAAAAAGAAAGTCTAG 1860
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QY 1921 AATCTAGTGTAGAGACTTGGAGTCAAGCAGTGAAGTGTGGGGCAGGAGTGG 1980
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QY 1981 GTACTGTATAACCTTTAAAGATGTTAATTCATTCAATAGATATTTATTAAGAACTTACT 2040
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OY	2461	TCCCTGACGCATATCTTGAATGGAGACCCTCCCTACCAAGTATGAAAAGTGTGAAAAACT	2520
Db	2461	TCCCTGACGCATATCTTGAATGGAGACCCTCCCTACCAAGTATGAAAAGTGTGAAAAACT	2520
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Db	2521	TAATAACAATGCTTGTGGCGAAGAATGGATTGAGATTATCTTCTCAGAAAGCA	2580
OY	2581	TTGTGAAGGAATTGAGCCAGATCTCTCCCTACTGCAAAACCCATTGTAGTAAAAAG	2640
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RESULT 2			
LOCUS	BD249810	2774 bp	DNA linear PAT 17-JUL-2003
DEFINITION	33 human secreted proteins.		
ACCESSION	BD249810		
VERSION	BD249810.1 GI:33059580		
KEYWORDS	JP 2002540763-A/12.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 2774) Rosen,C.A., Ruben,S.M., Ebner,R., Young,P.E., Ni,J., Soppet,D.R., Moore,P.A., Shi,Y., Lafleur,D.W., Olsen,H.S., Florence,K.A. and Komatsoulis,G. 33 human secreted proteins Patent: JP 2002540763-A 12 03-DEC-2002;		
AUTHORS	JOURNAL		
	HUMAN GENOME SCIENCES INC		
	OS Homo sapiens (human)		
	PN JP 2002540763-A/12		
	PD 03-DEC-2002		
	PF 08-FEB-2000 JP 2000598519		
	PR 10-FEB-1999 US 60/119468		
	PI CRAIG A ROSEN, STEVEN M RUBEN, REINHARD EBNER, PAUL E YOUNG, JIAN NI,		
	PI DANIEL R SOPPET, PAUL A MOORE, YANGGU SHI, DAVID W LAFLEUR, HENRIK		
	PI S OLSEN,		
	PI KIMBERLY A FLORENCE, GEORGE KOMATSOULIS		
	PC C12N15/09,A61K31/7115,A6IK38/00,A6IK48/00,A6IP1/00,A6IP1/04, PC A6IP1/16,		
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	PC C12Q1/68,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC C12N15/00,		
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Best Local Similarity	98.7%;	Pred. No. 0;	
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OY	61	GCCTCACCTCATCTATACTCTTTGGCAGCTCACAGGGTAGCAGCCTCTGGACCCTGA	120
Db	73	GCCTCACCTCATCTATACTCTTTGGCAGCTCACAGGGTAGCAGCCTCTGGACCCTGA	132
OY	121	AAGAGCTGGTCGGTCCGTTGGTGCGGCCGTGACTTCCCCCTGAAGTCCAAAGTAAAGC	180
Db	133	AAGAGCTGGTCGGTCCGTTGGTGCGGCCGTGACTTCCCCCTGAAGTCCAAAGTAAAGC	192
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OY	241	GGGGCACTATCATAGTAAGACCCAAATCGTATAGGAGAGAGTAGA CTTC CAGATGGAG	300
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OY	301	GCTACTCCCTGAAGCTCAGCAA ACTG AAG AAG AATGACTCAGGGA TCTACTATGTGGGA	360
Db	313	GCTACTCCCTGAAGCTCAGCAA ACTG AAG AAG AATGACTCAGGGA TCTACTATGTGGGA	372
OY	361	TATACAGCTCATCATCTCAGCAGC CCCTCC ACCCAGAGTAGTCTGCATGTCTACGAGC	420
Db	373	TATACAGCTCATCATCTCAGCAGC CCCTCC ACCCAGAGTAGTCTGCATGTCTACGAGC	432
OY	421	ACCTGTCAAGCCTAAGTCAACCATGGGCTGCAGAGCAATAAGATGGCACCCTGTGA	480
Db	433	ACCTGTCAAGCCTAAGTCAACCATGGGCTGCAGAGCAATAAGATGGCACCCTGTGA	492
OY	481	CCAATCTGACATGCTGTCATGGAACATGGGGAAGAGATGTGATTTATACCTGGAAGCCC	540
Db	493	CCAATCTGACATGCTGTCATGGAACATGGGGAAGAGATGTGATTTATACCTGGAAGCCC	552
OY	541	TGGGGCAAGCAGCCCAATGAGTCCCATATATGGGTCCATCTCTCCCATCTCTGAGATGG	600
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OY	661	GCCCCATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCAGATTCTCCATGG	720
Db	673	GCCCCATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCAGATTCTCCATGG	732
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Db	733	TCCTCCTGTGTCTCCTGTTGGTGCCCTCCTGCTCAGTCTTTGTACTGCGGTATTTTC	792
OY	781	TTTGGTTTCTGAAGAGAGAGACAAAGAAAGATACATTGAAGAAAGAAAGAGTGGACA	840
Db	793	TTTGGTTTCTGAAGAGAGAGACAAAGAAAGATACATTGAAGAAAGAAAGAGTGGACA	852
OY	841	TTTGTGGGAAACTCTTAACATATATGCCCCCATTTCTTGAGAGAAACACAGAGTACGACACAA	900

|||||
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Qy 901 TCCCTCACACTATAGAACATCCTAAAGAGATCCAGCAAAATACGGTTTACTCCACTG 960
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Qy 1321 TTAGAAGTATTCCTATAGAAATGTAAATGCAAGGTCAACATATTAATGACAGCCTGTTG 1380
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Qy 1441 AGGATTATACCAAGAGTCTTGCTACACAGAGGGCAAGAACCAAAACAGACAGACAAGT 1500
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ACCESSION AB027233
VERSION AB027233.1 GI:14517605
KEYWORDS membrane protein FOAP-12.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 2672)
Fujii,Y., Takayama,K., Tsuritani,K., Yajima,Y., Amemiya,T.,
Ukai,Y., Naito,K. and Kawaguchi,A.
Homo sapiens mRNA for FOAP-12 protein, complete cds
JOURNAL
Unpublished
2 (bases 1 to 2672)
Fujii,Y., Takayama,K., Tsuritani,K., Yajima,Y., Amemiya,T.,

TITLE Ukai,Y., Naito,K. and Kawaguchi,A.
Direct Submission
JOURNAL Submitted (12-MAY-1999) Yasuyuki Fujii, Taisho Pharmaceutical Co.,
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Saitama 3308530, Japan (E-mail: s17561@ccm.taisho.co.jp,
Tel: +81-48-663-1111, Fax: +81-48-652-7254)

FEATURES

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ORIGIN

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RESULT 4
 BC027867 2658 bp mRNA linear PRI 12-NOV-2003
 LOCUS Homo sapiens SLAM family member 7, mRNA (cDNA clone MGC:34188
 DEFINITION IMAGE:5203638) , complete cds.
 ACCESSION BC027867
 VERSION BC027867.1 GI:20380756

KEYWORDS
 SOURCE
 ORGANISM

MGC.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 AUTHORS

1 (bases 1 to 2658)
 Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Wille,J., Helton,E., Kettelman,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Buterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
 Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 22388257
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 2 (bases 1 to 2658)
 Strausberg,R.
 Direct Submission
 Submitted (08-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL

REMARK
 COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc_mgc@hgti.nih.gov
 Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Lalic,P., Legaspi,R., Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Stantiriop,S., Thomas,P.J., Touchman,J.W., Tsurgson,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
 Series: IRAC Plate: 49 Row: e Column: 22
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 19923571.

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ORIGIN

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DEFINITION Homo sapiens mRNA; cDNA DKFZp667F126 (from clone DKFZp667F126).
ACCESSION AL834424
VERSION AL834424.1 GI:21740141

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
1 (bases 1 to 2445)
AUTHORS Bloecker,H., Boecher,M., Brandt,P., Mewes,H.W., Weil,B. and Wiemann,S.
TITLE Direct Submission

JOURNAL
COMMENT

Submitted (09-JUL-2002) 1, D-85764 Neuberberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
Sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.
This clone (DKFZp667F126) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at <http://mips.gsf.de/proj/cDNA/>.

FEATURES

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ORIGIN

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LOCUS BD249841
DEFINITION 33 human secreted proteins.
ACCESSION BD249841
VERSION BD249841.1 GI:33059611
KEYWORDS JP 2002540763-A/43.
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2780)
Rosen,C.A., Ruben,S.M., Ebner,R., Young,P.E., Ni,J., Soppet,D.R.,
Moore,P.A., Shi,Y., Lafleur,D.W., Olsen,H.S., Florence,K.A. and

TITLE Komatsoulis,G.
JOURNAL 33 human secreted proteins
Patent: JP 2002540763-A 43 03-DEC-2002;
HUMAN GENOME SCIENCES INC
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PD 03-DEC-2002
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PI NI,
PI DANIEL R SOPPET,PAUL A MOORE,YANGU SHI,DAVID W LAFLEUR,HENRIK
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PI KIMBERLY A FLORENCE,GEORGE KOMATSOULIS
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QY 1540 AATTGGCTCTATAACTATGTGCCCCAGCACTATGCTGAGCTTACACTAATTGGTCAGACG 1599
Db 1616 AATTGGCTCTATAACTATGTGCCCCAGCACTATGCTGAGCTTACACTAATTGGTCAGACG 1675
QY 1600 TGCTGTGCTCCCTCATGAAATTTGGCTCCAAATGAATGAATCTACTTCATGAGCAGTTGTA 1659
Db 1676 TGCTGTGCTCCCTCATGAAATTTGGCTCCAAATGAATGAATCTACTTCATGAGCAGTTGTA 1735
QY 1660 GCAGGCTGACCAAGATTCACAGAGGCGCAGGTGTGATCCACAGACTTGAAAGTCAA 1719
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QY 1960 GTGGGGCAGCGGGGAGTGGTACTTGTAAACCTTAAAGATGTTAATTCAATCAATA 2019
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RESULT 7
HSM803118 3532 bp mRNA linear PRI 20-MAR-2002
LOCUS HSM803118
DEFINITION Homo sapiens mRNA; cDNA DKFZp667N1110 (from clone DKFZp667N1110).
ACCESSION AL713801
VERSION AL713801.1 GI:19584564
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 3532)
AUTHORS Duesterhoeft,A., Lauber,J., Mewes,H.W., Weil,B. and Wiemann,S.
TITLE Direct Submission
JOURNAL Submitted (12-MAR-2002) MIPS, Am Klopferpitz 18a, D-82152
Martinsried, GERMANY
COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Oigen (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.
This clone (DKFZp667N1110) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://mips.gsf.de/proj/cDNA/.
LOCATION/Qualifiers
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ORIGIN
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Best Local Similarity 99.2%; Pred. No. 0;
Matches 1780; Conservative 0; Mismatches 7; Indels 8; Gaps 4;
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Db 1921 ATTCTCGGCCCCAAGAAAAACAATCAGAGAATTCACTGATTGTGACTAGAAAACATCAAGGA 1980

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Db 1981 AGAATGAAGACGTTGACTTTTTCAGAGTAAATTATCTGTGATGCTTCTTAGATTTA 2040

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Db 3478 TTAATATCTTAATAAAAACAGATATTGTGAGATTACATAAAAAAA 3532

RESULT 8

AC068728

LOCUS

DEFINITION

AC068728 Homo sapiens chromosome 1 clone RP11-8D14, WORKING DRAFT SEQUENCE, 5 unordered pieces.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

JOURNAL

AUTHORS

TITLE

JOURNAL

COMMENT

On Mar 1, 2001 this sequence version replaced gi:11878529.

----- Genome Center

Center: Stanford DNA Sequencing and Technology Development Center

Center code: SDSJDC

Web site: <http://sequence-www.stanford.edu/group/human/>

Contact: hum-info@sequence.stanford.edu

----- Project Information
Center project name: 922
Center clone name: RP11-8D14
----- Summary Statistics
Sequencing Vector: M13mp18; X02513
Chemistry: Dye-primer; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 160988 bases at least Q40
Consensus quality: 161717 bases at least Q30
Consensus quality: 161956 bases at least Q20
Insert size: 164605; agarose-fp
Insert size: 165945; sum-of-ctnigs
Quality coverage: 9.0x in Q20 bases; agarose-fp
Quality coverage: 8.9x in Q20 bases; sum-of-ctnigs.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 1866: contig of 1866 bp in length
* 1867 1966: gap of unknown length
* 1967 3797: contig of 1831 bp in length
* 3798 3897: gap of unknown length
* 3898 23083: contig of 19186 bp in length
* 23084 23183: gap of unknown length
* 23184 62924: contig of 39741 bp in length
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ORIGIN

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repeat_region 23891. .24037 /note="MER91A repeat: matches 15. .171 of consensus"
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Best Local Similarity 98.9%; Pred. No. 0;
Matches 1704; Conservative 0; Mismatches 11; Indels 8; Gaps 4;
QY 976 AGATGAAATCCCACTCACTGCTCAGATGCCAGACACACCAAGGCTATTGCTATG 1035
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LOCUS

DEFINITION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

PN JP 2001522239-A/14

PD 13-NOV-2001

PF 19-MAR-1998 JP 1998542119

PR 21-MAR-1997 US 60/041281, 21-MAR-1997 US 60/041276 PR

21-MAR-1997 US 60/042344, 21-MAR-1997 US 60/041277 PR

30-MAY-1997 US 60/048355, 30-MAY-1997 US 60/048096 PR

30-MAY-1997 US 60/048351, 30-MAY-1997 US 60/048154 PR

30-MAY-1997 US 60/048160, 30-MAY-1997 US 60/048069 PR

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30-MAY-1997 US 60/048350, 05-AUG-1997 US 60/054804 PR

19-AUG-1997 US 60/056370, 02-OCT-1997 US 60/060862 PI PAUL

YOUNG, JOHN M GREENE, ANN M FERRIE, STEVEN M RUBEN, CRAIG A PI

ROSEN,

PI ROXANNE D DUAN, JING SHAN HU, KIMBERLY A FLORENCE, HENRIK S

OLSEN,

PI REINHARD EBNER, LAURIE A BREWER, PAUL A MOORE, YANGU SHI, DAVID W

PI LAFLEUR,

PI JIAN NI

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CC Strandedness: Double;

CC Topology: Linear;

FH Key Location/Qualifiers.

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VERSION AF390894.1 GI:16589010
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 1352)
AUTHORS Bouchon,A., Cella,M., Grierson,H.L., Cohen,J.I. and Colonna,M.
TITLE Cutting Edge: Activation of NK Cell-Mediated Cytotoxicity by a SAP-Independent Receptor of the CD2 Family
JOURNAL J. Immunol. 167 (2001) In press
REFERENCE 2 (bases 1 to 1352)
AUTHORS Colonna,M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2001) Basel Institute for Immunology, 487 Grenzacherstrasse, Basel CH-4005, Switzerland
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ACCESSION AL833025
VERSION AL833025.1 GI:21733615
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1250)
AUTHORS Ansoorge,W., Wirkner,U., Mewes,H.W., Weil,B. and Wiemann,S.
TITLE Direct Submission
JOURNAL Submitted (09-JUL-2002) 1, D-85764 Neuberberg, GERMANY
COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by EMBL (European Molecular Biology Laboratories, Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project.
This clone (DKFZp666F188) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/cDNA/.
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 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.

REFERENCE	1	(bases 1 to 1076)
AUTHORS	Winterbottom,J.M., Shimp,L., Boyce,T.M. and Kaes,D.	
TITLE	Implant, method of making same and use of the implant for the treatment of bone defects	
JOURNAL	Patent: US 6478825-A 252 12-NOV-2002;	
FEATURES	Location/Qualifiers	
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Matches 1076; Conservative	0;	Mismatches 0; Indels 0; Gaps 0;

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Qy	65	CACCTCATCTATATCCTTGGCAGCTCACAGAGGTCAAGCAGCCTCTGAGCCGTGAAGA	124
Db	61	CACCTCATCTATATCCTTGGCAGCTCACAGAGGTCAAGCAGCCTCTGAGCCGTGAAGA	120
Qy	125	GCTGGTCGGTTCGGTGGTGGGGCCGTGACTTTCCTCCCTGAAGTCCAAAGTAAAGCACT	184
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Qy	185	TGACTCTATTGTCTGGAACCTTCAACAACAACCCCTCTTGTTCACCATACAGCCAGAGGGG	244
Db	181	TGACTCTATTGTCTGGAACCTTCAACAACAACCCCTCTTGTTCACCATACAGCCAGAGGGG	240
Qy	245	CACTATCATAGTGACCCCAAAATCGTAATAGGAGAGAGTGAAGTCCAGATGAGGCTA	304
Db	241	CACTATCATAGTGACCCCAAAATCGTAATAGGAGAGAGTGAAGTCCAGATGAGGCTA	300
Qy	305	CTCCCTGAAGCTCAGCAAACTGAAGAAGATGACTCAGGATCTACTATGTGGGATATA	364
Db	301	CTCCCTGAAGCTCAGCAAACTGAAGAAGATGACTCAGGATCTACTATGTGGGATATA	360
Qy	365	CAGCTCATCACTCCAGAGCCCTCCACCCAGAGTACGTGTCATGTCTACGAGCACTT	424
Db	361	CAGCTCATCACTCCAGAGCCCTCCACCCAGAGTACGTGTCATGTCTACGAGCACTT	420
Qy	425	GTCAAAGCCTAAAGTCAACCATGGGCTCTGAGAGCAATGAATGGCACTGTGTACCA	484
Db	421	GTCAAAGCCTAAAGTCAACCATGGGCTCTGAGAGCAATGAATGGCACTGTGTACCA	480
Qy	485	TCTGCATGTCTGCATGGAACATGGGGAAAGAGATGTGATTTATACCTGGAAGCCCTGGG	544
Db	481	TCTGCATGTCTGCATGGAACATGGGGAAAGAGATGTGATTTATACCTGGAAGCCCTGGG	540
Qy	545	GCAAGCAGCCAATGAGTCCCATTAATGGGTCCATCTCCCATCTCTGAGATGGGAGA	604
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Qy	605	AAGTATATGACCTTCATCTGCGTTGCCAGGAACCTGTCAAGCAAACTTCTCAAGCCC	664
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Qy	725	CCTGTGTCTCCTGTGTGGTGGCCCTCCTGCTCAAGTCTCTTTGTACTGGGGCTATTTCTTTG	784
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Qy	785	GTTTCTGAAGAGAGAGACAAGAAGATGACATTGAAGAAGAAGAGAGTGAACATTTG	844
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Db 901 TCACACTAATAGAACATCCTAAAGAGATCCAGCAATAACGTTTACTCCACTGTGA 960
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LOCUS AX092314 Sequence 45 from Patent WO0116318.
DEFINITION AX092314
ACCESSION AX092314 GI:13444471
VERSION AX092314.1
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 Eaton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and
Wood,W.I.
Secreted and transmembrane polypeptides and nucleic acids encoding
the same

JOURNAL

Patent: WO 0116318-A 45 08-MAR-2001;
Genentech, Inc. (US)

FEATURES

Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 39.8%; Score 1076; DB 6; Length 1076;
Best Local Similarity 100.0%; Pred. No. 2.3e-293;
Matches 1076; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGGCTTCAATTCAGTGGCTGACTTCAGAGAGCAATATGGCTGTTCCCAACATGCCT 64
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Db 61 CACCCTCATCTATATCTCTTTGGCAGCTCACAGGCTCAGCAGCCTCTGACCCCGTGAAGA 120
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Db 121 GCTGTCGGTCCGTTGGTGGGGCCGTGACTTTCCTCCCTGAAGTCCAAAGTAAGCAAGT 180
QY 185 TGAATCTATTTGTTGAGACCTTCAACACAAACCCCTTGTCAACCATACAGCCAGAAAGGGG 244
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QY 245 CACTATCATAGTGAACCAAAATCGTAATAGGAGAGATAGACTTCCCAAGTGAAGGCTA 304
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QY 365 CAGCTCATCACTCAGCAGACCCCTCCACCCAGAGATACGTGCTCATGTCTACGACACCT 424
Db 361 CAGCTCATCACTCAGCAGACCCCTCCACCCAGAGATACGTGCTCATGTCTACGACACCT 420

QY 425 GTCAAGCCTTAAGTCAACCATGGGTCTGACAGCAATAAGATGGCACTGTGTGACCAA 484
Db 421 GTCAAGCCTTAAGTCAACCATGGGTCTGACAGCAATAAGATGGCACTGTGTGACCAA 480
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QY 905 TCACACTAATAGAACATCCTTAAGAGAGATCCAGCAATAACGTTTACTCCACTGTGA 964
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Job time : 11356 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 28, 2004, 03:55:11 ; Search time 8248 Seconds
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Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_est2: *
3: gb_hic: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_g881: *
9: gb_g882: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	776.4	28.7	784	6	CD364928 UI-H-FT2-
3	761.2	28.2	785	6	CD366908 UI-H-FT2-
4	760	28.1	1035	4	BM549959 AGENCOURT
5	746.6	27.6	876	5	BU166292 AGENCOURT
6	734.2	27.2	846	4	BG743877 602722632
7	734.2	27.2	1043	5	BQ053807 AGENCOURT
8	733.8	27.1	767	6	CB529471 UI-H-FT2-
9	732.8	27.1	904	5	BQ712547 AGENCOURT
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11	728.8	27.0	738	6	CD364943 UI-H-FT2-
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13	722.2	26.7	920	4	BI767020 603054228
14	716.4	26.5	739	6	CD366944 UI-H-FT2-
15	707.6	26.2	731	6	CB986561 AGENCOURT
16	697.8	25.8	1050	4	BM800975 AGENCOURT
17	697.4	25.8	704	6	CB529490 UI-H-FT2-
18	683.4	25.3	702	7	CN480770 UI-H-FT2-
19	670.6	24.8	761	6	CD630759 56071680U
20	665.6	24.6	672	1	AW003948 wg84h01.x
21	647.4	23.9	712	6	CD366710 UI-H-FT2-
22	647	23.9	714	4	BG743853 602722605
23	642.4	23.8	705	5	BQ000581 UI-H-DP0-
24	632.6	23.4	980	2	BF026131 601669819

25	624.4	23.1	789	1	AV713600	AV713600
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27	613	22.7	630	2	BE044439	BE044439 ho45e03.x
28	607.8	22.5	657	2	AW026300	AW026300 wv11d02.x
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32	600.8	22.2	648	6	CD687842	CD687842 EST4363 h
33	596.2	22.0	602	1	AI638519	AI638519 ct08f02.x
34	591.4	21.9	594	1	AI422743	AI422743 cf29g12.x
35	589	21.8	593	2	BE326659	BE326659 hr62h10.x
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ALIGNMENTS

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DEFINITION AGENCOURT 6544759 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5548139
5', mRNA sequence.

ACCESSION BM551726
VERSION BM551726.1 GI:18788997
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12256 row: j column: 12
High quality sequence stop: 552.

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/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."

ORIGIN

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Best Local Similarity 96.4%; Pred. No. 4.6e-137;
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QY	2086	GGAGGCCAAGGTGGGTGGTTCATCTGAGGTCAAGAGTTCAAGACCAAGCCTGGCCAACATG	2145
Db	298	GGAGGCCAAGGTGGGTGGTTCATCTGAGGTCAAGAGTTCAAGACCAAGCCTGGCCAACATG	357
QY	2146	GTGAAACCCCATCTCTACTAAAGAT--CAAAATTTGCTGAGCGGTGGTGTGCACCTGT	2203
Db	358	GTGAAACCCCATCTCTACTAAAGATCAAAAATTTGCTGAGCGGTGGTGTGCACCTGT	417
QY	2204	-ATCCCACTACTCGAGAGGCCAAGGCATGAGAATCGCTTGAACCTGG--AGGTAGGTT	2260
Db	418	AATCCCACTACTCGAGAGGCCAAGGCATGAGAATCGCTTGAACCTGGAGGTGAGGTT	477
QY	2261	GCAGTGAAGTGAGATGGCACCACCTGCACTCCGGCTTAGGCAACGAGCAAAACTCCAAT	2320
Db	478	GCAGTGAAGTGAGATGGCACCACCTGCACTCCGGCTTAGGCAACGAGCAAAACTCCAAT	537
QY	2321	ACAAACAACAACAACACCTGTGTAGGTCACTGTGACGTAAGATGAACATCCCTA	2380
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RESULT 2
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LOCUS UI-H-FT2-bjn-g-19-0-UI.s1 NCI CGAP_FT2 Homo sapiens cDNA clone
DEFINITION UI-H-FT2-bjn-g-19-0-UI 3', mRNA sequence.
ACCESSION CD364928
VERSION CD364928.1 GI:31149018
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 784)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.iowa.edu/distribution/cgap.html>
Seq primer: M13 FORWARD
POLYA=yes.

FEATURES
source

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/clone_lib="NCI_CGAP_FT2"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
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NCI CGAP FT2 is a subcloned cDNA library constructed from
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The mRNA samples
were a mixture of these conditions (times refer to
incubations following isolation by bronchoalveolar lavage)
(some normal donor macrophages were cultured in some of
the conditions, other donor macrophages in different
conditions). The mRNA samples were pooled for library
construction. Control 0 hours; LPS 100 ng/ml; control 24
hours; LPS 100 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph
aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours;
Adenoviral vector (Ads CMV eGFP), moi 500, 3 hours;
Adenoviral vector (Ads CMV eGFP), moi 500, 24 hours; wt
adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24
hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours;
wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours.
The library was subcloned according to Bonaldo, Lennon
and Soares, Genome Research, 6:791-806, 1996. The tissue
was provided by Dr. Gary W. Hunninghake of the University
of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT2
TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match 28.7%; Score 776.4; DB 6; Length 784;
Best Local Similarity 99.7%; Pred. No. 1.7e-129;
Matches 777; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 3
CD366908/c 785 bp mRNA linear EST 05-AUG-2004
LOCUS
DEFINITION
UI-H-FT2-bjp-a-22-0-UI.s1 NCI_CGAP_FT2 Homo sapiens cDNA clone
UI-H-FT2-bjp-a-22-0-UI 3', mRNA sequence.
ACCESSION
CD366908
VERSION
CD366908.1 GI:31150998
KEYWORDS
EST.
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SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE
1 (bases 1 to 785)
AUTHORS
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html
Seq primer: M13 FORWARD
POLYA=Yes.
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FEATURES
Source
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/organism="Homo sapiens"
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/clone="UI-H-FT2-bjp-a-22-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP FT2"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: Ecor I; Site_2: Not I;
NCI CGAP FT2 is a subcloned cDNA library constructed from
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The mRNA samples
were a mixture of these conditions (times refer to
incubations following isolation by bronchoalveolar lavage)
(some normal donor macrophages were cultured in some of
the conditions, other donor macrophages in different
conditions). The mRNA samples were pooled for library
construction. Control 0 hours; control 3 hours; control 24
hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph
aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours;
Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours;
Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt
adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24
hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours;
wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours.
The library was subcloned according to Bonaldo, Lennon
and Soares, Genome Research, 6:791-806, 1996. The tissue
was provided by Dr. Gary W. Hunninghake of the University
of Iowa.
TAG_ISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT2
TAG_SEQ=GGCCATGCCG"
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Query Match 28.2%; Score 761.2; DB 6; Length 785;
Best Local Similarity 99.1%; Pred. No. 9.3e-127;
Matches 774; Conservative 0; Mismatches 6; Indels 1; Gaps 1;
OY 312 AAGCTCAGCAAACTGAAGAAGATGACTCAGGATCTACTATGTGGGATATACAGCTCA 371
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Db 785 AAGCTCAGCAAACTGAAGAAGATGACTCAGGATCTACTATGTGGGATATACAGCTCA 727
OY 372 TCACCTCAGCAGCCCTCCACCAGAGTACGTCTGCATGTCTACGAGCACCTGTCAAG 431
    |||||||
Db 726 TCACCTCAGCAGCCCTCCACCAGAGTACGTCTGCATGTCTACGAGCACCTGTCAAG 667
OY 432 CCTAAAGTACCAATGGGTCTGCAGAGCAATAAGATGGCACCTGTGTGACCAATCTGACA 491
    |||||||
Db 666 CCTAAAGTACCAATGGGTCTGCAGAGCAATAAGATGGCACCTGTGTGACCAATCTGACA 607
OY 492 TGCTGCATGGAATGGGGAAGAGATGTATTATACCTGGAAGGCCCTGGGCAAGCA 551
    |||||||
Db 606 TGCTGCATGGAATGGGGAAGAGATGTATTATACCTGGAAGGCCCTGGGCAAGCA 547
OY 552 GCCAATGATCCCATTAATGGGTCCATCTCCCATCTCTCTGAGATGGGGAAGAAAGTAT 611
    |||||||
Db 546 GCCAATGATCCCATTAATGGGTCCATCTCCCATCTCTCTGAGATGGGGAAGAAAGTAT 487
OY 612 ATGACCTTCATCTGCGTTGCCAGGAACCTGTCAAGAACTTCTCAAGCCCCCATCTT 671
    |||||||
Db 486 ATGACCTTCATCTGCGTTGCCAGGAACCTGTCAAGAACTTCTCAAGCCCCCATCTT 427
OY 672 GCCAGGAAGCTCTGTGAAGGTGCTGTGATGACCCAGATTCTCTCCATGCTCTCTGTGT 731
    |||||||
Db 426 GCCAGGAAGCTCTGTGAAGGTGCTGTGATGACCCAGATTCTCTCCATGCTCTCTGTGT 367
OY 732 CTCCTGTGTGCCCCCTCTGCTCAGTCTCTTGTACTGGGGCTATTCTTTGGTTCTG 791
    |||||||
Db 366 CTCCTGTGTGCCCCCTCTGCTCAGTCTCTTGTACTGGGGCTATTCTTTGGTTCTG 307
OY 792 AAGAGAGAGACAAGAGAGTACATTGAAGAAGAAGAGAGTGGACATTTGTGCGGAA 851
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Db 306 AAGAGAGAGACAAGAGAGTACATTGAAGAAGAAGAGAGTGGACATTTGTGCGGAA 247
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QY 852 ACTCCTAACATATGCCCCCATTTCTGGAGAGAACACAGAGTAGACACAATCCCTCACACT 911
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Db 246 ACTCCTAACATATGCCCCCATTTCTGGAGAGAACACAGAGTAGACACAATCCCTCACACT 187
QY 912 AATAGAACATCCTAAAGGAAGATCCAGCAATAACGGTTTACTCCACTGTGGAATACCG 971
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Db 186 AATAGAACATCCTAAAGGAAGATCCAGCAATAACGGTTTACTCCACTGTGGAATACCG 127
QY 972 AAAAAGATGAAAATCCCCCACTCACTGCTCAACGATGCCAGACACACCAAGGCTATTGGCC 1031
|
Db 126 AAAAAGATGAAAATCCCCCACTCACTGCTCAACGATGCCAGACACACCAAGGCTATTGGCC 67
QY 1032 TATGAGATGTTATCTAGACAGCAGTGCACTCCCTAAGTCTCTGCTCAAAAAAAAAACA 1091
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Db 66 TATGAGATGTTATCTAGACAGCAGTGCACTCCCTAAGTCTCTGCTCAAAAAAAAAACA 7
QY 1092 A 1092
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Db 6 A 6
RESULT 4
BM549959 1035 bp mRNA linear EST 20-FEB-2002
LOCUS
DEFINITION AGENCOURT_6544167 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5745910
5', mRNA sequence.
ACCESSION BM549959
VERSION BM549959.1 GI:18785781
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1035)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM12769 row: j column: 23
High quality sequence start: 12
High quality sequence stop: 663.
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source location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5745910"
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/clone_lib="NIH_MGC_118"
/note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
(destroyed); RNA source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
and directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
1.2-3.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 027. Note:
this is a NIH_MGC Library."
ORIGIN
Query Match 28.1%; Score 760; DB 4; Length 1035;
Best Local Similarity 99.2%; Pred. No. 1.4e-126;
Matches 774; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 39 AATATGGCTGTTCCCAACATGCTCCACCTCATATATCCTTTGGCAGCTCAGAGG 98
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Db 23 AATATGGCTGTTCTCCAACATGCTCCACCTCATATATCCTTTGGCAGCTCAGAGG 82
QY 99 TCAGCAGCCTCTGAGACCCGTGAAGAAGCTGTCGGTTCGGTTGGGGCCGTGACTTTC 158
|
Db 83 TCAGCAGCCTCTGAGACCCGTGAAGAAGCTGTCGGTTCGGTTGGGGCCGTGACTTTC 142
QY 159 CCCCTGAAGTCCAAAGTAAAGCAAGTTGACTCTATTTGCTGGAACCTTCAACACACACCCCT 218
|
Db 143 CCCCTGAAGTCCAAAGTAAAGCAAGTTGACTCTATTTGCTGGAACCTTCAACACACACCCCT 202
QY 219 CTGTGACCATACAGCCAGAGGGGGCACTATCATAGTGACCCAAATCGTAATAGGGAG 278
|
Db 203 CTGTGACCATACAGCCAGAGGGGGCACTATCATAGTGACCCAAATCGTAATAGGGAG 262
QY 279 AGAGTAGACTTCCAGATGAGGCTACTCCCTGAAGCTCAGCAAACTGAAGAAGATGAC 338
|
Db 263 AGAGTAGACTTCCAGATGAGGCTACTCCCTGAAGCTCAGCAAACTGAAGAAGATGAC 322
QY 339 TCAGGATCTACTATGTGGGATATACAGCTCATCTCCAGCAGCCCTCCACCCAGAG 398
|
Db 323 TCAGGATCTACTATGTGGGATATACAGCTCATCTCCAGCAGCCCTCCACCCAGAG 382
QY 399 TACGTGCTGCATGTCTACAGACACCTGTCAAAGCCTTAAAGTCACCATGGGTCTGCAGAGC 458
|
Db 383 TACGTGCTGCATGTCTACAGACACCTGTCAAAGCCTTAAAGTCACCATGGGTCTGCAGAGC 442
QY 459 AATAAGATGGCACCTGTGTGACCAATCTGACATGCTGCATGGAACATGGGGAAGAGAT 518
|
Db 443 AATAAGATGGCACCTGTGTGACCAATCTGACATGCTGCATGGAACATGGGGAAGAGAT 502
QY 519 GTGATTTATACCTGGAAGGCCCTGGGGCAAGCAGCCAAATGAGTCCCATATATGGTCCATC 578
|
Db 503 GTGATTTATACCTGGAAGGCCCTGGGGCAAGCAGCCAAATGAGTCCCATATATGGTCCATC 562
QY 579 CTCGCCATCTCTCGAGATGGGGAAGAAAGTATATGACCTTCATCTGCGTTGCCAGGAAC 638
|
Db 563 CTCGCCATCTCTCGAGATGGGGAAGAAAGTATATGACCTTCATCTGCGTTGCCAGGAAC 622
QY 639 CCTGTACAGCAAACTTCTCAAGCCCCCATCTTCCAGGAAGCTCTGTGAAGTGTGCT 698
|
Db 623 CCTGTACAGCAAACTTCTCAAGCCCCCATCTTCCAGGAAGCTCTGTGAAGTGTGCT 682
QY 699 GATGACCCAGATTCCTCCATGTCTCTCTGTCTCTGTTGGTGGCCCTCTCTGCTCAGT 758
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Db 683 GATGA-CCAGATTCTCCATGTCTCTCTGTCTCTGTTGGTGGCCCTCTCTGCTCAGT 741
QY 759 CTCTTTGTACTGGGGCTATTCTTTGTTTCTGAAGAGAGAGACAGAAAGTAGTACATT 818
|
Db 742 CTCTTTGTACTGGGGCTATTCTTTGTTTCTGAAGAGAGAGACAGAAAGTAGTACATT 801
RESULT 5
BU166292 876 bp mRNA linear EST 04-SEP-2002
LOCUS
DEFINITION AGENCOURT_7944604 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6148660
5', mRNA sequence.
ACCESSION BU166292
VERSION BU166292.1 GI:22680244
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 876)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1AM13480 row: h column: 05
High quality sequence stop: 724.
Location/Qualifiers

FEATURES
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6148660"
/issue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."

ORIGIN
Query Match 27.6%; Score 746.6; DB 5; Length 876;
Best Local Similarity 97.3%; Pred. No. 3.8e-124;
Matches 823; Conservative 0; Mismatches 15; Indels 8; Gaps 6;

OY 947 GGTTCCTCCACTGTGGAATATCCGAAAAAGATGAAATCCCACTCACTGTCACGAT 1006
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DB 1 GGTTCCTCCACTGTGGAATATCCGAAAAAGATGAAATCCCACTCACTGTCACGAT 60
OY 1007 GCCAGACACACCAAGGCTATTGCTATGAGATGTTATCTAGACAGAGTGCCTCCC 1066
|||||
DB 61 GCCAGACACACCAAGGCTATTGCTATGAGATGTTATCTAGACAGAGTGCCTCCC 120
OY 1067 TAAGTCTGCTCAAAAAAACAATCTCGGCCCAAGAAAAACAATCAGAGAATTCA 1126
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DB 121 TAAGTCTGCTC-AAAAAAAACAATCTCGGCCCAAGAAAAACAATCAGAGAATTCA 179
OY 1127 CTGATTGACTAGAAACATCAAGGAAGATGAAGACGTGACTTTTCCAGATAAAT 1186
|||||
DB 180 CTGATTGACTAGAAACATCAAGGAAGATGAAGACGTGACTTTTCCAGATAAAT 239
OY 1187 TATCTGTGATGCTTTAGATTAAAGAGTTGTAATTCATCCACTGCTGAGAAATCTC 1246
|||||
DB 240 TATCTGTGATGCTTTAGATTAAAGAGTTGTAATTCATCCACTGCTGAGAAATCTC 299
OY 1247 CTCAAACCCAGAAGGTTAATCACTTCATCCCAAAAAATGGGATTGTAATGTCAGCAAAAC 1306
|||||
DB 300 CTCAAACCCAGAAGGTTAATCACTTCATCCCAAAAAATGGGATTGTAATGTCAGCAAAAC 359
OY 1307 CATAAAAAAAGTGCTTAGAATATCTCTATAGAAATGTAATGCAAGGTCAACATATTA 1366
|||||
DB 360 CATAAAAAAAGTGCTTAGAATATCTCTATAGAAATGTAATGCAAGGTCAACATATTA 419
OY 1367 ATGACAGCGCTGTTGTAATTAATGATGGCTCCAGGTCACTGCTGAGATTTCATTCATCCC 1426
|||||
DB 420 ATGACAGCGCTGTTGTAATTAATGATGGCTCCAGGTCACTGCTGAGATTTCATTCATCCC 479
OY 1427 AGGCTTGATGTCAAGATTATACCAAGAGTCTTGCTACCAAGAGGGCAAGAACCAAA 1486
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DB 480 AGGCTTGATGTCAAGATTATACCAAGAGTCTTGCTACCAAGAGGGCAAGAACCAAA 539
OY 1487 ACAGACAGACAAGTCCAGACAAGACAGATGACCTGACCAAAAAATGATGATTAATTGGC 1546
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DB 540 ACAGACAGACAAGTCCAGACAAGACAGATGACCTGACCAAAAAATGATGATTAATTGGC 599
OY 1547 TCTATAACTATGTGCCAGCACTATGTGAGCTTACATAATTGGTCAGACGTGCTGTC 1606
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DB 600 TCTATAACTATGTGCCAGCACTATGTGAGCTTACATAATTGGTCAGACGTGCTGTC 659
OY 1607 TGCCCTCATGAATGGCTCCAATGAATGAATCTTCATGAGCAGTGTGACAGGCC 1666
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DB 660 TGCCCTCATGAATTTGGCTCCAAATGAATGAATCTTTCATGAGCAGTTGTAGCAGGCC 719
OY 1667 TGACCACAGATTTCCAGAGGG--CCAGGTGGATCCACAGG--ACTTGAAGTCAAAAGT 1722
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DB 720 TGACCACAGATTTCCAGAGGGGCCAGGTGGATCCACAGGACTTGNAAGTCAAAAGT 779
OY 1723 TCACAAAGATG-AAGATCAGGGTAG-CTGACCAT-GTTGGCAGATATAATGAGAGA 1779
|||||
DB 780 TCACAAAGATGAAGAATCAGGGTAGNCTGACCATGTTTGGCAGATATAATGAGGGA 839
OY 1780 CACAGA 1785
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DB 840 GACACA 845

RESULT 6
BG743877
LOCUS
DEFINITION BG743877 846 bp mRNA linear EST 15-MAY-2001
602722632F1 NIH_MGC_106 Homo sapiens CDNA clone IMAGE:4849374 5',
mRNA sequence.
ACCESSION BG743877
VERSION BG743877
KEYWORDS BG743877.1 GI:14054530
SOURCE EST.
ORGANISM Homo sapiens (human)
Homo sapiens
Bukaryota; Euteleostomi;
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
TITLE NIH-MGC (bases 1 to 846)
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1CM1688 row: 0 column: 07
High quality sequence stop: 782.
Location/Qualifiers

FEATURES

Source

1. .846
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4849374"
/issue_type="natural killer cells, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_106"
/note="Organ: blood; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; CDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN

Query Match 27.2%; Score 734.2; DB 4; Length 846;
Best Local Similarity 93.5%; Pred. No. 6.5e-122;
Matches 788; Conservative 0; Mismatches 53; Indels 2; Gaps 2;
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DB 2 CAAGAAGAACTATCTTAAAGGAAGATCCAGCAATACGTTTACTCACTGTGAAAT 61
OY 968 ACCGAAAAAGATGAAAAATCCCACTGCTCAGCATGCCAGACACCAAGGCTATT 1027
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DB 62 ACCGAAAAAGATGAAAAATCCCACTGCTCAGCATGCCAGACACCAAGGCTATT 121
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QY	1028	TGCTATGAGAA	TGTATCTAGACAGCAGTCACTCCCTAAGTCTCTGCTCAAAAAA	1087
Db	122	TGCTATGAGAA	TGTATCTAGACAGCAGTCACTCCCTAAGTCTCTGCTCAAAAAA	181
QY	1088	AACAATTC	TGCGCCCAAGAAAACAATCAGAAAGAAATTCAGTGAATTCAGAAACATCA	1147
Db	182	AACAATTC	TGCGCCCAAGAAAACAATCAGAAAGAAATTCAGTGAATTCAGAAACATCA	241
QY	1148	AGGAAGATGAGA	ACGTTGACTTTTCCAGGATAAATTATCTGTGATGCTTCTTAGA	1207
Db	242	AGGAAGATGAGA	ACGTTGACTTTTCCAGGATAAATTATCTGTGATGCTTCTTAGA	301
QY	1208	TTTAAGAGTT	CGTAATTCATCCACTGCTGAGAAATCTCCTCAAAACCAGAGTTTAAT	1267
Db	302	TTTAAGAGTT	CGTAATTCATCCACTGCTGAGAAATCTCCTCAAAACCAGAGTTTAAT	361
QY	1268	CACATTCATCC	CAAAAAATGGGATGTGTAATGTCAACCAACCATTAATAAAGTCTTAGAAG	1327
Db	362	CACATTCATCC	CAAAAAATGGGATGTGTAATGTCAACCAACCATTAATAAAGTCTTAGAAG	421
QY	1328	TATTCCTATAGA	AAATGTTAAATGCAAGGTCAACATATTAATGACAGCTGTGTATTAAAT	1387
Db	422	TATTCCTATAGA	AAATGTTAAATGCAAGGTCAACATATTAATGACAGCTGTGTATTAAAT	481
QY	1388	GATGGCTC	CAGGTCAGTGTCTGAGTTTCATTCATCCAGGGCTTGATGTCAGGATTA	1447
Db	482	GATGGCTC	CAGGTCAGTGTCTGAGTTTCATTCATCCAGGGCTTGATGTCAGGATTA	541
QY	1448	TACCAAGAGT	CTTGCTACAGAGGGGCAAGAACCAAAACAGACAGCAAGTCCAGCAG	1507
Db	542	TACCAAGAGT	CTTGCTACAGAGGGGCAAGAACCAAAACAGACAGCAAGTCCAGCAG	601
QY	1508	AAGCAGATGCA	CCTGACAAAAATGGATGTAATTAATTGGCTCTATAAATATGTGCCAGC	1567
Db	602	AAGCAGATGCA	CCTGACAAAAATGGATGTAATTAATTGGCTCTATAAATATGTGCCAGC	660
QY	1568	ACTATGCT	GAGCTTAACACTAATTTGGTCACAGTGTCTGCTGCTCATGAATTTGGCTCC	1627
Db	661	ACTATGCT	GAGCTTAACACTAATTTGGTCACAGTGTCTGCTGCTCATGAATTTGGCTCC	720
QY	1628	AAATGAATGA	AACTACTTTTCATGAGCAGTTGTAGCAGGCTGACAGATTCAGAGGG	1687
Db	721	AAATGAATGA	AACTACTTTTCATGAGCAGTTGTGTAGCAGGCTGACAGATTCAGAGGG	779
QY	1688	CCAGGTG	TGATCCACAGACTTGAAGTCAAAAGTTCACAAAGATGAAGATCAGGCTAG	1747
Db	780	CCAGGTG	TGATCCACAGACTTGAAGGCAAAAGTCACAAGATGAAGATCAGGCTAGC	839
QY	1748	CTG	1750	
Db	840	ATG	842	
RESULT 7				
LOCUS	BQ053807	1043 bp	mRNA	linear EST 29-MAR-2002
DEFINITION	AGENCOURT_7027738 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5935701			
	5', mRNA sequence.			
ACCESSION	BQ053807			
VERSION	BQ053807.1	GI:19813147		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
AUTHORS	1 (bases 1 to 1043)			
TITLE	NIH-MGC http://mgc.nci.nih.gov/.			
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)			
COMMENT	Unpublished (1999)			
	Contact: Robert Strausberg, Ph.D.			
	Email: cga@bbs-r@mail.nih.gov			
	Tissue Procurement: Dr. Daniel McVicar, DBS/NCI			
	cDNA Library Preparation: Rubin Laboratory			

cdna library Arrayed by: The I.M.A.G.E. Consortium (LNL)									
DNA Sequencing by: Agencourt Bioscience Corporation									
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov									
Plate: LNCM2123 row: n column: 22									
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source									
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/note="Organ: blood; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dr priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."									
ORIGIN									
Query Match 27.2%; Score 734.2; DB 5; Length 1043;									
Best Local Similarity 98.2%; Pred. No. 6.3e-122;									
Matches 753; Conservative 0; Mismatches 13; Indels 1; Gaps 1;									
QY	368	CTCATCACTCCAGAGCCCTCCACCCAGAGTAGCTGCTGATGCTTACGAGCACCCTGTC	427						
Db	1	CTCATCACTCCAGAGCCCTCCACCCAGAGTAGCTGCTGATGCTTACGAGCACCCTGTC	60						
QY	428	AAAGCCTAAAGTCACCATGGGCTGTCAGAGCAATAAGATGGCACCTGTGTACCAATCT	487						
Db	61	AAAGCCTAAAGTCACCATGGGCTGTCAGAGCAATAAGATGGCACCTGTGTACCAATCT	120						
QY	488	GACATGCTGCATGGAACATGGGGAAGAGATGTGATTATACCTGGAAGGCCCTGGGCA	547						
Db	121	GACATGCTGCATGGAACATGGGGAAGAGATGTGATTATACCTGGAAGGCCCTGGGCA	180						
QY	548	AGCAGCCAATGAGTCCCATATATGGGTCCATCTCCCATCTCTGAGATGGGGAAGAAAG	607						
Db	181	AGCAGCCAATGAGTCCCATATATGGGTCCATCTCCCATCTCTGAGATGGGGAAGAAAG	240						
QY	608	TGATATGACCTTCATCTGCGTTGCCAGGAACCTGTGACAGAAACTTCTCAAGCCCCAT	667						
Db	241	TGATATGACCTTCATCTGCGTTGCCAGGAACCTGTGACAGAAACTTCTCAAGCCCCAT	300						
QY	668	CCTTGCCAGGAAGCTCTGTGAAGTGTCTGATGACCCAGATTCTTCATGCTCTCCT	727						
Db	301	CCTTGCCAGGAAGCTCTGTGAAGTGTCTGATGACCCAGATTCTTCATGCTCTCCT	360						
QY	728	GTTGTTCTCTGTTGGTGCCCCCTCTGCTCAGTCTCTTTGTACTGGGGCTATTCTTTGGTT	787						
Db	361	GTTGTTCTCTGTTGGTGCCCCCTCTGCTCAGTCTCTTTGTACTGGGGCTATTCTTTGGTT	420						
QY	788	TCTGAAGAGAGAGACAAGAGAGATACATTGAAGAGAAGAGAGATGGACATTTGTGCG	847						
Db	421	TCTGAAGAGAGAGACAAGAGAGATACATTGAAGAGAAGAGAGATGGACATTTGTGCG	480						
QY	848	GGAACCTCCTTAACATATGCCCCCATTTCTGAGAGAACACAGATGACACAATCCCTCA	907						
Db	481	GGAACCTCCTTAACATATGCCCCCATTTCTGAGAGAACACAGATGACACAATCCCTCA	540						
QY	908	CACATAATAGAACATCTTAAGAGAGATCCAGCAATACGGTTTACTCCACTGTGGAAT	967						
Db	541	CACATAATAGAACATCTTAAGAGAGATCCAGCAATACGGTTTACTCCACTGTGGAAT	600						
QY	968	ACCGAAAAAGATGGAATATCCCACTCACTGCTCAGATGCCAGACACCAAGGCTATT	1027						
Db	601	ACCGAAAAAGATGGAATATCCCACTCACTGCTCAGATGCCAGACACCAAGGCTATT	660						

QY 1028 TGCCATGAGATGTTATCTAGACAGCAGTGCACCTCCCTAAGTCTCTGCTCAAAAAA 1087
|||||
Db 661 TGCCTATGACAATGTATCTAAACCGCAGTGCACCTCCCTAAGTCTCTGCTCAAAAAA 720
QY 1088 AACAAATCTCGG-CCCAAGAAACAATCAGAAGATTCTACTGATT 1133
|||||
Db 721 AACCAATCTCGGCCCCCAGAAACCAATTCGAGCAATTCCTGATT 767
RESULT 8
CB529471/c 767 bp mRNA linear EST 05-AUG-2004
LOCUS UI-H-FT2-bjh-m-17-0-UI.s1 NCI CGAP_FT2 Homo sapiens cDNA clone
DEFINITION UI-H-FT2-bjh-m-17-0-UI 3', mRNA sequence.
ACCESSION CB529471
VERSION CB529471.1 GI:29390191
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS 1 (bases 1 to 767)
TITLE NCI-CGAP National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rc@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/cgap.html>
Seq primer: M13 FORWARD
POLYA=Yes.
FEATURES
source
1. 767
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT2-bjh-m-17-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_1lb="NCI-CGAP_FT2"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI-CGAP_FT2 is a subcloned cDNA library constructed from
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The mRNA samples
were a mixture of these conditions (times refer to
incubations following isolation by bronchoalveolar lavage)
(some normal donor macrophages were cultured in some of
the conditions, other donor macrophages in different
conditions). The mRNA samples were pooled for library
construction. Control 0 hours; control 3 hours; control 24
hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph
aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours;
Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours;
Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt
adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24
hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours;
wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours.
The library was subcloned according to Bonaldo, Lennon
and Soares, Genome Research, 6:791-806, 1996. The tissue
was provided by Dr. Gary W. Hunninghake of the University
of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT2

ORIGIN TAG_SEQ=GGCCATGCCG"
Query Match 27.1%; Score 733.8; DB 6; Length 767;
Best Local Similarity 99.2%; Pred. No. 7.9e-122;
Matches 757; Conservative 0; Mismatches 4; Indels 2; Gaps 2;
QY 331 AGAATGACTCAGGATCTACTATGTGGGATATACAGCTCATCTCAGCAGCCCTCCA 390
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Db 767 AGGATGACTCAGGATCTACTATGT-GGGATATACAGNTCATCTCAGCAGCCCTCCA 709
QY 391 C-CCAGAGTAGTGTCTGTCATGTCTACGACACCTGTCAAAAGCCTAAAGTCAACCATGGGT 449
|||||
Db 708 CMCAGAGTAGTGTCTGTCATGTCTACGACACCTGTCAAAAGCCTAAAGTCAACCATGGGT 649
QY 450 CTGCAGAGCAATAAGATGGCACCTGTGTACCAATCTGCATGCTGCATGGAACATGGG 509
|||||
Db 648 CTGCAGAGCAATAAGATGGCACCTGTGTACCAATCTGCATGCTGCATGGAACATGGG 589
QY 510 GAAGAGATGTGATTTATACCTGGAAGGCCCTGGGGCAAGCAGCCCAATGAGTCCCATAT 569
|||||
Db 588 GAAGAGATGTGATTTATACCTGGAAGGCCCTGGGGCAAGCAGCCCAATGAGTCCCATAT 529
QY 570 GGGTCCATCTCCCATCTCTCTGAGATGGGAGAAAGTATATGACTTCTATCTGCGTT 629
|||||
Db 528 GGGTCCATCTCCCATCTCTCTGAGATGGGAGAAAGTATATGACTTCTATCTGCGTT 469
QY 630 GCCAGAACCTGTACAGAGAACTTCTCAAGCCCATCTTCCAGAGACTCTGTGAA 689
|||||
Db 468 GCCAGAACCTGTACAGAGAACTTCTCAAGCCCATCTTCCAGAGACTCTGTGAA 409
QY 690 GGTGCTGTGATGACCCAGATTCCTCAATGTCCTCTGTCTCTGTTGGTGCCCTC 749
|||||
Db 408 GGTGCTGTGATGACCCAGATTCCTCAATGTCCTCTGTCTCTGTTGGTGCCCTC 349
QY 750 CTGCTCAGTCTTTTGTACTGCGGCTATTCTTTGTTCTGAAGAGAGAGACAAGAA 809
|||||
Db 348 CTGCTCAGTCTTTTGTACTGCGGCTATTCTTTGTTCTGAAGAGAGAGACAAGAA 289
QY 810 GAGTACATTGAAGAGAAAGAGAGAGATTTGTGCGGAACTCTTAACATATGCCCC 869
|||||
Db 288 GAGTACATTGAAGAGAAAGAGAGATTTGTGCGGAACTCTTAACATATGCCCC 229
QY 870 CATTCTGAGAGAACACAGAGTAGACACAATCCCTCACACTAATAGAACATCCTAAG 929
|||||
Db 228 CATTCTGAGAGAACACAGAGTAGACACAATCCCTCACACTAATAGAACATCCTAAG 169
QY 930 GAAGATCCAGCAATACGTTTACTCTCACTGTGGAATACCGAAGAAATGCC 989
|||||
Db 168 GAAGATCCAGCAATACGTTTACTCTCACTGTGGAATACCGAAGAAATGCC 109
QY 990 CACTCAGTCTCAGATGCCAGACACACCAAGGCTATTGCTTATGAGATGTATCTAG 1049
|||||
Db 108 CACTCAGTCTCAGATGCCAGACACACCAAGGCTATTGCTTATGAGATGTATCTAG 49
QY 1050 ACAGCAGTGCATCCCTAAGTCTTGTCTCAAAAAAACA 1092
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Db 48 ACAGCAGTGCATCCCTAAGTCTTGTCTCAAAAAAACA 6
RESULT 9
BQ712547 904 bp mRNA linear EST 16-JUL-2002
LOCUS BQ712547
DEFINITION AGENCOURT_8501546 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6303158
5', mRNA sequence.
ACCESSION BQ712547
VERSION BQ712547.1 GI:21851446
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 904)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
Plate: L1CM2521 row: m column: 15
High quality sequence stop: 637.

FEATURES
source 1. .904
Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6303158"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_113"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN
Query Match 27.1%; Score 732.8; DB 5; Length 904;
Best Local Similarity 91.6%; Pred. No. 1.2e-121;
Matches 826; Conservative 0; Mismatches 32; Indels 44; Gaps 3;

OY 62 CCTCACCCCTCATCTATATCCTTGGCAGCTCACAGGGTCAAGCCTCTGGACCCGTGAA 121
DB 1 CCTCACCCCTCATCTATATCCTTGGCAGCTCACAGGGTCAAGCCTCTGGACCCGTGAA 60
OY 122 AGAGCTGGTCGGTCCGTTGGTGGGGCGGTGACTTCCCGCTGAAGTCCAAAGTAAAGCA 181
DB 61 AGAGCTGGTCGGTCCGTTGGTGGGGCGGTGACTTCCCGCTGAAGTCCAAAGTAAAGCA 120
OY 182 AGTTGACTTATGTGTGACCTTCAACAACCCCTCTTGTCAACATACAGCCAGAGG 241
DB 121 AGTTGACTTATGTGTGACCTTCAACAACCCCTCTTGTCAACATACAGCCAGAGG 180
OY 242 GGGCACTATCATAGTGAACCCAAATCGTATAGGAGAGAGTAGTCCAGATGAGG 301
DB 181 GGGCACTATCATAGTGAACCCAAATCGTATAGGAGAGAGTAGTCCAGATGAGG 240
OY 302 CTACTCCCTGAAGCTCAGCAAACTGAAGAATGACTCAGGGATCTAATGTGGGGAT 361
DB 241 CTACTCCCTGAAGCTCAGCAAACTGAAGAATGACTCAGGGATCTAATGTGGGGAT 300
OY 362 ATACAGCTCATCTCCAGCAGCCCTCCACAGAGTAGTGTGATGTCTACGAGCA 421
DB 301 ATACAGCTCATCTCCAGCAGCCCTCCACAGAGTAGTGTGATGTCTACGAGCA 360
OY 422 CCTGTCAAAGCCTAAAGTCAACCATGGGTGTGAGAGCAATAAGATGGCACTGTGTGAC 481
DB 361 CCTGTCAAAGCCTAAAGTCAACCATGGGTGTGAGAGCAATAAGATGGCACTGTGTGAC 420
OY 482 CAATGTGACATGCTGCATGGAACATGGGGAAGAGATGTGATTATACCTGGAAGGCCCT 541
DB 421 CAATGTGACATGCTGCATGGAACATGGGGAAGAGATGTGATTATACCTGGAAGGCCCT 480
OY 542 GGGGCAAGCAGCCATGAGTCCCATATAGGGTCCATCCCATCTCCTGGAGATGGG 601
DB 481 GGGGCAAGCAGCCATGAGTCCCATATAGGGTCCATCCCATCTCCTGGAGATGGG 540
OY 602 AGAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCTGTACAGAGAAACTTCTCAAG 661

DB 541 AGAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCCGTGACAGAAACTTCTCAAG 600
OY 662 CCCGATCCTTGGCAGGAAGCTGTGAAG----- 690
DB 601 CCCGATCCTTGGCAGGAAGCTGTGAAGGTGACTGCCCTCTCCCTCTCCACAGAGACT 660
OY 691 -----GTGCTGTGATGACCCAGATTCTCCATGGTCTCTCTGTCTCTGTTGGT 742
DB 661 CTGCCCCAGTGCTGTGATGACCCAGATTCTCCATGGCCCTCTGTGTCTCTGTTGGT 720
OY 743 GCGCCCTCTGCTCAGTCTCTTTGTACTGGGCTATTCTTTGGTTTCTGAAGAGAGAGAG 802
DB 721 GCGCCCTCTGCTCAGTCTCTTTGTACTGGGCTATTCTTTGGTTTCTGAAGAGAGAGAG 780
OY 803 ACAAGAAGAGTACATTGAAGAAGAAGAGAGTGCATTTGTGCGG-AAACTCTTAACA 861
DB 781 ACCAGAAGAGGTCTTGAAGAAAAAAGAAAGTGAAGTCTTTGTGCGGAAAACTCCAAAA 840
OY 862 TATGCCCCCATTTCTGAGAGAACACAGAGTA----CGACCAATCCCTCACACTAATAGA 917
DB 841 TATGCCCCCATTTCTGAGAGAACACCCGAGTAGACGACCCATCCCTCCCTTAATAAA 900
OY 918 AC 919
DB 901 AC 902

RESULT 10
LOCUS CD630761 793 bp mRNA linear EST 12-JAN-2004
DEFINITION 56071688J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD630761
VERSION CD630761.1 GI:40279027
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com

FEATURES
source 1. .793
Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"

ORIGIN
Query Match 27.1%; Score 731.8; DB 6; Length 793;
Best Local Similarity 98.7%; Pred. No. 1.8e-121;
Matches 769; Conservative 0; Mismatches 7; Indels 3; Gaps 3;

OY 741 GTGCCCTCCTGCTCAGTCTCTTGTACTGGGCTATTCTTGGTTCTGAAGAGAGAG 800
DB 11 GTGTCCTCCTGCTCAGTCTC-TTGTACTGGGCTATTTC-TTGGTTCTGAAGAGAGAG 68
OY 801 AGACAAGAAGAGTACATTGAAGAAGAAGAGAGTGCATTTGTGCGGAAACTCCTAAC 860
DB 69 AGACAAGAAGAGTACATTGAAGAAGAAGAGAGTGCATTTGTGCGGAAACTCCTAAC 128
OY 861 ATATGCCCCCATTTCTGAGAGAACACAGAGTACGACAAATCCCTCACACTAATAGACA 920
DB 129 ATATGCCCCCATTTCTGAGAGAACACAGAGTACGACAAATCCCTCACACTAATAGACA 188

QY	921	ATCCTAAAGGAAGATCCAGCAAAATACGGTTTACTCCACTGTGGAAATATCCGAAAAAGATG	980
Db	189	ATCCTAAAGGAAGATCCAGCAAAATACGGTTTACTCCACTGTGGAAATATCCGAAAAAGATG	248
QY	981	GAATAATCCCACTCACTGCTCAGATGCCAGACACACCAAGGCTATTGGCTATGAGAAAT	1040
Db	249	GAATAATCCCACTCACTGCTCAGATGCCAGACACACCAAGGCTATTGGCTATGAGAAAT	308
QY	1041	GTTATCTAGACAGCAGTGCATCCCCCTAAGTCTCTGCTCAAAAAAAAAACAATTCTCGGC	1100
Db	309	GTTATCTAGACAGCAGTGCATCCCCCTAAGTCTCTGCTC-AAAAAAAAACAATTCTCGGC	367
QY	1101	CCAAAGAAAACAATCAGAAAGATTCACTGATTTGACTAGAAACATCAAGGAAGATGAAG	1160
Db	368	CCAAAGAAAACAATCAGAAAGATTCACTGATTTGACTAGAAACATCAAGGAAGATGAAG	427
QY	1161	AACGTGACTTTTTCAGAGTAAATTATCTCTGATGCTTCTTTAGATTTAAGATTCGT	1220
Db	428	AACGTGACTTTTTCAGAGTAAATTATCTCTGATGCTTCTTTAGATTTAAGATTCAT	487
QY	1221	AATTCATCCACTGCTGAGAAATCTCCTCAAAACCCAGAGGTTTATCACTTCATCCCA	1280
Db	488	AATTCATCCACTGCTGAGAAATCTCCTCAAAACCCAGAGGTTTATCACTTCATCCCA	547
QY	1281	AAATGGGATTGTGAATGTCAACAACCATMAAAAAAGTGCTTAGAAGTATTCCTATAGAA	1340
Db	548	AAATGGGATCGTGAATGTCAACAACCATMAAAAAAGTGCTTAGAAGTATTCCTATAGAA	607
QY	1341	ATGTAATGCAAGGTCAACATATTAATGACAGCCTGTGTATTAATGATGGCTCAGGT	1400
Db	608	ATGTAATGCAAGGTCAACATATTAATGACAGCCTGTGTATTAATGATGGCTCAGGT	667
QY	1401	CAGTGTCTGAGTTTCATTCATCCACAGGCTTGATGTCAAGATTATACCAAGAGTCTT	1460
Db	668	CAGTGTCTGAGTTTCATTCATCCACAGGCTTGATGTCAAGATTATACCAAGAGTCTT	727
QY	1461	GCTAACGAGAGGGCAAGAAAGCCAAAAACAGACAGACAAAGTCCAGCAGAGCAGATGCAC	1519
Db	728	GCTAACGAGAGGGCAAGAAAGCCAAAAACAGACAGACAAAGTCCAGCAGAGCAGATGCAC	786

RESULT 11	CD364943/c	LOCUS	CD364943	738 bp	mRNA	linear	EST 05-AUG-2004
DEFINITION	UI-H-FT2-bjn-k-01-0-UI.61		NCI CGAP_F12 Homo sapiens				CDNA clone
	UI-H-FT2-bjn-k-01-0-UI 3'		mRNA sequence.				

ACCESSION	CD364943	GI:31149033
VERSION	CD364943.1	
KEYWORDS	EST.	

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

REFERENCE
1 (bases 1 to 738)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 738)	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

**Tumor Gene Index
Unpublished (1997)**

COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/cgap.html>
 Seq primer: M13 FORWARD
 POLYA=Yes.

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  source      Location/Qualifiers
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/organism="Homo sapiens"
/mol type="mrna"
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/db_xref="taxon:9606"
 /clone="UI-H-FT2-bjn-k-01-0-UI"
 /tissue_type="Alveolar Macrophage"
 /dev_stage="Adult"
 /lab_host="DPH10B (Life Technologies)"
 /clone_11b="NCI_CGAP_FT2"
 /note="Organ: Lung; Vector: pRTT3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI_CGAP_FT2 is a subtracted cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; Adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG_TISSUE=Human Lung Alveolar Macrophage
 TAG_LIB=UI-H-FT2
 TAG_SEQ=GGCCCATGCCG"

ORIGIN

Query Match	27.0%	Score 728.8;	DB 6;	Length 738;
Best Local Similarity	99.6%	Pred. No. 6.3e-121;		
Matches 730; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

[illegible][illegible]

Qy 480 ACCAATCTGACATGCTGCATGGAACATGGGAGAGGATGTGATTTATACCTGGAAGGCC 539
|||||
618 ACCAATCTGACATTTCTGCATGGAACATGGGAGAGGATGTGATTTATACCTGGAAGGCC 559

QY	540 CTGGGCGAAGCAGCCCAATGAATGCCATAATGGGTCCATCTTCCCATTCTCTGGAGATGG	599
Db	558 CTGGGCGAAGCAGCCCAATGAATGCCATAATGGGTCCATCTTCCCATTCTCTGGAGATGG	499

Oy	600	GGAGAAAGTGATATGACCTTCATCTGCCTTCCAGGAACCCTGTCA	GAGAAAATTCTCA	659
Db	498	GGAGAAAGTGATATGACCTTCATCTGCCTTCCAGGAACCCTGTCA	GAGAAAATTCTCA	439

QY	660	AGCCCCATCCTTGCCAGGAAGCTCTGTGAAGTGCTGCTGATGACCCAGATTCTCCATG	719
Db	438	AGCCCCATCCTTGCCAGGAAGCTCTGTGAAGTGCTGCTGATGACCCAGATTCTCCATG	379

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Oy      720  GTCTCCTGTGTCTCTCCTGTGTGGATGCCCCCTCCGTCAAGTCTCTTTGTACTGGGGCTATTT  779
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Db      378  GTCTCCTGTGTCTCTCCTGTGTGGATGCCCCCTCCGTCAAGTCTCTTTGTACTGGGGCTATTT  319

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Oy      780 CTTTGGTTCTGAAGAGAGAGACAAGAAGATACATTGAAAGAAGAAGAGAGTGAC   839
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Db      318 CTTTGGTTCTGAAGAGAGAGACAAGAAGATACATTGAAGACAAGAAGAGAGTGAC   259
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oy 840 ATTTGTCGGAACTCCTAACATATGCCCATTTCTGAGAGAACACAGAGTAGACACA 899

Db

258

ATTGTGGGAAACTCCTACATATGCCCCATTTCTGGAGAGAAACACAGATACGACACA

199

Qy

900

ATCCCTCAGACTAATAGACAATCTCTAAAGAGATCCAGCAATACGGTTTACTCCACT

959

Db

198

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139

Qy

960

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1019

Db

138

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79

Qy

1020

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1079

Db

78

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19

Qy

1080

AAAAAAAAAAACAA

1092

Db

18

AAAAAAAAAAAAA

6

RESULT 12

CD366342/c

749 bp mRNA linear EST 05-AUG-2004

LOCUS

CD366342

UI-H-FT1-bjt-g-24-0-UI.s1 NCI CGAP_FTI Homo sapiens cDNA clone

DEFINITION

UI-H-FT1-bjt-g-24-0-UI 3', mRNA sequence.

ACCESSION

CD366342

VERSION

CD366342.1 GI:31150432

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 749)

AUTHORS

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL

Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at <http://genome.uiowa.edu/distribution/cgap.html>
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES

source

location/Qualifiers

1..749

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

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/tissue_type="Alveolar Macrophage"

/dev_stage="Adult"

/lab_host="DH10B (Life Technologies)"

/clone_lib="NCI CGAP_FTI"

/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI_CGAP_FTI is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500,

3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag (dT)18 tail. The sequence tag for this library is GCCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG_TISSUE=Human Lung Alveolar Macrophage

TAG_LIB=UI-H-FT1

TAG_SEQ=GCCCATGCCG"

ORIGIN

Query Match

27.0%; Score 728.8; DB 6; Length 749;

Best Local Similarity 99.7%; Pred. No. 6.3e-121;

Matches 730; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy

1307

CATAAAAAAAGTGCTTAGAGTATTCCTATAGAAATGTAATGCAAGGTCACACATATTA

1366

Db

749

CATAAAAAAAGTGCTAGAGACTATTCCTATAGAAATGTAATGCAAGGTCACACATATTA

690

Qy

1367

ATGACAGCCTGTGTATTAATGATGGCTCCAGGTCAGTGTCTGGAGTTTCATTCCATCCC

1426

Db

689

ATGACAGCCTGTGTATTAATGATGGCTCCAGGTCAGTGTCTGGAGTTTCATTCCATCCC

630

Qy

1427

AGGCTTGATGTACAGATTATACCAAGAGTCTTGCTAACGAGGGCAAGACCAAA

1486

Db

629

AGGCTTGATGTACAGATTATACCAAGAGTCTTGCTAACGAGGGCAAGACCAAA

570

Qy

1487

ACAGACAGACAAGTCCAGCAGAAGCAGATGCACCTGACAAAATGATGATTAATTGGC

1546

Db

569

ACAGACAGACAAGTCCAGCAGAAGCAGATGCACCTGACAAAATGATGATTAATTGGC

510

Qy

1547

TCTATAACTATGTGCCCGACACTATGCTGAGCTTACACTAATTGGTCAGACGCTGTC

1606

Db

509

TCTATAACTATGTGCCCGACACTATGCTGAGCTTACACTAATTGGTCAGACGCTGTC

450

Qy

1607

TGCCCTCATGAATTGGTCCCAATGAATGAATGAATCTTTCATGAGCAGTTGTAGACGCC

1666

Db

449

TGCCCTCATGAATTGGTCCCAATGAATGAATGAATCTTTCATGAGCAGTTGTAGACGCC

390

Qy

1667

TGACCAAGATTTCCAGAGGGCCAGGTGTGATCCACAGGACTTGAAGGTCAAAGTTTAC

1726

Db

389

TGACCAAGATTTCCAGAGGGCCAGGTGTGATCCACAGGACTTGAAGGTCAAAGTTTAC

330

Qy

1727

AAAGATGAAGATCAGGGTAGCTGACCATGTTTGGCAGATACTATAATGAGACACAGAA

1786

Db

329

AAAGATGAAGATCAGGGTAGCTGACCATGTTTGGCAGATACTATAATGAGACACAGAA

270

Qy

1787

GTGTGATGGCCCAAGACAAGGACCTCCAGCCAGGCTCATTTATGACACTTGTGCA

1846

Db

269

GTGTGATGGCCCAAGACAAGGACCTCCAGCCAGGCTCATTTATGACACTTGTGCA

210

Qy

1847

AAAGAAAAGTCTAGGTTTAAAGGCTGTGCCAGAACCCATCCCAATAAAGAGACGAGTCT

1906

Db

209

AAAGAAAAGTCTAGGTTTAAAGGCTGTGCCAGAACCCATCCCAATAAAGAGACGAGTCT

150

Qy

1907

GAACTCATTGTAAATCTAGTGTAGAGACTTGGAGTCAAGGAGTGAAGTGGTGGGC

1966

Db

149

GAACTCATTGTAAATCTAGTGTAGAGACTTGGAGTCAAGGAGTGAAGTGGTGGGC

90

Qy

1967

ACGGGGGCGAGTGGTACTGTAAACCTTTAAAGTGGTTAATTCATTCAATAGATATT

2026

Db

89

ACGGGGGCGAGTGGTACTGTAAACCTTTAAAGTGGTTAATTCATTCAATAGATATT

30

Qy

2027

ATTAGAACCTA

2038

Db

2027

ATTAGAACCTA

2038

Db 29 ATTAAGAACCTA 18

RESULT 13
BI767020 920 bp mRNA linear EST 25-SEP-2001
DEFINITION 603054228F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5203638 5',
mRNA sequence.
ACCESSION BI767020
VERSION BI767020.1 GI:15758598
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: L1AM1510 row: h column: 07
High quality sequence stop: 743.
Location/Qualifiers
1. 920
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5203638"
/lab_host="DH10B"
/clone_lib="NIH_MGC_122"
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
Site 1: NotI; Site 2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dr
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 026. Note:
this is a NIH_MGC Library."

ORIGIN

Query Match 26.7%; Score 722.2; DB 4; Length 920;
Best Local Similarity 97.4%; Pred. No. 9.2e-120;
Matches 755; Conservative 0; Mismatches 18; Indels 2; Gaps 2;

QY 31 CAGAGAGCAATATGGCTGTTCCCAACATGCTCACCCCTCATATATCTTTGGCAGC 90
|||||
Db 1 CAGAGAGCAATATGGCTGTTCCCAACATGCTCACCCCTCATATATCTTTGGCAGC 60

QY 91 TCACAGGGTACAGCAGCCTCTGGACCCGTGAAGAAGCTGTCGGTCCGTTGGTGGGCCG 150
|||||
Db 61 TCACAGGGTACAGCAGCCTCTGGACCCGTGAAGAAGCTGTCGGTCCGTTGGTGGGCCG 120

QY 151 TGAATTTCCCTGTAAGTCCAAAGTAAAGCAAGTTGACTTATTGTCTGGAAGCTTCAACA 210
|||||
Db 121 TGAATTTCCCTGTAAGTCCAAAGTAAAGCAAGTTGACTTATTGTCTGGAAGCTTCAACA 180

QY 211 CAACCCCTCTTGTCAACATACAGCCAGAGGGGGGCACTATCATAGTGACCAAAATCGTA 270
|||||
Db 181 CAACCCCTCTTGTCAACATACAGCCAGAGGGGGGCACTATCATAGTGACCAAAATCGTA 240

QY 271 ATAGGAGAGAGTAGACTTCCAGATGAGGGCTACTCCCTGAAGCTCAGCAAACTGAAGA 330
|||||
Db 241 ATAGGAGAGAGTAGACTTCCAGATGAGGGCTACTCCCTGAAGCTCAGCAAACTGAAGA 300

QY 331 AGAATGACTCAGGATCTACTATGTGGGATATACAGCTCATCTACCTCCAGACCCCTCCA 390
|||||
Db 301 AGAATGACTCAGGATCTACTATGTGGGATATACAGCTCATCTACCTCCAGACCCCTCCA 360

QY 391 CCCAGAGTACGCTGTCATGTCTACGAGCAGCTGTCAAAAGCCTAAAGTCACCATGGGTC 450
|||||
Db 361 CCCAGAGTACGCTGTCATGTCTACGAGCAGCTGTCAAAAGCCTAAAGTCACCATGGGTC 420

QY 451 TGCAGAGCAATAGAATGGCAGCCTGTGTGACCAATCTGACATGCTGCAATGGAATGGGG 510
|||||
Db 421 TGCAGAGCAATAGAATGGCAGCCTGTGTGACCAATCTGACATGCTGCAATGGAATGGGG 480

QY 511 AAGAGATGTATTTATACCTGGAAGGCCCTGGGGCAAGCAGCAATGATGCCATATATG 570
|||||
Db 481 AAGAGATGTATTTATACCTGGAAGGCCCTGGGGCAAGCAGCAATGATGCCATATATG 540

QY 571 GGTCCATCTCCCATCTCTCTGAGATGGGGA-GAAAGTATATGACCTTCATCTGCGTT 629
|||||
Db 541 GGTCCATCTCCCATCTCTCTGAGATGGGGA-GAAAGTATATGACCTTCATCTGCGTT 600

QY 630 GCCAGGAACCTGTGTCAGCAGAACTTCTCAAGCCCCATCTTGCCAGAGACTCTGTGAA 689
|||||
Db 601 GCCAGGAACCTGTGTCAGCAGAACTTCTCAAGCCCCATCTTGCCAGAGACTCTGTGAA 660

QY 690 GGTGCTGTGATGACCCAGATTCCTCCATGCTCTCTGCTGTCTCTGTGCTGCTGCTC 749
|||||
Db 661 GGTGCTGTGATGACCCAGATTCCTCCATGCTCTCTGCTGTCTCTGTGCTGCTGCTC 720

QY 750 C-TGCTCAGTCTTTGTACTGGGGCTATTCTTTGTTTCTGAAGAGAGAGA 803
|||||
Db 721 CTGCTCAGTCTTTGTACTGGGGCTATTCTCTTGATTTCTGAAGAGAGAGA 775

RESULT 14
CD366944/c 739 bp mRNA linear EST 05-AUG-2004
LOCUS UI-H-FT2-bjp-1-06-0-UI.s1 NCI CGAP_FT2 Homo sapiens cDNA clone
DEFINITION UI-H-FT2-bjp-1-06-0-UI 3', mRNA sequence.
ACCESSION CD366944
VERSION CD366944.1 GI:31151034
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS 1 (bases 1 to 739)
TITLE NCI-CGAP National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html
Seq primer: M13 FORWARD
POLYA=yes.

FEATURES
source
1. 739
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT2-bjp-1-06-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP_FT2"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;

NCI_CGAP_FT2 is a subtracted cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was substracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT2
TAG_SEQ=GCCATGCCG"

ORIGIN

Query Match 26.5%; Score 716.4; DB 6; Length 739;
Best Local Similarity 99.2%; Pred. No. 1.1e-118;
Matches 728; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

OY	360	ATATACGCTCATCTACTCCAGCAGCCCTCCACCCA-GGAGTACGCTGCATGTCTACGA	418
DB	739	ATATACGCTCATCTACTCCAGCAGCCCTCCACCCAAGGAGTACGCTGCATGTCTACGA	680
OY	419	GCACCTGTCAAGCCTAAAGTCACCATGGGTCTGCAGAGCAATAGAATGGCACCTGTGT	478
DB	679	GCACCTGTCAAGCCTAAAGTCACCATGGGTCTGCAGAGCAATAGAATGGCACCTGTGT	620
OY	479	GACCAATGTGACATGCTGCATGGAACATGGGAAGAGATGATTTATACCTGGAAGGC	538
DB	619	GACCAATGTGACATGCTGCATGGAACATGGGAAGAGATGATTTATACCTGGAAGGC	560
OY	539	CCTGGGGCAAGCAGCCATGAGTCCCATTAATGGGTCCATCCTCCCATCTCCTGAGATG	598
DB	559	CCTGGGGCAAGCAGCCATGAGTCCCATTAATGGGTCCATCCTCCCATCTCCTGAGATG	500
OY	599	GGGAGAAAGTATATGACCTTCATCTGCGTTGCCAGGAACCCCTGTCAAGAACTTCTC	658
DB	499	GGGAGAAAGTATATGACCTTCATCTGCGTTGCCAGGAACCCCTGTCAAGAACTTCTC	440
OY	659	AAGCCCCATCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCAT	718
DB	439	AAGCCCCATCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCAT	380
OY	719	GGTCTCTGTGTCTCTGTTGGTGGCCCTCCTGCTCAGTCTCTTTGTACTGGGGCTATT	778
DB	379	GGTCTCTGTGTCTCTGTTGGTGGCCCTCCTGCTCAGTCTCTTTGTACTGGGGCTATT	320
OY	779	TCTTGGTTTCTGAAGAGAGAGACAAGAAGTACATTTGAAGAGAAGAAGAGTGA	838
DB	319	TCTTGGTTTCTGAAGAGAGAGACAAGAAGTACATTTGAAGAGAAGAAGAGTGA	260
OY	839	CATTGTGCGGAAAACCTCCTAACATATGCCCATTTCTGAGAGAACACAGAGTACGACAC	898
DB	259	CATTGTGCGGAAAACCTCCTAACATATGCCCATTTCTGAGAGAACACAGAGTACGACAC	200
OY	899	AATCCCTCACACTAATAGAACAACTCTAAAGGAAGATCCAGCAATAACGGTTTACTCCAC	958
DB	199	AATCCCTCACACTAATAGAACAACTCTAAAGGAAGATCCAGCAATAACGGTTTACTCCAC	140
OY	959	TGTGAAATATCCGAAAAGATGAAAATCCCACTCACTGCTCAGATGCCAGACACACC	1018

DB	139	TGTGAAATATACCGAAAAAGATGAAAATCCCACTCACTGCTCAGATGCCAGACACACC	80
OY	1019	AAGGCTATTGGCTTATGAGATGTTATCTAGACAGCAGTGCACTCCCTAAGTCTTGCT	1078
DB	79	AAGGCTATTGGCTTATGAGATGTTATCTAGACAGCAGTGCACTCCCTAAGTCTTGCT	20
OY	1079	CAAAAAAAAAAAACAA	1092
DB	19	CAAAAAAAAAAAAA	6

RESULT 15

CB986561
LOCUS
DEFINITION
AGENCOURT 13646958 NIH_MGC_184 Homo sapiens cDNA clone
IMAGE:30327727 5', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

NIH-MGC <http://mgc.nci.nih.gov/>.
1 (bases 1 to 731)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: NDCM137 row: d column: 08
High quality sequence stop: 599.

FEATURES
source

location/Qualifiers
1..731
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30327727"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_184"
/note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1: SfiI (ggccatratggcc); Site_2: SfiI (ggccgcctcgcc); Library is oligo-dT primed and directionally cloned. cDNA was prepared from a glandular pool of tissues from thyroid, parathyroid, adrenal, cortex and pineal gland. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-ATTCTAGAGCGCGGCGGCGGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.38 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 26.2%; Score 707.6; DB 6; Length 731;
Best Local Similarity 99.3%; Pred. No. 4.1e-117;
Matches 721; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

OY	14	TTTCAGTGGCTGACTTCCAGAGAGCAATATGGCTGTTCCCAACATGCTCACCCCTCAT	73
DB	6	TTTCAGTGGCTGACTTCCAGAGAGCAATATGGCTGTTCCCAACATGCTCACCCCTCAT	65
OY	74	CTATATCCTTTGGCAGCTCACAGGGTACAGAGCCTCTTGACCCCGTGAAGAGCTGTGG	133
DB	66	CTATATCCTTTGGCAGCTCACAGGGTACAGAGCCTCTTGACCCCGTGAAGAGCTGTGG	125

QY	134	TTCCGTTGGTGGGGCCGTGACTTTCCCTCCGTAAGTCCAAAGTAAAGCAAGTTGACTCTAT	193
Db	126	TTCCGTTGGTGGGGCCGTGACTTTCCCTCCGTAAGTCCAAAGTAAAGCAAGTTGACTCTAT	185
QY	194	TGCTGTGACCTTCAACACAAACCCTCTTGTCAACCATACAGCCAGAGGGGGCACTATCAT	253
Db	186	TGCTGTGACCTTCAACACAAACCCTCTTGTCAACCATACAGCCAGAGGGGGCACTATCAT	245
QY	254	AGTGACCCAAATCGTAATAGGAGAGAGTAGACTTCCAGATGAGGCTACTCCCTGAA	313
Db	246	AGTGACCCAAATCGTAATAGGAGAGAGTAGACTTCCAGATGAGGCTACTCCCTGAA	305
QY	314	GCTCAGCAAACTGAAGAAGATGACTCAGGGATCTACTATGTGGGATATACAGCTCATC	373
Db	306	GCTCAGCAAACTGAAGAAGATGACTCAGGGATCTACTATGTGGGATATACAGCTCATC	365
QY	374	ACTCCAGCAGCCCTCCACCAGAGAGTAGTGCTGCATGTCTACGAGCACCTGTCAAAGCC	433
Db	366	ACTCCAGCAGCCCTCCACCAGAGAGTAGTGCTGCATGTCTACGAGCACCTGTCAAAGCC	425
QY	434	TAAAGTCACCATGGGCTCTGCAGAGCAATAAGATGGCACCTGTGTGACCAATCTGACATG	493
Db	426	TAAAGTCACCATGGGCTCTGCAGAGCAATAAGATGGCACCTGTGTGACCAATCTGACATG	485
QY	494	CTGCATGGAACATGGGGAAGAGATGATTTATACCTGGAAGCCCTGGGGCAAGCAGC	553
Db	486	CTGCATGGAACATGGGGAAGAGATGATTTATACCTGGAAGCCCTGGGGCAAGCAGC	545
QY	554	CAATGAGTCCCATATATGGGTCATCTTCCCCCATCTCTCTGAGATGGGGAGAAAGTGATAT	613
Db	546	CAATGAGTCCCATATATGGGTCATCTTCCCCCATCTCTGAGATGGGGAGAAAGTGATAT	605
QY	614	GACCTTCATCTGCGTTGCCAGGAACCTGTCAAGCAAGAACTTCTCAAGCCCCATCTTGC	673
Db	606	GACCTTCATCTGCGTTGCCAGGAACCTGTCAAGCAAGAACTTCTCAAGCCCCATCTTGC	665
QY	674	CAGGAAGCTCTGTGAAGTGCTGTGATGACCAGATTCTCTCATGGT - CTTCTGTGTC	732
Db	666	CAGGAAGCTCTGTGGAAGTGCTGTGATGACCAGAAATTCTCCATGGTCTCCTCTGTGTC	725
QY	733	TCCTGT 738	
Db	726	TCCTGT 731	

Search completed: October 28, 2004, 10:16:56
Job time : 8258 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 28, 2004, 03:09:04 ; Search time 1275 Seconds
(without alignments)
11132.890 Million cell updates/sec

Title: US-09-745-605-1

Perfect score: 2704

Sequence: 1 ggaagtgcgttcatttcagt.....aaaaaaaaaaaaaaaa 2704

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04:*

1: geneseqn1980s:*

2: geneseqn1990s:*

3: geneseqn2000s:*

4: geneseqn2001as:*

5: geneseqn2001bs:*

6: geneseqn2002as:*

7: geneseqn2002bs:*

8: geneseqn2003as:*

9: geneseqn2003bs:*

10: geneseqn2003cs:*

11: geneseqn2003ds:*

12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2704	100.0	2704	5	AAC86114	Aac86114 APEX-1 CD
2	2617.2	96.8	2774	3	AAC55192	Aac55192 Human sec
3	2604.6	96.3	2672	10	ADD67524	Add67524 Human Lyl
4	2186.4	80.9	2780	3	AAC55223	Aac55223 Human sec
5	1728.8	63.9	3651	12	ADQ24216	Adq24216 Human sof
6	1369.4	50.6	1412	2	AAx00615	Aax00615 Human sec
7	1369.4	50.6	1412	3	AAC55224	Aac55224 Human sec
8	1369.4	50.6	1412	8	ADA40261	Ada40261 Human sec
9	1369.4	50.6	1412	10	ADA56425	Ada56425 Gene enco
10	1256.6	46.5	1272	3	AAZ51572	Aaz51572 Human cel
11	1082	40.0	1082	3	ACC72129	Acc72129 Human NOV
12	1076	39.8	1076	3	AAZ65040	Aaz65040 Membrane-
13	1076	39.8	1076	4	AAS46020	Aas46020 Human DNA
14	1076	39.8	1076	4	AAF92080	Aaf92080 Human PRO
15	1076	39.8	1076	5	AAF44186	Aaf44186 Human PRO
16	1076	39.8	1076	6	ABS74400	Abs74400 Human CDN
17	1076	39.8	1076	8	ACA89470	Aca89470 CDNA enco
18	1076	39.8	1076	8	ACA73480	Aca73480 Human sec
19	1076	39.8	1076	8	ACA05795	Aca05795 Human sec
20	1076	39.8	1076	8	ACA66629	Aca66629 CDNA enco
21	1076	39.8	1076	8	ACA64332	Aca64332 Novel hum

22	1076	39.8	1076	8	ACA91186	Aca91186 Novel hum
23	1076	39.8	1076	8	ACD81563	Acd81563 Human CDN
24	1076	39.8	1076	8	ACF20204	Acf20204 Human sec
25	1076	39.8	1076	8	ACF19590	Acf19590 Human sec
26	1076	39.8	1076	8	ACD21878	Acd21878 Human sec
27	1076	39.8	1076	8	ACF13043	Acf13043 Human sec
28	1076	39.8	1076	8	ACD25146	Acd25146 Human sec
29	1076	39.8	1076	8	ACF00195	Acf00195 Human sec
30	1076	39.8	1076	8	ACA60385	Aca60385 Novel hum
31	1076	39.8	1076	8	ACA72252	Aca72252 Novel hum
32	1076	39.8	1076	8	ACD04776	Acd04776 Novel hum
33	1076	39.8	1076	8	ACD18237	Acd18237 Human sec
34	1076	39.8	1076	8	ACD08244	Acd08244 Human sec
35	1076	39.8	1076	8	ACA88678	Aca88678 Novel hum
36	1076	39.8	1076	8	ACA70120	Aca70120 Human sec
37	1076	39.8	1076	8	ACD12342	Acd12342 Novel hum
38	1076	39.8	1076	8	ACC74257	Acc74257 Human sec
39	1076	39.8	1076	8	ACD15885	Acd15885 Human sec
40	1076	39.8	1076	8	ACD25453	Acd25453 Novel hum
41	1076	39.8	1076	8	ACD17930	Acd17930 Human sec
42	1076	39.8	1076	8	ACC88217	Acc88217 Human sec
43	1076	39.8	1076	8	ACD21571	Acd21571 Human sec
44	1076	39.8	1076	8	ACD18638	Acd18638 Human sec
45	1076	39.8	1076	8	ACA58832	Aca58832 CDNA enco

ALIGNMENTS

RESULT 1	
AAC86114	
ID	AAC86114 standard; CDNA; 2704 BP.
XX	
AC	AAC86114;
XX	
DT	29-AUG-2001 (first entry)
XX	
DE	APEX-1 CDNA.
XX	
KW	Antigen presenting cell expression protein; APEX-1; APEX-2; APEX-3; extracellular domain; immunoglobulin-like domain; Ig-like structure;
KW	N-glycosylation site; transmembrane domain; cytoplasmic domain;
KW	SH2-binding motif; aschma; arteriosclerosis; AIDS; cirrhosis;
KW	Crohn's disease; atopic dermatitis; autoimmune anaemia; bursitis;
KW	cholecystitis; diabetes mellitus; emphysema; atrophic gastritis;
KW	inflammatory bowel disease; multiple sclerosis; myasthenia gravis;
KW	myocardial inflammation; pericardial inflammation; osteoarthritis;
KW	osteoporosis; psoriasis; Reiter's syndrome; rheumatoid arthritis;
KW	inflammation; cancer; autoimmune disease; graft rejection;
KW	graft versus host disease; systemic lupus erythematosus; ss.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	42..1049
FT	/*tag= a
FT	/product= "APEX-1"
FT	sig_peptide
FT	42..107
FT	/*tag= b
FT	mat_peptide
FT	108..1046
FT	/*tag= c
XX	
PN	WO200146260-A2.
XX	
PD	28-JUN-2001.
XX	
PF	22-DEC-2000; 2000WO-US034963.
XX	
PR	23-DEC-1999; 99US-0172025P.
XX	
PA	(BRIM) BRISTOL-MYERS SQUIBB CO.
XX	
PI	Starling GC, Finger J;

XX WPI; 2001-418044/44.
DR P-PSDB; AAB47321.
XX
PT Novel Antigen presenting cell expression protein useful for treating
PT asthma, arteriosclerosis, autoimmune diseases, AIDS, cirrhosis, Crohn's
PT disease and atopic dermatitis.

XX Claim 2; Fig 2; 112pp; English.

XX
XX The sequences given in AAC86114-16 encode antigen presenting cell
CC expression (APEX)-1, APEX-2 and APEX-3 proteins. APEX-1 and APEX-2
CC comprise an extracellular domain having one immunoglobulin (Ig)-like
CC structure and N-glycosylation site, a transmembrane domain, and a
CC cytoplasmic domain having at least one SH2-binding motif. APEX proteins
CC and antibodies are useful in the study, diagnosis, prevention and
CC treatment of disease associated with the presence of an APEX protein
CC e.g., asthma, arteriosclerosis, AIDS, cirrhosis, Crohn's disease, atopic
CC dermatitis, autoimmune anaemia, bursitis, cholecystitis, diabetes
CC mellitus, emphysema, atrophic gastritis, inflammatory bowel disease,
CC multiple sclerosis, myasthenia gravis, myocardial or pericardial
CC inflammation, osteoarthritis, osteoporosis, psoriasis, Reiter's syndrome,
CC rheumatoid arthritis, inflammation, cancer, immune disorders, autoimmune
CC diseases, graft rejections, graft versus host reaction and systemic lupus
CC erythematosus. APEX proteins are useful as diagnostic and/or prognostic
CC markers on APCs or APEX expressing cells, the ability to elicit the
CC generation of antibodies and as targets for various therapeutic
CC modalities. APEX proteins are also useful for identifying and isolating
CC ligand that bind APEX
XX

SQ Sequence 2704 BP; 824 A; 618 C; 629 G; 633 T; 0 U; 0 Other;

Query Match 100.0%; Score 2704; DB 5; Length 2704;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2704; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGTGGCTTCATTTCAGTGGCTGACTTCCAGAGCAATATGGCTGTCCTCCCAACAT 60
Db 1 GGAAGTGGCTTCATTTCAGTGGCTGACTTCCAGAGCAATATGGCTGTCCTCCCAACAT 60
QY 61 GCCTCACCTCATCTATATCCTTTGGCAGCTCAGAGGTGAGCCTCTGACCCCTGA 120
Db 61 GCCTCACCTCATCTATATCCTTTGGCAGCTCAGAGGTGAGCCTCTGACCCCTGA 120
QY 121 AAGAGCTGGTCGGTTCGGTGGGGCGGTGACTTCCCCCTGAAGTCCAAAGTAAAGC 180
Db 121 AAGAGCTGGTCGGTTCGGTGGGGCGGTGACTTCCCCCTGAAGTCCAAAGTAAAGC 180
QY 181 AAGTGACTCTATTGTCTGGACCTTGAACAACACCCCTCTGTCAACATACAGCCAGAAG 240
Db 181 AAGTGACTCTATTGTCTGGACCTTGAACAACACCCCTCTGTCAACATACAGCCAGAAG 240
QY 241 GGGGCATCTATAGTGACCCCAAATCGTAATAGGGAGAGATGACTTCCAGATGAG 300
Db 241 GGGGCATCTATAGTGACCCCAAATCGTAATAGGGAGAGATGACTTCCAGATGAG 300
QY 301 GCTACTCCCTGAAGCTCAGCAAACCTGAAGAATGACTCAGGGATCTACTATGTGGGA 360
Db 301 GCTACTCCCTGAAGCTCAGCAAACCTGAAGAATGACTCAGGGATCTACTATGTGGGA 360
QY 361 TATACAGCTCATCTCCAGCAGCCCTCCACCAGAGATAGTGTGATGTCTACGAGC 420
Db 361 TATACAGCTCATCTCCAGCAGCCCTCCACCAGAGATAGTGTGATGTCTACGAGC 420
QY 421 ACCTGTCAAAGCCTTAAAGTCACCATGGGTCTGACAGCAATAAGATGGACCTGTGTA 480
Db 421 ACCTGTCAAAGCCTTAAAGTCACCATGGGTCTGACAGCAATAAGATGGACCTGTGTA 480
QY 481 CCAATCTGCATGCTGCATGGAACATGGGGAAGAGATGTGATTATACCTGGAAGGCC 540
Db 481 CCAATCTGCATGCTGCATGGAACATGGGGAAGAGATGTGATTATACCTGGAAGGCC 540
QY 541 TGGGGCAAGCAGCCAATGAGTCCCATATGGGTCCATCTCCCATCTCTGAGATGGG 600

Db 541 TGGGGCAAGCAGCCAATGAGTCCCATATGGGTCCATCTCCCATCTCTGAGATGGG 600
QY 601 GAGAAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCTGTACAGAAACTTCTCA 660
Db 601 GAGAAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCTGTACAGAAACTTCTCA 660
QY 661 GCCCCATCTTGCCAGGAAGCTCTGTGAAGGTGCTGTGATGACCCAGATTCCTCCATGG 720
Db 661 GCCCCATCTTGCCAGGAAGCTCTGTGAAGGTGCTGTGATGACCCAGATTCCTCCATGG 720
QY 721 TCCTCTGTGTCCTCTGTTGGTGGCCCTCCTGCTCAGTCTTGTGTAATGAGGCTATTTTC 780
Db 721 TCCTCTGTGTCCTCTGTTGGTGGCCCTCCTGCTCAGTCTTGTGTAATGAGGCTATTTTC 780
QY 781 TTTGGTTTCTGAAGAGAGACAAGAAGTACATTGAAGAAGAAGAGAGTGAACA 840
Db 781 TTTGGTTTCTGAAGAGAGACAAGAAGTACATTGAAGAAGAAGAGAGTGAACA 840
QY 841 TTTGTCGGGAAACTCCTAACAATATGCCCCCATTTCTGAGAGAACACAGATAGACACAA 900
Db 841 TTTGTCGGGAAACTCCTAACAATATGCCCCCATTTCTGAGAGAACACAGATAGACACAA 900
QY 901 TCCTTCACACTAATAGAACAAATCCTTAAAGGAAGATCCAGCAATACGGTTTACTCCACTG 960
Db 901 TCCTTCACACTAATAGAACAAATCCTTAAAGGAAGATCCAGCAATACGGTTTACTCCACTG 960
QY 961 TGGAAATACCGAAAAAGATGGAATAATCCCACTCAGTCTCAGATGCCAGACACACCAA 1020
Db 961 TGGAAATACCGAAAAAGATGGAATAATCCCACTCAGTCTCAGATGCCAGACACACCAA 1020
QY 1021 GGTATTGTCCTATGAGATGTTATCTAGACAGCAGTGCACTCCCTAAGTCTCTGCTCA 1080
Db 1021 GGTATTGTCCTATGAGATGTTATCTAGACAGCAGTGCACTCCCTAAGTCTCTGCTCA 1080
QY 1081 AAAAAAACAATTCCTGGCCCAAGAAAAACAATCAGAAATTCAGTATTGACTAGA 1140
Db 1081 AAAAAAACAATTCCTGGCCCAAGAAAAACAATCAGAAATTCAGTATTGACTAGA 1140
QY 1141 AACATCAAGGAAGAATGAGAACGTTGACTTTTTCAGAGTAATATCTGTAGTCTT 1200
Db 1141 AACATCAAGGAAGAATGAGAACGTTGACTTTTTCAGAGTAATATCTGTAGTCTT 1200
QY 1201 CTTTGAATTTAAGATTCGTAATTCATCCACTGCTGAGAAATCTCTCAAAACCCAGAAG 1260
Db 1201 CTTTGAATTTAAGATTCGTAATTCATCCACTGCTGAGAAATCTCTCAAAACCCAGAAG 1260
QY 1261 GTTTAATCACTTCAATCCCAAAATGGGATGTGAAATGTCAGCAAAACATAAAAAAGTGC 1320
Db 1261 GTTTAATCACTTCAATCCCAAAATGGGATGTGAAATGTCAGCAAAACATAAAAAAGTGC 1320
QY 1321 TTGAAAGTATTCCTATAGAAATGTAAATGCAAGGTCAACATATTAATGACAGCCTGTTG 1380
Db 1321 TTGAAAGTATTCCTATAGAAATGTAAATGCAAGGTCAACATATTAATGACAGCCTGTTG 1380
QY 1381 TATTAATGATGGCTCCAGGTCAGTGCTGAGATTTCATCCATCCAGGCTTGATGTC 1440
Db 1381 TATTAATGATGGCTCCAGGTCAGTGCTGAGATTTCATCCATCCAGGCTTGATGTC 1440
QY 1441 AGGATTATACCAAGAGTCTTGCTAACAGAGGGCAAGAACCAAAACAGACAGCAAGT 1500
Db 1441 AGGATTATACCAAGAGTCTTGCTAACAGAGGGCAAGAACCAAAACAGACAGCAAGT 1500
QY 1501 CCAAGCAAGCAGATGCACCTGACAAAAATGGATGTATTAATTGGCTCTATTAACATATGT 1560
Db 1501 CCAAGCAAGCAGATGCACCTGACAAAAATGGATGTATTAATTGGCTCTATTAACATATGT 1560
QY 1561 GCCCAGCACTATGCTGAGCTTACACTAATTTGTCAGACGTGCTGCCCCCATGAATAAT 1620
Db 1561 GCCCAGCACTATGCTGAGCTTACACTAATTTGTCAGACGTGCTGCCCCCATGAATAAT 1620
QY 1621 TGGCTCCAAATGAATGAATTAATTTCATGAGCAGTTGTAGCAGGCTGACCAAGATTCC 1680
Db 1621 TGGCTCCAAATGAATGAATTAATTTCATGAGCAGTTGTAGCAGGCTGACCAAGATTCC 1680

Db	1621	TGGCTCCAATGAATGAACCTTTCATGAGCAGTTGTAGCAGGCTGACCA	CAGATTCC	1680
QY	1681	CAGAGGGCCAGGTGTGATCCAGGACTTGAAGGTCAAAGTTC	CAAGATGAAGATC	1740
Db	1681	CAGAGGGCCAGGTGTGATCCAGGACTTGAAGGTCAAAGTTC	CAAGATGAAGATC	1740
QY	1741	AGGGTAGCTGACCATGTTGGCAGATACTATATATGAGACA	CAGAAGTGTGCATGGCCCA	1800
Db	1741	AGGGTAGCTGACCATGTTGGCAGATACTATATATGAGACA	CAGAAGTGTGCATGGCCCA	1800
QY	1801	AGGACAAGGACCTCCAGCCAGGCTTCATTATGCACTTGTCTG	CAAAAGAAAAGTCTAG	1860
Db	1801	AGGACAAGGACCTCCAGCCAGGCTTCATTATGCACTTGTCTG	CAAAAGAAAAGTCTAG	1860
QY	1861	GTTTAAAGGCTGTGCCAAGAACCCATCCCAATAAAGACCGA	GTCTGAAGTCACTTGTGA	1920
Db	1861	GTTTAAAGGCTGTGCCAAGAACCCATCCCAATAAAGACCGA	GTCTGAAGTCACTTGTGA	1920
QY	1921	AATCTAGTAGAGACTTGSAGTCAAGCAGTGAAGCTGTGGGCA	CGGGGGCAGTGG	1980
Db	1921	AATCTAGTAGAGACTTGSAGTCAAGCAGTGAAGCTGTGGGCA	CGGGGGCAGTGG	1980
QY	1981	GTACTTGTAAACCTTTAAAGATGTTAATTCATTCAATAGAT	ATTATTAAAGACTACT	2040
Db	1981	GTACTTGTAAACCTTTAAAGATGTTAATTCATTCAATAGAT	ATTATTAAAGACTACT	2040
QY	2041	ATGCGGGCCCGCATGTGGTCAACCTGTATCCCACTTTGGAGG	CCCAAGTGGG	2100
Db	2041	ATGCGGGCCCGCATGTGGTCAACCTGTATCCCACTTTGGAGG	CCCAAGTGGG	2100
QY	2101	TGGGTCACTGAGGTCAAGAGTCAAGACCAGCCCTGGCCAAC	ATGTTGAAAACCCATCTC	2160
Db	2101	TGGGTCACTGAGGTCAAGAGTCAAGACCAGCCCTGGCCAAC	ATGTTGAAAACCCATCTC	2160
QY	2161	TACTTAAAGATCAAAATTTGCTGAGCGTGTGTGTGCACTGT	ATCCAGCTACTCGAGA	2220
Db	2161	TACTTAAAGATCAAAATTTGCTGAGCGTGTGTGTGCACTGT	ATCCAGCTACTCGAGA	2220
QY	2221	GGCCAAGGCATGAGAATCGCTTGAACCTGAGGTGAGTTGCA	GTGAGCTGAGATGGCAC	2280
Db	2221	GGCCAAGGCATGAGAATCGCTTGAACCTGAGGTGAGTTGCA	GTGAGCTGAGATGGCAC	2280
QY	2281	CACTGCACCTCCGCGCTAGGCAACGAGCAAAACCTCCAATA	CAAAACAACAACACAC	2340
Db	2281	CACTGCACCTCCGCGCTAGGCAACGAGCAAAACCTCCAATA	CAAAACAACAACACAC	2340
QY	2341	CTGTGCTAGGTCACTGCGCAGTAAGATGAACATCCCTACCA	ACACAGAGCTCACCATC	2400
Db	2341	CTGTGCTAGGTCACTGCGCAGTAAGATGAACATCCCTACCA	ACACAGAGCTCACCATC	2400
QY	2401	TCTTACTTAAAGTGAAGAAACATGGGGAAGGGAATGGCTGT	TTTGATATGT	2460
Db	2401	TCTTACTTAAAGTGAAGAAACATGGGGAAGGGAATGGCTGT	TTTGATATGT	2460
QY	2461	TCCCTGACGCATATCTTGAATGGAAGCTCCCTACCAAGTGA	AAAGTGTGAAAAACT	2520
Db	2461	TCCCTGACGCATATCTTGAATGGAAGCTCCCTACCAAGTGA	AAAGTGTGAAAAACT	2520
QY	2521	TAATAACAATGCTTGTGGCAAGAATGGGATTTGAGATTATCT	TCTCTCAGAAAAAGCA	2580
Db	2521	TAATAACAATGCTTGTGGCAAGAATGGGATTTGAGATTATCT	TCTCTCAGAAAAAGCA	2580
QY	2581	TTGTGAAGGAATTGAGCCAGATCTCTCCCTACTGCAAAACC	TATTGTAGTAAAAAAG	2640
Db	2581	TTGTGAAGGAATTGAGCCAGATCTCTCCCTACTGCAAAACC	TATTGTAGTAAAAAAG	2640
QY	2641	TCTTCTTACTATCTTAATAAAACAGATATTGTGAGATTCA	CATAAAAAAGAAAAAA	2700
Db	2641	TCTTCTTACTATCTTAATAAAACAGATATTGTGAGATTCA	CATAAAAAAGAAAAAA	2700
QY	2701	AAAA	2704	
Db	2701	AAAA	2704	

RESULT 2	
AAC5192	
ID AAC5192 standard; cDNA; 2774 BP.	
XX	
AC AAC5192;	
DT 16-JAN-2001 (first entry)	
XX	
DE Human secreted protein gene 3 SEQ ID NO:13.	
XX	
KW Human; secreted protein; cytosolic; immunostimulant; antiproliferative;	
KW cardiant; antiarrhythmic; antiviral; antibacterial; antifungal; cancer;	
KW antiparasitic; neuroprotective; nootropic; antiinflammatory; anti-HIV;	
KW antiangiogenic; antiarteriosclerotic; diagnosis; immune disorder; AIDS;	
KW autoimmune disease; haematopoietic cell disorder; blood protein disorder;	
KW agammaglobulinaemia; hyperproliferative disease; Gaucher's disease;	
KW cardiovascular disorder; congenital heart defect; pulmonary atresia;	
KW arrhythmia; ischaemia; angiogenesis related disorder; Crohn's disease;	
KW atherosclerosis; neurological disease; Alzheimer's disease; Huntington's;	
KW infectious disease; cat-scratch disease; chromosome 1; ss.	
XX	
OS Homo sapiens.	
XX	
PN WO200047602-A1.	
XX	
PD 17-AUG-2000.	
XX	
PF 08-FEB-2000; 2000WO-US003062.	
XX	
PR 10-FEB-1999; 99US-0119468P.	
XX	
PA (HUMA-) HUMAN GENOME SCI INC.	
XX	
PI Rosen CA, Ruben SM, Ebnur R, Young PE, Ni J, Soppet DR;	
PI Moore PA, Shi Y, Lafleur DW, Olsen HS, Florence KA, Komatsoulis G;	
XX	
DR WPI; 2000-543578/49.	
DR P-PSDB; AAB32373.	
XX	
PT New human nucleic acids encoding secreted proteins, useful in the	
PT treatment, prevention or diagnosis of immune disorders (e.g. autoimmune	
PT diseases), blood protein disorders and hyperproliferative diseases (e.g.	
PT Gaucher's disease).	
XX	
PS Claim 1; Page 392-393; 488pp; English.	
XX	
CC The polynucleotide sequences given in AAC5190 to AAC55235 encode the	
CC human secreted proteins given in AAB32371 to AAB32484. Human secreted	
CC proteins have activities based on the tissues and cells the genes are	
CC expressed in. Examples of activities include: cytosolic; immunostimulant	
CC ; antiproliferative; cardiant; antiarrhythmic; antiviral; antibacterial;	
CC antifungal; antiparasitic; neuroprotective; nootropic; antiinflammatory;	
CC antiangiogenic; anti-HIV; and antiarteriosclerotic. The polynucleotides	
CC and polypeptides, or their agonists and antagonists, can be used for	
CC treating, preventing or diagnosing immune disorders (e.g. cancer,	
CC autoimmune diseases), disorders of haematopoietic cells, blood protein	
CC disorders (e.g. agammaglobulinaemia), hyperproliferative diseases (e.g.	
CC Gaucher's disease), cardiovascular disorders (e.g. congenital heart	
CC defects, pulmonary atresia, arrhythmias, ischaemia), angiogenesis related	
CC disorders (e.g. Crohn's disease, atherosclerosis), neurological diseases	
CC (e.g. Alzheimer's disease, Huntington's chorea), infectious diseases	
CC (e.g. AIDS, cat-scratch disease and other bacterial, viral, parasitic or	
CC fungal diseases). AAC5181 to AAC55189 and AAB32370 represent sequences	
CC used in the exemplification of the present invention	
XX	
SQ Sequence 2774 BP; 841 A; 632 C; 645 G; 644 T; 0 U; 12 Other;	

Query Match 96.8%; Score 2617.2; DB 3; Length 2774;
Best local Similarity 98.7%; Pred. No. 0;
Matches 2669; Conservative 6; Mismatches 22; Indels 7; Gaps 4;

QY 1 GGAAGTGGCTTCATTTTCAGTGGCTGACTTCCAGAGACAATATGGCTGGTCCCAACAT 60
| | | | |
Db 13 GGAAGTGGCTTCATTTTCAGTGGCTGACTTCCAGAGACAATATGGCTGGTCCCAACAT 72
QY 61 GCCTCACCCCTCATCTATATCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGAACCCGTGA 120
| | | | |
Db 73 GCCTCACCCCTCATCTATATCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGAACCCGTGA 132
QY 121 AAGAGCTGGTCGGTCCGTTGGTGGGGCCGTGACTTCCCCCTGAAGTCCAAAGTAAAGC 180
| | | | |
Db 133 AAGAGCTGGTCGGTCCGTTGGTGGGGCCGTGACTTCCCCCTGAAGTCCAAAGTAAAGC 192
QY 181 AAGTGACTCTATTGTCTGGACCTTCAACACAAACCCCTCTGTCAACCATACAGCCAGAAG 240
| | | | |
Db 193 AAGTGACTCTATTGTCTGGACCTTCAACACAAACCCCTCTGTCAACCATACAGCCAGAAG 252
QY 241 GGGGCACTATCATAGTGACCCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCAAGATGGAG 300
| | | | |
Db 253 GGGGCACTATCATAGTGACCCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCAAGATGGAG 312
QY 301 GCTACTCCCTGGAAGCTCAGCAAACTGAAAGAAATGACTCAGGGATCTACTATGTGGGGA 360
| | | | |
Db 313 GCTACTCCCTGGAAGCTCAGCAAACTGAAAGAAATGACTCAGGGATCTACTATGTGGGGA 372
QY 361 TATACAGCTCATCACTCCAGCAGCCCTCCACCCAGAGAGTACGTGCTGATGTCTACGAGC 420
| | | | |
Db 373 TATACAGCTCATCACTCCAGCAGCCCTCCACCCAGAGAGTACGTGCTGATGTCTACGAGC 432
QY 421 ACCTGTCAAAAGCCTAAAGTCACCATGGGTCTGCAGAGCAATAAGAAATGGCACCTGTGTGA 480
| | | | |
Db 433 ACCTGTCAAAAGCCTAAAGTCACCATGGGTCTGCAGAGCAATAAGAAATGGCACCTGTGTGA 492
QY 481 CCAATCTGACATGCTGCATGGAACATGGGGAGAGAGATGTGATTTATACCTGGAAGGCC 540
| | | | |
Db 493 CCAATCTGACATGCTGCATGGAACATGGGGAGAGAGATGTGATTTATACCTGGAAGGCC 552
QY 541 TGGGGCAAGCAGCCCAATGAGTCCCATTAATGGGTCCATCCTCCCATCTCTGAGATGGG 600
| | | | |
Db 553 TGGGGCAAGCAGCCCAATGAGTCCCATTAATGGGTCCATCCTCCCATCTCTGAGATGGG 612
QY 601 GAGAAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCCCTGTCAAGAGAACTTCTCAA 660
| | | | |
Db 613 GAGAAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCCCTGTCAAGAGAACTTCTCAA 672
QY 661 GCCCCATCTTGGCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCATGG 720
| | | | |
Db 673 GCCCCATCTTGGCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCATGG 732
QY 721 TCCTCCTGTGTCCTCTGTTGGTGCCCTCCTGCTCAGTCTCTTTGTACTGGGGCTATTTC 780
| | | | |
Db 733 TCCTCCTGTGTCCTCTGTTGGTGCCCTCCTGCTCAGTCTCTTTGTACTGGGGCTATTTC 792
QY 781 TTTGGTTTCTGAAGAGAGAGAGACAAGAGATACATTGAAGAGAAAGAGAGAGTGACA 840
| | | | |
Db 793 TTTGGTTTCTGAAGAGAGAGAGACAAGAGATACATTGAAGAGAAAGAGAGTGACA 852
QY 841 TTTGTGGGAAACTCTTAACATATGCCCCCACTTCTGAGAGAAACAGAGTACGACACAA 900
| | | | |
Db 853 TTTGTGGGAAACTCTTAACATATGCCCCCACTTCTGAGAGAAACAGAGTACGACACAA 912
QY 901 TCCCTCACACTAATAGAACAAATCCTAAAGAGAATCCAGCAAAATACGGTTTACTCCACTG 960
| | | | |
Db 913 TCCCTCACACTAATAGAACAAATCCTAAAGAGAATCCAGCAAAATACGGTTTACTCCACTG 972
QY 961 TGAATAATCCGAAAAAGATGAAAAATCCCACTCACTGCTCAGCATGCAAGACACACCAA 1020
| | | | |
Db 973 TGAATAATCCGAAAAAGATGAAAAATCCCACTCACTGCTCAGCATGCAAGACACACCAA 1032
QY 1021 GGCTATTTGCTATGAGATGTATCTAGACAGCAGTGCACCTCCCTAAGTCTGTCTCA 1080
| | | | |
Db 1033 GGCTATTTGCTATGAGATGTATCTAGACAGCAGTGCACCTCCCTAAGTCTGTCTCA 1092
QY 1081 AAAAAAACAATTTCTCGGCCCAAGAAAAACAATCAGAAAGATTCACTGATTTGACTAGA 1140

Db 1093 AAAAAAACAATTTCTCGGCCCAAGAAAAACAATCAGAAAGATTCACTGATTTGACTAGA 1152
QY 1141 AACATCAAGGAAGAATGAAGACGTTGACTTTTTCAGAGATAAATTATCTGTAGTCTT 1200
| | | | |
Db 1153 AACATCAAGGAAGAATGAAGACGTTGACTTTTTCAGAGATAAATTATCTGTAGTCTT 1212
QY 1201 CTTAGATTTAAGAGTTCGTATTCATCCACTGCTGAGAAATCTCCTCAACCCAGAAAG 1260
| | | | |
Db 1213 CTTAGATTTAAGAGTTCGTATTCATCCACTGCTGAGAAATCTCCTCAACCCAGAAAG 1272
QY 1261 GTTTAATCACTTCACTCCCAAAATGGGATTGTGAATGTCAACCAACCATMAAAAAAGTGC 1320
| | | | |
Db 1273 GTTTAATCACTTCACTCCCAAAATGGGATTGTGAATGTCAACCAACCATMAAAAAAGTGC 1332
QY 1321 TTAGAATAATTCCTATAGAAATGTAAATGCAAGGTCAACATATTAATGACAGCCTGTTG 1380
| | | | |
Db 1333 TTAGAATAATTCCTATAGAAATGTAAATGCAAGGTCAACATATTAATGACAGCCTGTTG 1392
QY 1381 TATTAAATGATGGCTCCAGGTCAAGTGTCTGAGTTTCATTCCATCCCAAGGCTTGAATGTC 1440
| | | | |
Db 1393 TATTAAATGATGGCTCCAGGTCAAGTGTCTGAGTTTCATTCCATCCCAAGGCTTGAATGTC 1452
QY 1441 AGGATTAATCAAGAGTCTTGTCTACAGAGGGCAAGAACCAAAACAGACAGACAAGT 1500
| | | | |
Db 1453 AGGATTAATCAAGAGTCTTGTCTACAGAGGGCAAGAACCAAAACAGACAGACAAGT 1512
QY 1501 CCAGCAGAAAGCAGATGCACCTGCACAAAAATGGAATGTATTAATTGGCTCTATAAATCTATGT 1560
| | | | |
Db 1513 CCAGCAGAAAGCAGATGCACCTGCACAAAAATGGAATGTATTAATTGGCTCTATAAATCTATGT 1572
QY 1561 GCCCAGCACTATGTCTGAGCTTCACTAATTGGTCAGACGTGCTGTGCCCTCATGAAT 1620
| | | | |
Db 1573 GCCCAGCACTATGTCTGAGCTTCACTAATTGGTCAGACGTGCTGTGCCCTCATGAAT 1632
QY 1621 TGGCTCCAATGAATGAATGAATCTTTCATGAGCAGTGTGACAGGCTGACACAGATTCC 1680
| | | | |
Db 1633 TGGCTCCAATGAATGAATGAATCTTTCATGAGCAGTGTGACAGGCTGACACAGATTCC 1692
QY 1681 CAGAGGGCCAGGTGTGATCCACAGAGCTTGAAGGTCAAAGTCAAGAGTAAGATC 1740
| | | | |
Db 1693 CAGAGGGCCAGGTGTGATCCACAGAGCTTGAAGGTCAAAGTCAAGAGTAAGATC 1752
QY 1741 AGGTAAGCTGACCATGTTTGGCAGATACTATATGAGACACAGAAGTGTGCATGGCCA 1800
| | | | |
Db 1753 AGGTAAGCTGACCATGTTTGGCAGATACTATATGAGACACAGAAGTGTGCATGGCCA 1812
QY 1801 AGGACAAGGACCTCCAGCCAGGCTTCATTATATGACATTGTGCTCAAAAAGAAAGTCTAG 1860
| | | | |
Db 1813 AGGACAAGGACCTCCAGCCAGGCTTCATTATATGACATTGTGCTCAAAAAGAAAGTCTAG 1872
QY 1861 GTTTTAAAGGCTGTGCCAGAACCCATCCCAATMAAGAGACGAGTCTGAAGTCAATGTGA 1920
| | | | |
Db 1873 GTTTTAAAGGCTGTGCCAGAACCCATCCCAATMAAGAGACGAGTCTGAAGTCAATGTGA 1932
QY 1921 AATCTAGTGAAGAGACTTGAAGTCAAGGAGTGAAGTGGTGGGGCACGCGGGGCAAGTGG 1980
| | | | |
Db 1933 AATCTAGTGAAGAGACTTGAAGTCAAGGAGTGAAGTGGTGGGGCACGCGGGGCAAGTGG 1992
QY 1981 GTACTGTGAACCTTTAAGATGTTAATTCATTCAATAGATATTTATTAAGAACTACT 2040
| | | | |
Db 1993 GTACTGTGAACCTTTAAGATGTTAATTCATTCAATAGATATTTATTAAGAACTACT 2049
QY 2041 ATGCGGCCCGGCATGCTGGCTCAACCTGTATCCAGCACTTTGGAGGCCCAAGGTGGG 2100
| | | | |
Db 2050 ATGCGGCCCGGCATGCTGGCTCAACCTGTATCCAGCACTTTGGAGGCCCAAGGTGGG 2109
QY 2101 TGGGTATCTGAGGTCAAGAGTTCAGAGCCAGCCTGGCCCAATGTGTAAGAACCC-CATCT 2159
| | | | |
Db 2110 TGGGTATCTGAGGTCAAGAGTTCAGAGCCAGCCTGGCCCAATGTGTAAGAACCCCATCTCT 2169
QY 2160 CTACTAAAGATCAAAATTTGCTGAGCGGTGTGTGTGCACCTGT-ATCCAGCTACTCGA 2218
| | | | |

Db	2170	ACTAMAGATACAAAMATTGCTGAGCGTGTGTGTGCACTGTATCCAGCTACTCGA	2229
Oy	2219	GAGGCCAAGCATGAGAAATCGCTTGAACCTGG--AGGTGAGTTGACGTGAGCTGAGATG	2276
Db	2230	GAGGCCAAGCATGAGAAATCGCTTGAACCTGGAGGTGGAGTTGCAGTGAAGTGAATG	2289
Oy	2277	GCACCACTGCACCTCCGGCTAGGCAACGAGAGCAAACTCCATATCAACAACAACA	2336
Db	2290	GCACCACTGCAYTCCGGCTAGGCAACGAGAGCAAACTCCAATACAACAACAACA	2349
Oy	2337	ACAACCTGTGCTAGGTCACTGTGGCAGCTAAGATGAACATCCCTACCAACACAGAGCTCAC	2396
Db	2350	ACAACCTGTGCTAGGTCACTGTGGCAGCTAAGATGAACATCCCTACCAACACAGAGCTCAC	2409
Oy	2397	CATCTCTTACTTAAAGTGAAGAAACATGGGGAAGGGGAATGGCTGTTTGAT	2456
Db	2410	CATCTCTTACTTAAAGTGAAGAAACATGGGGAAGGGGAATGGCTGTTTGAT	2469
Oy	2457	ATGTTCCCTGACGCAATCTTGAATGAGACCTCCCTACCAAGTGAAGTGTGAAA	2516
Db	2470	ATGTTCCCTGACACATCTTGAATGAGACCTCCCTACCAAGTGAAGTGTGAAA	2529
Oy	2517	AACTTAATACAATGCTTGTGGCAAGAATGGATTTAGAGATTATCTCTCAGAAA	2576
Db	2530	AACTTAATACAATGCTTGTGGCAAGAATGGATTTAGAGATTATCTCTCAGAAA	2589
Oy	2577	GGCATTGTGAAGGAATGAGCCAGATCTCTCTCCCTACTGCAAAACCCTATTGTAGTAA	2636
Db	2590	GGCATTGTGAAGGAATGAGCCAGATCTCTCTCCCTACTGCAAAACCCTATTGTAGTAA	2649
Oy	2637	AAAGTCTTCTTACTTATCTTAATAAAACAGATATTGTGAGATTACATATAAAAAA	2696
Db	2650	AAAGTCTTCTTACTTATCTTAATAAAACAGATATTGTGAGAMAMAMAAAAA	2709
Oy	2697	AAAA 2700	
Db	2710	AAAA 2713	
RESULT 3			
ID	ADD67524	standard; cDNA; 2672 BP.	
XX	AC	ADD67524;	
XX	DT	15-JAN-2004 (first entry)	
XX	DE	Human Ly1728P encoding cDNA SEQ ID NO:1.	
XX	KM	haematological malignancy; immunocjugate; cytostatic; immunostimulant;	
KM		vaccine; immunotherapy; cancer; multiple myeloma cell;	
KM		chronic lymphocytic leukaemia; B cell leukaemia; lymphoma; anti-cancer;	
KM		human; gene; ss.	
OS		Homo sapiens.	
XX	PN	WO2003062401-A2.	
XX	PD	31-JUL-2003.	
XX	PF	22-JAN-2003; 2003WO-US002353.	
XX	PR	22-JAN-2002; 2002US-00057475.	
XX	PA	(CORI-) CORIXA CORP.	
XX	PI	Galger A, Algate PA, Mannion J, Clapper JD, Wang A, Ordonez N;	
XX	PI	Carter L, McNeill PD;	
XX	DR	WPI; 2003-598749/56.	
XX	DR	P-PSDB; ADD67525.	
PT		New hematological malignancy-related genes and polypeptides, useful for	

PT	screening anti-cancer agents, and generating antibodies or	
PT	immunocjugates for treating e.g. multiple myeloma cell or chronic	
PT	lymphocytic leukemia.	
PS	Claim 1; SEQ ID NO 1; 307pp; English.	
XX		
CC	The present invention describes an isolated polynucleotide (I), which is	
CC	overexpressed in haematological malignancies, and which encodes a	
CC	polypeptide or an immunogenic fragment of the polypeptide. Also	
CC	described: (1) an isolated polypeptide; (2) an expression vector	
CC	comprising (I) operably linked to an expression control sequence; (3) a	
CC	host cell comprising an expression vector; (4) an isolated antibody that	
CC	specifically binds to the polypeptide or its immunogenic fragment; and	
CC	(5) immunocjugates comprising the antibody above, or an antibody that	
CC	specifically binds to a polypeptide, or its immunogenic fragment, encoded	
CC	by (I). (I) has cytostatic and immunostimulant activities, and can be	
CC	used in vaccines and immunotherapy. The immunocjugates are useful in	
CC	the manufacture of a medicament, particularly as active ingredients in a	
CC	composition for treating cancer, e.g. multiple myeloma cell, chronic	
CC	lymphocytic leukaemia, B cell leukaemias, or lymphomas in humans, sheep,	
CC	primates, goats, bovines, equines, porcines, lupines, canines or felines.	
CC	The polynucleotide (I) or polypeptide can be used for screening anti-	
CC	cancer agents, and generating antibodies or immunocjugates for treating	
CC	or preventing the above-mentioned diseases. The polynucleotide,	
CC	polypeptide or antibody can be used for detecting, diagnosing or	
CC	prognosticating the haematological malignancies described above. The	
CC	present sequence is used in the exemplification of the present invention.	
XX		
SQ	Sequence 2672 BP; 818 A; 611 C; 620 G; 623 T; 0 U; 0 Other;	
	Query Match	
	Best Local Similarity 96.3%; Score 2604.6; DB 10; Length 2672;	
	Matches 2658; Conservative 0; Mismatches 9; Indels 8; Gaps 4;	
OY	27 CTTCCAGAGAGCAATATGGCTGTGTTCCCAACATGCTCACCTCATCTATATCCTTTGG	86
DB	1 CTTCCAGAGAGCAATATGGCTGTGTTCCCAACATGCTCACCTCATCTATATCCTTTGG	60
OY	87 CAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAGAGAGCTGGTCCGTTGGTGG	146
DB	61 CAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAGAGAGCTGGTCCGTTGGTGG	120
OY	147 GCCGTGACTTTCCCTCCCTGAAGTCCAAAGTAAAGCAAGTGACTCTATTTGCTGGA	206
DB	121 GCCGTGACTTTCCCTCCCTGAAGTCCAAAGTAAAGCAAGTGACTCTATTTGCTGGA	180
OY	207 AACACAACCCCTCTTGTCCACCATACAGCCAGAAAGGGGCACCTATCATAGTAC	266
DB	181 AACACAACCCCTCTTGTCCACCATACAGCCAGAAAGGGGCACCTATCATAGTAC	240
OY	267 CGTAATAGGAGAGAGTAGACTTCCAGATGAGGCTACTCCCTGAAGCTCAGCAAA	326
DB	241 CGTAATAGGAGAGAGTAGACTTCCAGATGAGGCTACTCCCTGAAGCTCAGCAAA	300
OY	327 AAGAAGAATGACTCAGGATCTACTATGTGGGATATACAGCTCATCTCCAGCAG	386
DB	301 AAGAAGAATGACTCAGGATCTACTATGTGGGATATACAGCTCATCTCCAGCAG	360
OY	387 TCCACCCAGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAAGCCTAAAGTC	446
DB	361 TCCACCCAGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAAGCCTAAAGTC	420
OY	447 GGTCTGACAGCAATTAAGATGGCACCTGTGTGACCAATCTGACATGCTCATGGA	506
DB	421 GGTCTGACAGCAATTAAGATGGCACCTGTGTGACCAATCTGACATGCTCATGGA	480
OY	507 GGGGAAGAGATGTGATTTTATACCTGGAAGGCCCTGGGGCAAGCAATGAGTCC	566
DB	481 GGGGAAGAGATGTGATTTTATACCTGGAAGGCCCTGGGGCAAGCAATGAGTCC	540
OY	567 AATGGGTCCATCTCCCATCTCTGAGATGGGAGAAAGTGAATGACCTTCATCTGC	626
DB	541 AATGGGTCCATCTCCCATCTCTGAGATGGGAGAAAGTGAATGACCTTCATCTGC	600

QY	627	GTGGCCAGGAACCCCTGTGCAGAGAAACTTCTCAAGCCCCATCTTGGCCAGGAAGCTCTGT	686
Db	601	GTGGCCAGGAACCCCTGTGCAGAGAAACTTCTCAAGCCCCATCTTGGCCAGGAAGCTCTGT	660
QY	687	GAAGGTGCTGTGATGACCCAGATTCTCCATGTGCTCTGTGTCTCTGTGTGTC	746
Db	661	GAAGGTGCTGTGATGACCCAGATTCTCCATGTGCTCTGTGTCTCTGTGTGTC	720
QY	747	CTCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTCTGAAGAGAGAGACAA	806
Db	721	CTCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTCTGAAGAGAGAGACAA	780
QY	807	GAAGATACATTGAAGAGAGAGAGAGTGGACATTTGTCCGGGAAACTCCTAACATATGC	866
Db	781	GAAGATACATTGAAGAGAGAGAGAGTGGACATTTGTCCGGGAAACTCCTAACATATGC	840
QY	867	CCCCATTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAATAGAACAACTCTA	926
Db	841	CCCCATTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAATAGAACAACTCTA	900
QY	927	AAGGAAGATCCAGCAAAATACGGTTTACTCCACTGTGAAATACCGAAAAAGATGAAAT	986
Db	901	AAGGAAGATCCAGCAAAATACGGTTTACTCCACTGTGAAATACCGAAAAAGATGAAAT	960
QY	987	CCCCACTCACTGCTCACAGATGCCAGACACACCAAGGCTAATTGCTATGAGAAATTTATC	1046
Db	961	CCCCACTCACTGCTCACAGATGCCAGACACACCAAGGCTAATTGCTATGAGAAATTTATC	1020
QY	1047	TAGACAGCAGTGCACCTCCCTAAGTCTCTGCTCAAAAAAACAATTTCTCGGCCCAAG	1106
Db	1021	TAGACAGCAGTGCACCTCCCTAAGTCTCTGCTCAAAAAAACAATTTCTCGGCCCAAG	1080
QY	1107	AAAACAATCAGAAGAAATTCATGATTTGACTAGAAACATCAAGGAAGATGAAGACGTT	1166
Db	1081	AAAACAATCAGAAGAAATTCATGATTTGACTAGAAACATCAAGGAAGATGAAGACGTT	1140
QY	1167	GACTTTTTTCAGGATAAATATCTCTGATGCTTCTTAGATTTAAGATTGTAATTC	1226
Db	1141	GACTTTTTTCAGGATAAATATCTCTGATGCTTCTTAGATTTAAGATTGTAATTC	1200
QY	1227	ATCCACTGCTGAGAAATCTCTCAAAACCAGAAAGTTTAATCACTCATCCCAAAATGG	1286
Db	1201	ATCCACTGCTGAGAAATCTCTCAAAACCAGAAAGTTTAATCACTCATCCCAAAATGG	1260
QY	1287	GATTGTGAATGTACGAAACCATTAAAAAAGTCTTAGAATATTCTATAGAAATGTAA	1346
Db	1261	GATTGTGAATGTACGAAACCATTAAAAAAGTCTTAGAATATTCTATAGAAATGTAA	1320
QY	1347	ATGCAAGGTACACATAATTAATGACAGCCTGTTGTAATTAATGATGCTCCAGTCAGTGT	1406
Db	1321	ATGCAAGGTACACATAATTAATGACAGCCTGTTGTAATTAATGATGCTCCAGTCAGTGT	1380
QY	1407	CTGAGTTTCATTCCATCCCAAGGCTTGATGTCAAGATTATACCAAGAGCTTGTCTACC	1466
Db	1381	CTGAGTTTCATTCCATCCCAAGGCTTGATGTGAAGATTATACCAAGAGCTTGTCTACC	1440
QY	1467	AGGAGGGCAAGAACCAAAACAGACAGACAAAGTCCAGAGACAGATGCACTGACAA	1526
Db	1441	AGGAGGGCAAGAACCAAAACAGACAGACAAAGTCCAGAGACAGATGCACTGACAA	1500
QY	1527	AAATGATGTATTAATGGCTCTATAAACTATGTGCCAGCACTATGCTGAGCTTACACT	1586
Db	1501	AAATGATGTATTAATGGCTCTATAAACTATGTGCCAGCACTATGCTGAGCTTACACT	1560
QY	1587	AATTGTCAGACGTGCTGTCTGCCCTCATGAATTTGGTCCAATGATGAATTAATTTT	1646
Db	1561	AATTGTCAGACGTGCTGTCTGCCCTCATGAATTTGGTCCAATGATGAATTAATTTT	1620
QY	1647	ATGAGCAGTTGTAGCAGGCTGACACACAGATTCCACAGAGGCCAGGTGTGATCCACAGG	1706
Db	1621	ATGAGCAGTTGTAGCAGGCTGACACACAGATTCCACAGAGGCCAGGTGTGATCCACAGG	1680

QY	1707	ACTTGAAGGTC	CAAAAGTTCA	CAAGAATGA	AGAAATCAGGGTAG	CTGACCATGTTGGCAGAT	1766			
Db	1681	ACTTGAAGGTC	CAAAAGTTCA	CAAGAATGA	AGAAATCAGGGTAG	CTGACCATGTTGGCAGAT	1740			
QY	1767	ACTATAATG	AGACACAC	AGAAAGTGTG	ATGGCCCAAGGACA	AGGACCTCCAGCCAGGCTTC	1826			
Db	1741	ACTATAATG	AGACACAC	AGAAAGTGTG	ATGGCCCAAGGACA	AGGACCTCCAGCCAGGCTTC	1800			
QY	1827	ATTATATG	CACTGTGCTG	CAAAAGAAAAGT	CTAGGTTTTAAGGCTGTG	CCAGAACCATC	1886			
Db	1801	ATTATATG	CACTGTGCTG	CAAAAGAAAAGT	CTAGGTTTTAAGGCTGTG	CCAGAACCATC	1860			
QY	1887	CCAATAAAG	AGACCCGAGT	CTGAAGTCA	CATTGTAAATCTAGTGTAG	GAGACTTGGAGTCA	1946			
Db	1861	CCAATAAAG	AGACCCGAGT	CTGAAGTCA	CATTGTAAATCTAGTGTAG	GAGACTTGGAGTCA	1920			
QY	1947	GGCAGTGA	CACTGGTGGG	GCACGGGGGGG	GCAGTGGGTACTTGTAA	ACCTTAAAGATGGTT	2006			
Db	1921	GGCAGTGA	CACTGGTGGG	GCACGGGGGGG	GCAGTGGGTACTTGTAA	ACCTTAAAGATGGTT	1980			
QY	2007	AATTCATT	CAATAGATAT	TTATTATTA	GAACCTACTATGCGGCCG	GCATGGTGGCTCACAC	2066			
Db	1981	AATTCATT	CAATAGATAT	TTATTATTA	GAACCTACTATGCGGCCG	GCATGGTGGCTCACAC	2037			
QY	2067	CTGTAAAT	CCAGCACTTT	TGGAGGCGCA	AGGTGGTGGTCACTGAGGT	CAGAGTTCAA	2126			
Db	2038	CTGTAAAT	CCAGCACTTT	TGGAGGCGCA	AGGTGGTGGTCACTGAGGT	CAGAGTTCAA	2097			
QY	2127	GACCAGC	CTGGCCCA	ACATGTGTAA	ACCCCATCTCTACTAA	AAGAT--CAAAATTGCTGAG	2184			
Db	2098	GACCAGC	CTGGCCCA	ACATGTGTAA	ACCCCATCTCTACTAA	AAGATCAAAAAATTGCTGAG	2157			
QY	2185	CGTGTGTG	TGTGCA	CCCTGT-AT	CCCACTACTCGAGAGG	CCAAAGCATGAGAA	TCGCTTG	2243		
Db	2158	CGTGTGTG	TGTGCA	CCCTGTAA	TCCCACTACTCGAGAGG	CCAAAGCATGAGAA	TCGCTTG	2217		
QY	2244	AACCTGG--	AGGTGAGT	TGCACTGAG	CTGAGATGGCA	CACTGCAC	TCGCGCTAGGCA	2301		
Db	2218	AACCTGG	AGGTGAGT	TGCACTGAG	CTGAGATGGCA	CACTGCAC	TCGCGCTAGGCA	2277		
QY	2302	ACGAGAG	CAAAACTCC	AATACAA	CAACAACA	CAACACTGTG	CTAGGTCA	GTGCGCA	2361	
Db	2278	ACGAGAG	CAAAACTCC	AATACAA	CAACAACA	CAACACTGTG	CTAGGTCA	GTGCGCA	2337	
QY	2362	CGTAAGAT	GAAACAT	CCCTAC	CAACACAGAG	CTCACCATCTT	TATCTTA	CTTAAGTGA	AAAAAC	2421
Db	2338	CGTAAGAT	GAAACAT	CCCTAC	CAACACAGAG	CTCACCATCTT	TATCTTA	CTTAAGTGA	AAAAAC	2397
QY	2422	ATGGGGA	AGGGGAA	GGGGAATG	GTCTTTG	ATATGTCCCTG	ACGCATAT	CTTGAAT		2481
Db	2398	ATGGGGA	AGGGGAA	GGGGAATG	GTCTTTG	ATATGTCCCTG	ACGCATAT	CTTGAAT		2457
QY	2482	GGAGAC	TCCTTAC	CAAGTGA	TGAAGTGT	TGAAAAA	CTTAATA	CAAAATGCT	GTGTTGGG	2541
Db	2458	GGAGAC	TCCTTAC	CAAGTGA	TGAAGTGT	TGAAAAA	CTTAATA	CAAAATGCT	GTGTTGGG	2517
QY	2542	CAAGAAT	GGGATTG	AGATTAT	CTTCTCT	CAGAAAG	CAATTGT	TGAAGGAA	TTGAGCCAGA	

RESULT 4	
AAC55223	
ID AAC55223	standard; cDNA; 2780 BP.
XX	

AC AAC55223;
XX 16-JAN-2001 (first entry)
XX Human secreted protein gene 3 SEQ ID NO:44.
DB
XX Human; secreted protein; cyostatic; immunostimulant; antiproliferative;
KM cardiatic; antiarhythmic; antiviral; antibacterial; antifungal; cancer;
KM antiparasitic; neuroprotective; nootropic; antiinflammatory; anti-HIV;
KM antiangiogenic; antiarteriosclerotic; diagnosis; immune disorder; AIDS;
KM autoimmune disease; haematopoietic cell disorder; blood protein disorder;
KM agammaglobulinaemia; hyperproliferative disease; Gaucher's disease;
KM cardiovascular disorder; congenital heart defect; pulmonary atresia;
KM arhythmia; ischaemia; angiogenesis related disorder; Crohn's disease;
KM atherosclerosis; neurological disease; Alzheimer's disease; Huntington's;
KM infectious disease; cat-scratch disease; chromosome 1; ss.
XX Homo sapiens.
XX WO200047602-A1.
PN 17-AUG-2000.
XX 08-FEB-2000; 2000WO-US003062.
PF 10-FEB-1999; 99US-0119468P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Ruben SM, Ebner R, Young PE, Ni J, Soppet DR;
PI Moore PA, Shi Y, Lafleur DW, Olsen HS, Florence KA, Komatsoulis G;
XX WPI; 2000-543578/49.
DR P-PSDB; AAB32404.
XX New human nucleic acids encoding secreted proteins, useful in the
PT treatment, prevention or diagnosis of immune disorders (e.g. autoimmune
PT diseases), blood protein disorders and hyperproliferative diseases (e.g.
PT Gaucher's disease).
XX Claim 1; Page 411-412; 488pp; English.
XX The polynucleotide sequences given in AAC55190 to AAC55235 encode the
CC human secreted proteins given in AAB32371 to AAB32484. Human secreted
CC proteins have activities based on the tissues and cells the genes are
CC expressed in. Examples of activities include: cyostatic; immunostimulant
CC ; antiproliferative; cardiatic; antiarhythmic; antiviral; antibacterial;
CC antifungal; antiparasitic; neuroprotective; nootropic; antiinflammatory;
CC antiangiogenic; anti-HIV; and antiarteriosclerotic. The polynucleotides
CC and polypeptides, or their agonists and antagonists, can be used for
CC treating, preventing or diagnosing immune disorders (e.g. cancer,
CC autoimmune diseases), disorders of haematopoietic cells, blood protein
CC disorders (e.g. agammaglobulinaemia), hyperproliferative diseases (e.g.
CC Gaucher's disease), cardiovascular disorders (e.g. congenital heart
CC defects, pulmonary atresia, arhythmias, ischaemia), angiogenesis related
CC disorders (e.g. Crohn's disease, atherosclerosis), neurological diseases
CC (e.g. Alzheimer's disease, Huntington's chorea), infectious diseases
CC (e.g. AIDS, cat-scratch disease and other bacterial, viral, parasitic or
CC fungal diseases). AAC55181 to AAC55189 and AAB32370 represent sequences
CC used in the exemplification of the present invention
XX Sequence 2780 BP; 819 A; 658 C; 652 G; 651 T; 0 U; 0 Other;
SQ
Query Match 80.9%; Score 2186.4; DB 3; Length 2780;
Best Local Similarity 90.7%; Pred. No. 0;
Matches 2530; Conservative 0; Mismatches 136; Indels 122; Gaps 14;

DB 64 GCAGCTCACAGGGTACGACGACCTCTGACCCCGTGAAGAAGCTGTGCTCCGTTGCTG 123
QY 146 GGCCGTGACTTTCCCTCCCTGAAGTCCAAAGTAAGCAAGTTGACTCTATTGCTGACCTT 205
DB 124 GGCCGTGACTTTCCCTCCCTGAAGTCCAAAGTAAGCAAGTTGACTCTATTGCTGACCTT 183
QY 206 CAACACAACCCCTCTTGTCCACCATACAGCCAGAAAGGGGCACTATCATAGTACCACAAA 265
DB 184 CAACACAACCCCTCTTGTCCACCATACAGCCAGAAAGGGGCACTATCATAGTACCACAAA 243
QY 266 TCCTATAGGAGAGAGAGTAGACTTCCCAAGTAGAGGCTACTCCCTGAAGCTCAGCAAACT 325
DB 244 TCCTATAGGAGAGAGAGTAGACTTCCCAAGTAGAGGCTACTCCCTGAAGCTCAGCAAACT 301
QY 326 GAAGAAGATGACTCAGGATCTACTATGTGGGATATACAGCTCATCTCCAGCAGCC 385
DB 302 GAAGAAGATGACTCAGGATCTACTATGTGGGATATACAGCTCATCTCA -TCCAGCAGCC 360
QY 386 CTCACCCAGAGTAGCTGCTGATGCTACGACGACCTGTCAAAAGCTAAAGTCACCAT 445
DB 361 CTCACCCAGAGTAGCTGCTGATGCTACGATCACCTGTCAAAAGCTAAAGTCACCAT 420
QY 446 GGGTCTGACAGCAATAAGATGGACCTGTGTGACCAATCTGACATGCTGATGAACA 505
DB 421 GGGTCTGACAGCAATAAGATGGACCTGTGTGACCAATCTGACATGCTGATGAACA 480
QY 506 TGGGAGAGAGATGTGATTATACCTGGAAGCCCTGGGGCAAGCACAATGAGTCCCA 565
DB 481 TGGGAGAGAGATGTGA -TTATTCTGGAAGGCC -TGGGAGAGCACAATGAGTCCCA 536
QY 566 TAATGGGTCCATCTCTCCCATCTCTGAGATGGGAGAAAGTATGACCTTATCTG 625
DB 537 TAATGGGTCCATCTCTCCCATCTCTGAGATGGGAGAAAGTATGACCTTATCTG 596
QY 626 CGTTGCCAGGAACCTGTGACAGAGAACTTCTCAAGCCCCCATCTTCCAGAGAACTCTG 685
DB 597 CGTTGCCAGGAACCTGTGACAGAGAACTTCTCAAGCCCCCATCTTCCAGAGAACTCTG 656
QY 686 TGAAGTGTGCTGATGACCC-----AGATTCTCCATGTCCTCTGTCTCC 735
DB 657 TGAAGTGTGCTGCTCTCTCCCTCTCCAGAGAGACTCTGCCAGGCTCTACACCTTCTC 716
QY 736 TGTGTGCTCCCT 795
DB 717 AGCTCTAGCCCT 776
QY 796 GAGAGAGACAGAAGATGATCTTGAAGAGAAAGAGAGAGAGATGACATTTGTCGGAACT- 854
DB 777 CAGGCTGGAGAGAGGTGGCAGGTGCTTCAAGACCTGGGTCTTCTCTGAGCTGACTTT 836
QY 855 -----CCTAATATGCCCCCA-----TTCTGAGAGAACACAGATACGA 895
DB 837 TCTCCCTTCCCTGTGCTCTCCACCATCTCTGAAGGTGCTGATGACCCAGATTCTCTC 896
QY 896 CACAATCCCTC----- 906
DB 897 CATGTCCTCTCTGTCTCTCTGTGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 956
QY 907 -----ACATAATAGAACATCTTAAAGAGATCCAG 939
DB 957 ATTTCTTTGTTTCTGAAGAGAGAGACAGAAGAACATCTTAAAGAGATCCAG 1016
QY 940 CAATACGGTTTACTCTCACTGTGGAATAACGAAAAAGATGGAATACTCCCACTACTGC 999
DB 1017 CAATACGG -TTACTCTCACTGTGGAATAACGAAAAAGATGGAATACTCCCACTACTGC 1075
QY 1000 TCACGATGCCAGACACACCAAGGCTATTGCTCTATGAGAAATGTTATCTAGACAGCAGTGC 1059
DB 1076 TCACGATGCCAGACACACCAAGGCTATTGCTCTATGAGAAATGTTATCTAGACAGCAGTGC 1135
QY 1060 ACTCCCTTAAGTCTCTGCTCAAAAAAACAATTTCTCGGCCCAAGAAACAATCAGAA 1119
DB 1136 ACTCCCTTAAGTCTCTGCTCAAAAAAACAATTTCTCGGCCCAAGAAACAATCAGAA 1195

QY 1120 GAATTCACCTGATTGAGTGAACATCAAGAGAAGATGAGAACGTTGACTTTTCCAG 1179
Db 1196 GAATTCACCTGATTGAGTGAACATCAAGAGAAGATGAGAACGTTGACTTTTCCAG 1255
QY 1180 GATAAATATATCTGATGCTTCTTAGATTAAAGAGTTCGTAATTCACCTGCTAG 1239
Db 1256 GATAAATATATCTGATGCTTCTTAGATTAAAGAGTTCATATTCACCTGCTAG 1315
QY 1240 AAATCTCCTCAAAACCCAGAAAGGTTTAATCACTTCAATCCAAAAATGGGATTTGAAATGTC 1299
Db 1316 AAATCTCCTCAAAACCCAGAAAGGTTTAATCACTTCAATCCAAAAATGGGATTTGAAATGTC 1375
QY 1300 AGCAAAACCATAAAAAAAGTGCTTAGAAGTATTCCTATAGAAATGTAAATGCAAGGTCACA 1359
Db 1376 AGCAAAACCATAAAAAAAGTGCTTAGAAGTATTCCTATAGAAATGTAAATGCAAGGTCACA 1435
QY 1360 CATATTAAATGACAGCCTGTTGTATTAAATGATGGCTCCAGGTCAGTGTCTGGAATTCATT 1419
Db 1436 CATATTAAATGACAGCCTGTTGTATTAAATGATGGCTCCAGGTCAGTGTCTGGAATTCATT 1495
QY 1420 CCATCCCAAGGCTTGATGTCAGGATTATATCAAGAGTCTTGCTACAGAGGCAAGAA 1479
Db 1496 CCATCCCAAGGCTTGATGTCAGGATTATATCAAGAGTCTTGCTACAGAGGCAAGAA 1555
QY 1480 GACCAAAAACAGACAGACAGTCCAGCAGAAACAGATGCACTGTACAAAAATGGATGTATT 1539
Db 1556 GACCAAAAACAGACAGACAGTCCAGCAGAAACAGATGCACTGTACAAAAATGGATGTATT 1615
QY 1540 AATTGGCTCTATAAACTATGTGCCCCAGCACTATGCTGAGCTTACATTAATTGGTCAGACG 1599
Db 1616 AATTGGCTCTATAAACTATGTGCCCCAGCACTATGCTGAGCTTACATTAATTGGTCAGACG 1675
QY 1600 TGCTGTCTGCCCTCATGAAATTGGCTCCAATGAATGAATGAATCTACTTTCATGAGCAGTTGTA 1659
Db 1676 TGCTGTCTGCCCTCATGAAATTGGCTCCAATGAATGAATGAATCTACTTTCATGAGCAGTTGTA 1735
QY 1660 GCAGGCTTGACCAAGATTTCCAGAGGGCCAGGTGTGATCCACAGACTTGAAGGTCAA 1719
Db 1736 GCAGGCTTGACCAAGATTTCCAGAGGGCCAGGTGTGATCCACAGACTTGAAGGTCAA 1795
QY 1720 AGTTCACAAAGATGAAGATCAGGGTAGCTGACCATGTTTGGCAGATACTATAATGAGA 1779
Db 1796 AGTTCACAAAGATGAAGATCAGGGTAGCTGACCATGTTTGGCAGATACTATAATGAGA 1855
QY 1780 CACAGAAGTGTGATGCCCCAAGACCAAGGACCTCCAGCCAGGCTTCAATTTATGCACTTG 1839
Db 1856 CACAGAAGTGTGATGCCCCAAGGACCAAGGACCTCCAGCCAGGCTTCAATTTATGCACTTG 1915
QY 1840 TGCTGCAAAAAGAAAGTCTAGGTTTAAAGCTGTGCCAGAACCCATCCCAATAAAGAGAC 1899
Db 1916 TGCTGCAAAAAGAAAGTCTAGGTTTAAAGCTGTGCCAGAACCCATCCCAATAAAGAGAC 1975
QY 1900 CGAGTCTGAAGTCACATTTGTAATCTAGTGTAGAGACTTGAAGTCAAGGCACTGAGACTG 1959
Db 1976 CGAGTCTGAAGTCACATTTGTAATCTAGTGTAGAGACTTGAAGTCAAGGCACTGAGACTG 2035
QY 1960 GTGGGGCACGGGGGCGAGTGGTACTTGTAAACCTTTAAAGATGGTTAATTCATTCAATA 2019
Db 2036 GTGGGGCACGGGGGCGAGTGGTACTTGTAAACCTTTAAAGATGGTTAATTCATTCAATA 2095
QY 2020 GATATTTATTAAGAACCTACTATCGGGCCCGGCATGGTGGCTCACACTGTATCCAGC 2079
Db 2096 GATATTTATTAAGAACCTAC--GCGGCCCGCATGGTGGCTCACACTGTATCCAGC 2152
QY 2080 ACTTTGGAGGCCAAGGTGGGTGATCTGAGGTCAAGGTTCAAGACCAAGCCTGGCC 2139
Db 2153 ACTTTGGAGGCCAAGGTGGGTGATCTGAGGTCAAGGTTCAAGACCAAGCCTGGCC 2212
QY 2140 AACATGGTGAACCCCATCTCTACTAAAGAT--CAAAATTTGCTGAGCGTGTGTGTGC 2197
Db 2213 AACATGGTGAACCCCATCTCTACTAAAGATACAAAAATTTGCTGAGCGTGTGTGTGC 2272

QY 2198 ACCTGT-ATCCAGCTACTCTGAGAGGCCCAAGGCATGAGAAATCCCTTGAACCTGG--AGGT 2254
Db 2273 ACCTGTAATCCAGCTACTCTGAGAGGCCCAAGGCATGAGAAATCCCTTGAACCTGGAGGTG 2332
QY 2255 GAGTTGCAAGTGAAGTGAAGTGGCAACCACTGCACTCCGGCTTAGGCAACGAGAGCAAAAC 2314
Db 2333 GAGTTGCAAGTGAAGTGAAGTGGCAACCACTGCACTCCGGCTTAGGCAACGAGAGCAAAAC 2392
QY 2315 TCCATATCAAAACAAACAAACCAACCACTGTGCTAGGTGAGTCTGGCACGTAAAGATGACA 2374
Db 2393 TCCATATCAAAACAAACAAACCAACCACTGTGCTAGGTGAGTCTGGCACGTAAAGATGACA 2452
QY 2375 TCCCTAACCAACACAGAGCTGACCATCTCTATATCTTAAGTGAAGAAAAATGAGGAGGGA 2434
Db 2453 TCCCTAACCAACACAGAGCTGACCATCTCTATATCTTAAGTGAAGAAAAATGAGGAGGGA 2512
QY 2435 AAGGGAATGGCTGCTTTGATATGTTCCTGACCGCATATCTGAATGAGACCTCCCTA 2494
Db 2513 AAGGGAATGGCTGCTTTGATATGTTCCTGACCATATCTTGAATGAGACCTCCCTA 2572
QY 2495 CCAAGTATGAAAGTGTGAAAAAATTATTAACAAATGCTTGTGGCAAGATGGGATT 2554
Db 2573 CCAAGTATGAAAGTGTGAAAAAATTATTAACAAATGCTTGTGGCAAGATGGGATT 2632
QY 2555 GAGGATATCTTCTCTCAGAAAGCATTTGTGAAGGAATGAGCCAGATCTCTCCCTAC 2614
Db 2633 GAGGATATCTTCTCTCAGAAAGCATTTGTGAAGGAATGAGCCAGATCTCTCCCTAC 2692
QY 2615 TGCAAAAACCTATTGTAGTAAAAAAGTCTTCTTACTATCTTAATAAAACAGATATTGTG 2674
Db 2693 TGCAAAAACCTATTGTAGTAAAAAAGTCTTCTTACTATCTTAATAAAACAGATATTGTG 2752
QY 2675 AGATTCACATAAAAAAGTCTTCTTACTATCTTAAATAAAACAGATATTGTG 2702
Db 2753 AGATTCACATAAAAAAGTCTTCTTACTATCTTAAATAAAACAGATATTGTG 2780

RESULT 5
ADQ24216
ID ADQ24216 standard; DNA; 3651 BP.
XX
AC ADQ24216;
XX
DT 26-AUG-2004 (first entry)
XX
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7036.
XX
KW soft tissue sarcoma; cytoslastic; gene therapy; vaccine; screening; human;
XX
OS Homo sapiens.
XX
PN WO2004048938-A2.
XX
PD 10-JUN-2004.
XX
PF 26-NOV-2003; 2003WO-US038193.
XX
PR 26-NOV-2002; 2002US-0429739P.
XX
PA (PROT-) PROTEIN DESIGN LABS INC.
XX
PI Aziz N, Ginsburg WM, Zlotnick A;
XX
DR WPI; 2004-441208/41.
XX
PT Early detection of soft tissue sarcoma comprises determining expression
PT of a gene in a first soft tissue sample and a normal soft tissue sample
PT and comparing the gene expression, also useful in treating soft tissue
PT sarcoma.
XX
PS Example 2; SEQ ID NO 7036; 210pp; English.
XX

CC The invention relates to a novel method for detecting soft tissue sarcoma
CC which comprises obtaining a first soft tissue sample from an individual
CC and a normal soft tissue sample from the same or different individual,
CC determining the expression of a gene in both samples and comparing the
CC expression of the gene in both soft tissue samples, where a higher level
CC of protein expression in the first soft tissue sample indicates the
CC presence of soft tissue sarcoma. The method of the invention has
CC cytosolic applications and may be useful for detecting soft tissue
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC DNA of the invention. The current sequence is not shown within the
CC specification per se but was submitted in CD format by the inventor.
XX

Sequence 3651 BP; 996 A; 837 C; 769 G; 926 T; 0 U; 123 Other;

Query Match 63.9%; Score 1728.8; DB 12; Length 3651;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 1781; Conservative 0; Mismatches 7; Indels 8; Gaps 4;

QY 912 AATAGAACATCCTAAAGAGATCCAGCAATACGGTTTACTCCACTGTGAAATACCG 971
DB 1752 AAGAGAACATCCTAAAGAGATCCAGCAATACGGTTTACTCCACTGTGAAATACCG 1811
QY 972 AAAAAGATGAAAATCCCACTCACTGCTCAGATGCGACACACCAAGGCTATTGGC 1031
DB 1812 AAAAAGATGAAAATCCCACTCACTGCTCAGATGCGACACACCAAGGCTATTGGC 1871
QY 1032 TATGAGATGTTATCTAGACAGCAGTGCACTCCCTAAGTCTCTGCTCAAAAAAACA 1091
DB 1872 TATGAGATGTTATCTAGACAGCAGTGCACTCCCTAAGTCTCTGCTCAAAAAAACA 1931
QY 1092 ATTCTCGGCCCAAGAAAACAATCAGAAATTCAGTATTGACTAGAAACATCAGGA 1151
DB 1932 ATTCTCGGCCCAAGAAAACAATCAGAAATTCAGTATTGACTAGAAACATCAGGA 1991
QY 1152 AGAATGAAGACGTTGACTTTTCCAGGATTAATATCTGATGCTCTTTAGATTTA 1211
DB 1992 AGAATGAAGACGTTGACTTTTCCAGGATTAATATCTGATGCTCTTTAGATTTA 2051
QY 1212 AGATTCGTAATTCATCCACTGCTGAGAATCTCCTCAACCAGAGGTTTAATCACT 1271
DB 2052 AGATTCATATATTCATCCACTGCTGAGAATCTCCTCAACCAGAGGTTTAATCACT 2111
QY 1272 TCATCCCAAAATGGGATGTGAATGTCAAGCAAAACCAATAAAAAAGTCTTAGAATTT 1331
DB 2112 TCATCCCAAAATGGGATGTGAATGTCAAGCAAAACCAATAAAAAAGTCTTAGAATTT 2171
QY 1332 CCTATGAATGTAAATGCAAGGTCACACATATTATGACAGCCTGTTGATTATGATG 1391
DB 2172 CCTATGAATGTAAATGCAAGGTCACACATATTATGACAGCCTGTTGATTATGATG 2231
QY 1392 GCTCCAGGTCAGTGTCTGAGATTTCATTCATCCCAAGGCTTGATGTCAAGATTATAC 1451
DB 2232 GCTCCAGGTCAGTGTCTGAGATTTCATTCATCCCAAGGCTTGATGTCAAGATTATAC 2291
QY 1452 AAGAGTCTGCTACCAAGGCGCAAGAAGACCAAAACAGACAGCAAGTCCAGCAAGC 1511
DB 2292 AAGAGTCTGCTACCAAGGCGCAAGAAGACCAAAACAGACAGCAAGTCCAGCAAGC 2351
QY 1512 AGATGCACTGACAAAATGGAATGATATTAATTGGCTCTATAAACTATGTGCCAGCACTA 1571
DB 2352 AGATGCACTGACAAAATGGAATGATATTAATTGGCTCTATAAACTATGTGCCAGCACTA 2411
QY 1572 TGCTGAGCTTACACTAATTTGCTCAGACGCTGTCTGCTCATGAAATTTGGCTCCAAT 1631
DB 2412 TGCTGAGCTTACACTAATTTGCTCAGACGCTGTCTGCTCATGAAATTTGGCTCCAAT 2471
QY 1632 GAATGAATCTTTATGAGCAGTGTGACAGGCTGACCAAGATTCCAGAGGCGCAG 1691
DB 2472 GAATGAATCTTTATGAGCAGTGTGACAGGCTGACCAAGATTCCAGAGGCGCAG 2531
QY 1692 GTGTGATCCACAGACTTGAAGGTCAAAGTTCAAAAGATGAAGATCAGGGTAGCTGA 1751

DB 2532 GTGTGATCCACAGACTTGAAGGTCAAAGTTCAAAAGATGAAGATCAGGGTAGCTGA 2591
QY 1752 CCATGTTTGGCAGATACTATAATGAGACACAGAAAGTGCATGCGCCCAAGACAGAAC 1811
DB 2592 CCATGTTTGGCAGATACTATAATGAGACACAGAAAGTGCATGCGCCCAAGACAGAAC 2651
QY 1812 CTCACGAGGCTTCATTTATGCACTTGTGCTGCAAAAAGTCTAGGTTTAAGGCT 1871
DB 2652 CTCACGAGGCTTCATTTATGCACTTGTGCTGCAAAAAGTCTAGGTTTAAGGCT 2711
QY 1872 GTGCCAGAACCCATCCCAATPAAAGAGACCGAGTCTGAAGTCAATTGTAATCTAGTGA 1931
DB 2712 GTGCCAGAACCCATCCCAATPAAAGAGACCGAGTCTGAAGTCAATTGTAATCTAGTGA 2771
QY 1932 GGAGACTTGAGTCAAGCAGTGAGACTGTGGGGACCGGGGGCAGTGGTACTTGTAA 1991
DB 2772 GGAGACTTGAGTCAAGCAGTGAGACTGTGGGGACCGGGGGCAGTGGTACTTGTAA 2831
QY 1992 CCTTTAAAGATGTTAATTCATTCAATAGATATTTAAGAACCCTACTATGCGGCCCG 2051
DB 2832 CCTTTAAAGATGTTAATTCATTCAATAGATATTTAAGAACCCTACTATGCGGCCCG 2888
QY 2052 CATGCTGCTCACACCTGTAATCCAGACCTTTGGAGGCCCAAGGTGGTGGTCACTG 2111
DB 2889 CATGCTGCTCACACCTGTAATCCAGACCTTTGGAGGCCCAAGGTGGTGGTCACTG 2948
QY 2112 AGTCAAGAGTCAAGACCAAGCCTGGCCAACTGGTGAACCCCATCTCTAATAAGAT - 2170
DB 2949 AGTCAAGAGTCAAGACCAAGCCTGGCCAACTGGTGAACCCCATCTCTAATAAGAT - 3008
QY 2171 -CAAAATTTGCTGAGCGTGGTGGTGTGACACTGT -ATCCAGCTACTGAGAGCCCAAG 2228
DB 3009 CAAAATTTGCTGAGCGTGGTGGTGTGACACTGTATATCCAGCTACTGAGAGCCCAAG 3068
QY 2229 CATGAGATCGCTTGAACCTGG -AGTGAAGTTGCAAGTGAAGTGAAGTGAAGTGAAGTGA 2286
DB 3069 CATGAGATCGCTTGAACCTGGAGGTTGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 3128
QY 2287 ACTCCGGCCTAGGCAAGAGACCAAACTCCAAATACAAACAAACAAACCAACTGTGC 2346
DB 3129 ACTCCGGCCTAGGCAAGAGACCAAACTCCAAATACAAACAAACCAACCAACTGTGC 3188
QY 2347 TAGTCAAGTCTGGCAGTAAAGATGAACATCCCTACCAACACAGAGCTCACCATCTTAT 2406
DB 3189 TAGTCAAGTCTGGCAGTAAAGATGAACATCCCTACCAACACAGAGCTCACCATCTTAT 3248
QY 2407 ACTTAAGTGAATAATGAGGGAAGGGAAGGGAATGCTGCTTTGATATGTTCCCTG 2466
DB 3249 ACTTAAGTGAATAATGAGGGAAGGGAAGGGAATGCTGCTTTGATATGTTCCCTG 3308
QY 2467 AGCATATCTTGAATGAGACCTCCCTACCAAGTGAAGAGTGTGAATACTTAATA 2526
DB 3309 ACACATATCTTGAATGAGACCTCCCTACCAAGTGAAGAGTGTGAATACTTAATA 3368
QY 2527 CAATGCTTGTGGCAAGAAATGGGATTAATCTTCTCTCAGAAAGGCAATGTGA 2586
DB 3369 CAATGCTTGTGGCAAGAAATGGGATTAATCTTCTCTCAGAAAGGCAATGTGA 3428
QY 2587 AGGAATTGAGCCAGATCTCTCCCTACTGCAAAACCCTATTGTAGTAAAGAGTCTTCT 2646
DB 3429 AGGAATTGAGCCAGATCTCTCCCTACTGCAAAACCCTATTGTAGTAAAGAGTCTTCT 3488
QY 2647 TTAATCTTTAATAAAGAGATATTGTGAGATTCAATATAAAAAAAGTCTTCT 2702
DB 3489 TTAATCTTTAATAAAGAGATATTGTGAGATTCAATATAAAAAAAGTCTTCT 3544

RESULT 6
AAK00615
ID AAK00615 standard; DNA; 1412 BP.
XX
AC AAK00615;

XX 25-MAR-1999 (first entry)
DT
XX
DE Human secreted protein gene 5 clone HASAV70.
XX
KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS Homo sapiens.
XX
PN WO9842738-A1.
XX
PD 01-OCT-1998.
XX
PF 19-MAR-1998; 98WO-US005311.
XX
PR 21-MAR-1997; 97US-0041276P.
PR 21-MAR-1997; 97US-0041277P.
PR 21-MAR-1997; 97US-0041281P.
PR 21-MAR-1997; 97US-0042344P.
PR 30-MAY-1997; 97US-0048069P.
PR 30-MAY-1997; 97US-0048094P.
PR 30-MAY-1997; 97US-0048095P.
PR 30-MAY-1997; 97US-0048096P.
PR 30-MAY-1997; 97US-0048099P.
PR 30-MAY-1997; 97US-0048131P.
PR 30-MAY-1997; 97US-0048135P.
PR 30-MAY-1997; 97US-0048154P.
PR 30-MAY-1997; 97US-0048160P.
PR 30-MAY-1997; 97US-0048186P.
PR 30-MAY-1997; 97US-0048187P.
PR 30-MAY-1997; 97US-0048188P.
PR 30-MAY-1997; 97US-0048351P.
PR 30-MAY-1997; 97US-0048352P.
PR 30-MAY-1997; 97US-0048355P.
PR 30-MAY-1997; 97US-0050937P.
PR 05-AUG-1997; 97US-0054804P.
PR 19-AUG-1997; 97US-0056370P.
PR 02-OCT-1997; 97US-0060862P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Young P, Greene JM, Ferrie AM, Ruben SM, Rosen CA, Duan R, Hu J;
PI Florence KA, Olsen HS, Ebner R, Brewer LA, Moore PA, Shi Y;
PI Lafleur DW, Ni J;
XX
XX WPI; 1999-070066/06.
DR P-PSDB; AAW67811.
XX
PT New isolated human genes and the secreted polypeptides they encode -
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders.
XX
XX
PS Claim 1; Page 171-172; 385pp; English.
XX
CC This sequence represents a nucleic acid molecule which encodes a secreted
CC human protein. The gene number, and the clone it is derived from, are
CC detailed in the descriptor line. The gene can be used to generate fusion
CC proteins by linking to the gene to a human immunoglobulin Fc portion
CC (e.g. AAX00602) for increasing the stability of the fused protein as
CC compared to the human protein only. The invention of the relates to 87 novel
CC genes and their fragments (nucleic acid sequences: AAX00611-X00724; amino
CC acid sequences AAW67807-W68004) which are useful for preventing, treating
CC or ameliorating medical conditions e.g. by protein or gene therapy. Also,
CC pathological conditions can be diagnosed by determining the amount of the
CC new polypeptides in a sample or by determining the presence of mutations
CC in the new polynucleotides. Specific uses are described for each of the

CC 87 polynucleotides, based on which tissues they are most highly expressed
CC in (see AAX00611 for described uses)
XX
SQ Sequence 1412 BP; 439 A; 310 C; 310 G; 348 T; 0 U; 5 Other;

Query Match 50.6%; Score 1369.4; DB 2; Length 1412;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1384; Conservative 2; Mismatches 11; Indels 1; Gaps 1;

QY 616 CCTTCATCTGCGTTGCCAGGAAACCCTGTCAAGCAGAAACTTCTCAAGCCCCCATCTTGCCA 675
DB 2 CCTTCATCTGCGTTGCCAGGAAACCCTGTCAAGCAGAAACTTCTCAAGCCCCCATCTTGCCA 61

QY 676 GGAAGCTCTGTGAAGGTGCTGATGACCCAGATTCTTCATGGTCTCCTGTGTCTCC 735
DB 62 GGAAGCTCTGTGAAGGTGCTGATGACCCAGATTCTTCATGGTCTCCTGTGTCTCC 121

QY 736 TGTGTGCCCCCTCTGCTCACTCTTTGTACTGGGCTATTCTTGTGTTCTGAAGA 795
DB 122 TGTGTGCCCCCTCTGCTCACTCTTTGTACTGGGCTATTCTTGTGTTCTGAAGA 181

QY 796 GAGAGACAAGAAGATACATGAAGAAGAAGAAGATGACATTTGTCGGAATCTC 855
DB 182 GAGAGACAAGAAGATACATGAAGAAGAAGAAGATGACATTTGTCGGAATCTC 241

QY 856 CTACATATGCCCCCATTTCTGAGAGAAACACAGAGTACGACAAATCCCTCACACTAATA 915
DB 242 CTACATATGCCCCCATTTCTGAGAGAAACACAGAGTACGACAAATCCCTCACACTAATA 301

QY 916 GAACATCTCTAAAGGAAGATCCAGCAAAATACGGTTTACTCTCACTGTGAAATACCGAAA 975
DB 302 GAACATCTCTAAAGGAAGATCCAGCAAAATACGGTTTACTCTCACTGTGAAATACCGAAA 361

QY 976 AGATGAAAAATCCCCACTCACTGCTCAAGATGCCAGACACCAAGGCTATTGGCCTATG 1035
DB 362 AGATGAAAAATCCCCACTCACTGCTCAAGATGCCAGACACCAAGGCTATTGGCCTATG 421

QY 1036 AGAATGTTATCTAGACAGACAGTCACTCCCCCTAAGTCTCTGCTCAAAAAAACAATTC 1095
DB 422 AGAATGTTATCTAGACAGACAGTCACTCCCCCTAAGTCTCTGCTCAAAAAAACAATTC 481

QY 1096 TCGGCCCAAGAAAAACAATCAGAAATTCACGTATTGACTAGAACAACATCAAGAGAAG 1155
DB 482 TCGGCCCAAGAAAAACAATCAGAAATTCACGTATTGACTAGAACAACATCAAGAGAAG 541

QY 1156 TGAAGAACGTTGACTTTTTCAGAGATAAATTATCTTGATGCTTCTTAGATTAAAG 1215
DB 542 TGAAGAACGTTGACTTTTTCAGAGATAAATTATCTTGATGCTTCTTAGATTAAAG 601

QY 1216 TTCGTAATTCATCCACTGCTGAGAAATCTCCTCAAAACCAGAAAGTTAATCACTTCAT 1275
DB 602 TTCGTAATTCATCCACTGCTGAGAAATCTCCTCAAAACCAGAAAGTTAATCACTTCAT 661

QY 1276 CCCAAAAATGGATTGTGAATGTCAAGCAAAACCATAAAAAAGTCTTAGAAGTATTCCTA 1335
DB 662 CCCAAAAATGGATTGTGAATGTCAAGCAAAACCATAAAAAAGTCTTAGAAGTATTCCTA 721

QY 1336 TAGAAATGTAATGCAAGGTCAACATATTAATGACAGCCTGTGTATTAATGATGGCTC 1395
DB 722 TAGAAATGTAATGCAAGGTCAACATATTAATGACAGCCTGTGTATTAATGATGGCTC 781

QY 1396 CAGGTCAAGTCTGAGTTTCAATTCATCCAGGGCTTGATGTCAGGATTATACCAAGA 1455
DB 782 CAGGTCAAGTCTGAGTTTCAATTCATCCAGGGCTTGATGTCAGGATTATACCAAGA 841

QY 1456 GTCTTGCTACAGAGGGCAAGAACCAAAACAGACAGCAAGTCCAGCAGAGCAGAT 1515
DB 842 GTCTTGCTACAGAGGGCAAGAACCAAAACAGACAGCAAGTCCAGCAGAGCAGAT 901

QY 1516 GCACCTGACAAAAATGATGTAATTAATGGCTCTATAAACTATGTGCCAGCACTATGCT 1575
DB 902 GCACCTGACAAAAATGATGTAATTAATGGCTCTATAAACTATGTGCCAGCACTATGCT 961

QY	1576	GAGCTTACACTAATTGGTCAGACGTGCTGTCTGCCCCCTCATGAAAATTGGCTCCAAATGAAT	1635
			:
Db	962	GAGCTTACACTAATTGGTCAGACATGCTGTCTGCCCCCTCATGAAAATTGGCTCCAAATGAMT	1021
QY	1636	GAACCTACTTTCATGAGCAGCTGTGTAGCAGGCCCTGACCACAGATTCACAGAGGGCCAGGTGT	1695
Db	1022	GAACCTACTTTCATGAGCAGCTGTGTAGCAGGCCCTGACCACAGATTCACAGAGGGCCAGGTGT	1081
QY	1696	GGATCCACAGAGCTTGAAGCTCAAAGTTCACAAAGATGAAGAAATCAGGGTAGCTGACCAT	1755
Db	1082	GGATCCACAGAGCTTGAAGCTCAAAGTTCACAAAGATGAAGAAATCAGGGTAGCTGACCAT	1141
QY	1756	GTTTGGCAGATACTATATATGGAGACACAGAAGTGTGATGGCCCAAGACAAAGACCTCC	1815
Db	1142	GTTTGGCAGATACTATATATGGAGACACAGAAGTGTGATGGCCCAAGACAAAGACCTCC	1201
QY	1816	AGCCAGGCTTCATTTATGCACTTGTGCTGCAAAAGAAAGTCTAGGTTTAAAGCTGTGC	1875
Db	1202	AGCCAGGCTTCATTTATGCACTTGT - CTGCAAAAGAAAGTCTAGGTTTAAAGCTGTGC	1260
QY	1876	CAGAACCATCCCAATATAAGAGACCGAGTCTGAAGTCAATGTAAATCTAGTGTAGAG	1935
Db	1261	CAGAACCATCCCAATATAAGAGACCGAGTCTGAAGTCAATGTAAATCTAGTGTAGAG	1320
QY	1936	ACTTGAGTCAGGCAGTGTGACTGTGTTGGGACACGGGGGGCAGTGGGTACTTGTAAACCTT	1995
Db	1321	ACTTGAGTCAGGCAGTGTGACTGTGTTGGGACACGGGGGGCANTGGGTANTGTAAACCTTT	1380
QY	1996	TAAAGATGTTAATTCAT 2013	
Db	1381	TAAAGATGTTAATTCAT 1398	

RESULT	7
AAC55224	
ID	AAC55224 standard; cDNA; 1412 BP.
XX	
AC	AAC55224;
XX	
DT	16-JAN-2001 (first entry)
XX	
DE	Human secreted protein gene 3 SEQ ID NO:45.
XX	
KW	Human; secreted protein; cytostatic; immunostimulant; antiproliferative;
KW	cardiant; antiarrhythmic; antiviral; antibacterial; antifungal; cancer;
KW	antiparasitic; neuroprotective; nootropic; antiinflammatory; anti-HIV;
KW	antiangiogenic; arteriosclerotic; diagnosis; immune disorder; AIDS;
KW	autoimmune disease; haematopoietic cell disorder; blood protein disorder;
KW	agamaglobulinaemia; hyperproliferative disease; Gaucher's disease;
KW	cardiovascular disorder; congenital heart defect; pulmonary atresia;
KW	arhythmia; ischaemia; angiogenesis related disorder; Crohn's disease;
KW	atherosclerosis; neurological disease; Alzheimer's disease; Huntington's;
KW	infectious disease; cat-scratch disease; chromosome 1; ss.
XX	
OS	Homo sapiens.
PN	WO200047602-A1.
XX	
PD	17-AUG-2000.
XX	
PF	08-FEB-2000; 2000WO-US003062.
XX	
PR	10-FEB-1999; 99US-0119468P.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
PI	Rosen CA, Ruben SM, Ebner R, Young PE, Ni J, Soppet DR;
PI	Moore PA, Shi Y, Lafleur DW, Olsen HS, Florence KA, Komatrboulis G;
XX	
DR	WPI; 2000-543578/49.
XX	P-PSDB; AAB32405.
PT	New human nucleic acids encoding secreted proteins, useful in the

PT treatment, prevention or diagnosis of immune disorders (e.g. autoimmune PT diseases), blood protein disorders and hyperproliferative diseases (e.g. PT Gaucher's disease).

PS Claim 1; Page 413; 488pp; English..

CC The polynucleotide sequences given in AAC55190 to AAC55235 encode the
CC human secreted proteins given in AAB32371 to AAB32484. Human secreted
CC proteins have activities based on the tissues and cells the genes are
CC expressed in. Examples of activities include: cytostatic; immunostimulant
CC ; antiproliferative; cardiac; antiarrhythmic; antiviral; antibacterial;
CC antifungal; antiparasitic; neuroprotective; nootropic; antiinflammatory;
CC antiangiogenic; anti-HIV; and antiarteriosclerotic. The polynucleotides
CC and polypeptides, or their agonists and antagonists, can be used for
CC treating, preventing or diagnosing immune disorders (e.g. cancer,
CC autoimmune diseases), disorders of haematopoietic cells, blood protein
CC disorders (e.g. agammaglobulinaemia), hyperproliferative diseases (e.g.
CC Gaucher's disease), cardiovascular disorders (e.g. congenital heart
CC defects, pulmonary atresia, arrhythmias, ischaemia), angiogenesis related
CC disorders (e.g. Crohn's disease, atherosclerosis), neurological diseases
CC (e.g. Alzheimer's disease, Huntington's chorea), infectious diseases
CC (e.g. AIDS, cat-scratch disease and other bacterial, viral, parasitic or
CC fungal diseases). AAC55181 to AAC55189 and AAB32370 represent sequences
CC used in the exemplification of the present invention

SQ Sequence 1412 BP; 439 A; 310 C; 310 G; 348 T; 0 U; 5 Other;

Query Match 50.6%; Score 1369.4; DB 3; Length 1412;

Matches 1384; Conservative 2; Mismatches 11; Indels 1; Gaps 1;

[illegible]

Oy	676	GGAA	CTCT	GTGA	AGGT	CTCT	GTAT	GA	TGAC	CCAG	ATTCC	TCCAT	GGT	CCTC	CTGT	GTCT	CC	735
Db	62	GGAA	CTCT	GTGA	AGGT	CTCT	GTAT	GA	TGAC	CCAG	ATTCC	TCCAT	GGT	CCTC	CTGT	GTCT	CC	121

[illegible][illegible]

Qy	856	CTAACATATGCCCCCATTTCTGGAGAAACAAGAGTACGACACAAATCCCTCACACTAATA	915
Db	242	CTAACATATGCCCCCATTTCTGGAGAGAACACAGAGTACGACACAAATCCCTCACACTAATA	301

[illegible]

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Qy      976 AGATGAAATCCCCACTCATCTGCTCAGATGCCAGACACACCAGGCTATTGGCTATG 103
          |||||
Db      362 AGATGAAATCCCCACTCATCTGCTCAGATGCCAGACACACCAGGCTATTGGCTATG 421

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Oy	1036	AGAATGTTATCTAGACAGCAGTGCCTCCCCTAAGTCCTGCTCAAAAAAAAAA	CAATTTC	109
Db	422	AGAATGTTATCTAGACAGCAGTGCCTCCCCTAAGTCCTGCTCAAAAAAAAAA	CAATTTC	481

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Qy      1096 TCGGCCCCAAGAAAACAATCAGAGAATTCACTGATTGACTAGAAACATCAAGGAGAA 115
          |||||
Db      482 TCGGCCCCAAGAAAACAATCAGAGAATTCACTGATTGACTAGAAACATCAAGGAGAA 541

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Oy      1156 TGAAGAACGTGACTTTTTCACGATAAATTATCTCTGATGCTTCTTTAGATTTAAGAG 121
        |||||
Db      542 TGAAGAACGTGACTTTTTCACGATAAATTATCTCTGATGCTTCTTTAGATTTAAGAG 601

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QY 1216 TTGTAATTCACCTCCACTGCTGAGAAATCTCCTCAAAACCAGAAAGTTTAATCACTTCAT 1227

Db 602 TTCATAATTCATCCACTGCTGAGAAATCTCTCAAAACCAGAGGTTTAATCACTTCAT 661
QY 1276 CCCAAAAATGGGATTGTGAATGTCAGCAAAACCATAAAAAAGTCTTAGAAGTATTCCTA 1335
Db 662 CCCAAAAATGGGATTGTGAATGTCAGCAAAACCATAAAAAAGTCTTAGAAGTATTCCTA 721
QY 1336 TAGAAATGTAATGCAAGGTCACACATATTAATGACAGCCCTGTTGATTAATGATGGCTC 1395
Db 722 TAAAAATGTAATGCAAGGTCACACATATTAATGACAGCCCTGTTGATTAATGATGGCTC 781
QY 1396 CAGGTCAAGTGTCTGAGGTTTCATCCATCCAGGGCTTGATGTGAGGATTATACCAAGA 1455
Db 782 CAGGTCAAGTGTCTGAGGTTTCATCCATCCAGGGCTTGATGTGAGGATTATACCAAGA 841
QY 1456 GTCTTGCTACAGAGGGCAAGAGCCAAAAACAGACAGACAAGTCCAGCAGAGAGAGAT 1515
Db 842 GTCTTGCTACAGAGGGCAAGAGCCAAAAACAGACAGACAAGTCCAGCAGAGAGAGAT 901
QY 1516 GCACCTGACAAAAATGGATGTATTAATTGGCTCTATAAACTATGTGCCACAGAYTATGCT 1575
Db 902 GCACCTGACAAAAATGGATGTATTAATTGGCTCTATAAACTATGTGCCACAGAYTATGCT 961
QY 1576 GAGCTTACATAATTGTCAGACGTCGTCTGCCCTCATGAAATGGCTCCAAATGAAT 1635
Db 962 GAGCTTACATAATTGTCAGACATGCTGTCTGCCCTCATGAAATGGCTCCAAATGAAT 1021
QY 1636 GAACTACTTTCATGAGCAGTTGTAGCAGGCTTGACCACAGATTCAGAGGGCCAGGTGT 1695
Db 1022 GAACTACTTTCATGAGCAGTTGTAGCAGGCTTGACCACAGATTCAGAGGGCCAGGTGT 1081
QY 1696 GGATCCACAGAGCTTGAAGGTCAAAGTTCACAAAAGATGAAGAAATCAGGGTAGCTGACCAT 1755
Db 1082 GGATCCACAGAGCTTGAAGGTCAAAGTTCACAAAAGATGAAGAAATCAGGGTAGCTGACCAT 1141
QY 1756 GTTTGGCAGATACTATATGAGACACAGAAGTGTGCATGGCCCAAGACAAGACCTCC 1815
Db 1142 GTTTGGCAGATACTATATGAGACACAGAAGTGTGCATGGCCCAAGACAAGACCTCC 1201
QY 1816 AGCCAGGCTTCATTATGACACTTGTGTGCAAAAAGAAAGTCTAGGTTTAAAGGCTGTGC 1875
Db 1202 AGCCAGGCTTCATTATGACACTTGT-CTGCAAAAAGAAAGTCTAGGTTTAAAGGCTGTGC 1260
QY 1876 CAGAACCCATCCCAATAAAGAGACCGAGTCTGAAGTCACATTGTAATCTAGTGTAGAG 1935
Db 1261 CAGAACCCATCCCAATAAAGAGACCGAGTCTGAAGTCACATTGTAATCTAGTGTAGAG 1320
QY 1936 ACTTGAAGTCAGGCAGTGAGACTGTGTGGGGCACGGGGGCAGTGGGTACTTGTAAACCTT 1995
Db 1321 ACTTGAAGTCAGGCAGTGAGACTGTGTGGGGCACGGGGGCAGTGGGTANTGTAAACCTTT 1380
QY 1996 TAAAGATGGTTAATTCAT 2013
Db 1381 TAAAGATGGTTAATTCAT 1398

RESULT 8
ADA40261
ID ADA40261 standard; cDNA; 1412 BP.

XX ADA40261;
XX 20-NOV-2003 (first entry)
DE Human secreted protein encoding cDNA.
XX
KW Human; secreted protein; cancer; hyperproliferative disorder;
KW rheumatoid arthritis; autoimmune disorder; haematopoietic disorder;
KW anaemia; allergic reaction; asthma; cardiovascular disorder;
KW wound healing; cytostatic; immunosuppressive; nootropic; neuroprotective;
KW antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory;
KW vulnerary; cardiant; gene therapy; ss.
XX
OS Homo sapiens.

XX WO2002102993-A2.
PN
XX 27-DEC-2002.
PD
XX
XX 19-MAR-2002; 2002WO-US008123.
PF
XX 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PI Rosen CA, Ruben SM;
XX
XX WPI; 2003-175238/17.
DR
XX
XX
PT New human secreted proteins and nucleic acid molecules, useful for
PT preparing a diagnostic or pharmaceutical composition for diagnosing,
PT preventing or treating cancer or other hyperproliferative disorder,
PT asthma, allergies or AIDS.
XX
XX
PS Claim 9; SEQ ID NO 643; 3205bp; English.

XX The invention relates to novel genes ADA39629-ADA40565 and proteins
XX ADA40566-ADA41501 for human secreted proteins, useful for preventing,
CC treating or ameliorating medical conditions e.g. by protein or gene
CC therapy. The polypeptides, nucleic acid molecules, antibodies or their
CC fragments, and agonists or antagonists that bind to the polypeptide are
CC useful for preparing a diagnostic or pharmaceutical composition for
CC diagnosing or treating cancer or other hyperproliferative disorder. The
CC polypeptides and nucleic acid molecules are also useful for detecting,
CC preventing, diagnosing, prognosticating, treating or ameliorating cancer
CC or other hyperproliferative disorders including neoplasms, autoimmune
CC disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus
CC erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic
CC anaemia), haematopoietic or haematological disorders (e.g. anaemia,
CC thrombocytopenia), allergic reactions including asthma or eczema,
CC inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory
CC bowel disease or Crohn's disease), neurodegenerative disorders (e.g.
CC Alzheimer's disease or Parkinson's disease), cardiovascular disorders
CC (e.g. atherosclerosis, myocarditis), infectious diseases (bacterial,
CC fungal or viral infections including HIV/AIDS), or wound healing and
CC disorders of epithelial cell proliferation. The nucleic acids are also
CC useful for chromosome identification, radiation hybrid mapping or long-
CC range restriction mapping, as molecular weight markers, or as
CC hybridization or diagnostic probes. The polypeptides and antibodies are
CC useful for providing immunological probes for differential identification
CC of the tissues immunohistochemistry assays. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_jct_sequences.
XX
SQ Sequence 1412 BP; 439 A; 310 C; 310 G; 348 T; 0 U; 5 Other;

Query Match 50.6%; Score 1369.4; DB 8; Length 1412;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1384; Conservative 2; Mismatches 11; Indels 1; Gaps 1;

QY 616 CCTTCATCTGCGTGGCCAGGAACCCCTGTCAAGAGAACTTCTCAAGCCCCCATCTTGCA 675
Db 2 CCTTCATCTGCGTGGCCAGGAACCCCTGTCAAGAGAACTTCTCAAGCCCCCATCTTGCA 61
QY 676 GGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCCTCCATGGTCTCTGTGTCTCC 735
Db 62 GGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCCTCCATGGTCTCTGTGTCTCC 121
QY 736 TGTGTGCCCCCTCTGCTCAGTCTCTTGTACTGGGGCTATTCTTGTGGTTCTGAAGA 795
Db 122 TGTGTGCCCCCTCTGCTCAGTCTCTTGTACTGGGGCTATTCTTGTGGTTCTGAAGA 181
QY 796 GAGAGAGACAAGAAGATCATTTGAAGAGAAGAAGAGAGTGAACATTTGTGGGAAACTC 855

Db 182 GAGAGAGACAAGAGTACATTGAAGAGAAGAGAGTGACATTGTGCGGAAACTC 241
QY 856 CTAACATATGCCCCATTCTGGAGAGAACACAGAGTACGACAAATCCCTCAGACTAATA 915
Db 242 CTAACATATGCCCCATTCTGGAGAGAACACAGAGTACGACAAATCCCTCAGACTAATA 301
QY 916 GAACAATCCTAAAGAGATCCAGCAATACGGTTTACTCCACTGTGGAATACCGAAA 975
Db 302 GAACAATCCTAAAGAGATCCAGCAATACGGTTTACTCCACTGTGGAATACCGAAA 361
QY 976 AGATGAAAAATCCCCACTCACTGCTCAGATGCCAGACACACCAAGGCTATTGGCTATG 1035
Db 362 AGATGAAAAATCCCCACTCACTGCTCAGATGCCAGACACACCAAGGCTATTGGCTATG 421
QY 1036 AGAATGTTATCTAGACAGAGTGCACTCCCCCTAAGTCTGCTCAAAAAAACAATTC 1095
Db 422 AGAATGTTATCTAGACAGAGTGCACTCCCCCTAAGTCTGCTCAAAAAAACAATTC 481
QY 1096 TCGGCCCAAGAAAAACAATCAGAAAGATTCACTGATTGACTAGAAACATCAAGAGAA 1155
Db 482 TCGGCCCAAGAAAAACAATCAGAAAGATTCACTGATTGACTAGAAACATCAAGAGAA 541
QY 1156 TGAAGACGTTGACTTTTCCAGATAAATTATCTGATGCTCTTTAGATTAAAG 1215
Db 542 TGAAGACGTTGACTTTTCCAGATAAATTATCTGATGCTCTTTAGATTAAAG 601
QY 1216 TTCGTAATCCACTGCTGAGAAATCTCCTCAAAACCAGAGGTTTAATCACTTCAT 1275
Db 602 TTCATTAATCCACTGCTGAGAAATCTCCTCAAAACCAGAGGTTTAATCACTTCAT 661
QY 1276 CCCAAAAATGGGATTGGAATGTCAGCAAAACATAAAAAGTGCTTAGAATTCCTA 1335
Db 662 CCCAAAAATGGGATTGGAATGTCAGCAAAACATAAAAAGTGCTTAGAATTCCTA 721
QY 1336 TAGAATGTAAATGCAAGSTCACACATATTAAATGACAGCTGTGTTAATGATGGCTC 1395
Db 722 TAAAAATGTAAATGCAAGSTCACACATATTAAATGACAGCTGTGTTAATGATGGCTC 781
QY 1396 CAGGTCAGTGCTGGAGTTTCATTCATCCCAAGGCTTGATGTCAAGATTATCAAGA 1455
Db 782 CAGGTCAGTGCTGGAGTTTCATTCATCCCAAGGCTTGATGTCAAGATTATCAAGA 841
QY 1456 GTCTTGCTACGAGAGGGCAAGAACCAAAACAGACAGCAAGTCCAGCAAGACAGAT 1515
Db 842 GTCTTGCTACGAGAGGGCAAGAACCAAAACAGACAGCAAGTCCAGCAAGACAGAT 901
QY 1516 GCACCTGACAAAAATGATGTATTAAATGGCTCTATAAATATGTGCCAGCACTATGCT 1575
Db 902 GCACCTGACAAAAATGATGTATTAAATGGCTCTATAAATATGTGCCAGCACTATGCT 961
QY 1576 GAGCTTACACTAATGGTCAGACGTGCTGTGCTCATGAATGGCTCCAAATGAAT 1635
Db 962 GAGCTTACACTAATGGTCAGACGTGCTGTGCTCATGAATGGCTCCAAATGAAT 1021
QY 1636 GAACTACTTTCATGACAGTTGTAGCAGGCTGACACAGATTCCAGAGGCGCAGGTGT 1695
Db 1022 GAACTACTTTCATGACAGTTGTAGCAGGCTGACACAGATTCCAGAGGCGCAGGTGT 1081
QY 1696 GGATCCACAGACTTGAAGGTCAAAGTTCACAAAGATGAAGAATCAGGGTAGTCAACAT 1755
Db 1082 GGATCCACAGACTTGAAGGTCAAAGTTCACAAAGATGAAGAATCAGGGTAGTCAACAT 1141
QY 1756 GTTTGGCAGATACTATAATGAGACACAGAAAGTGTGATGGCCCAAGGACAGACCTCC 1815
Db 1142 GTTTGGCAGATACTATAATGAGACACAGAAAGTGTGATGGCCCAAGGACAGACCTCC 1201
QY 1816 AGCCAGGCTTCATTATGCACTGTGCTGCAAAAAGAAAGTCTAGGTTTAAAGCTGTGC 1875
Db 1202 AGCCAGGCTTCATTATGCACTTGT-CTGCAAAAAGAAAGTCTAGGTTTAAAGCTGTGC 1260
QY 1876 CAGAACCCATCCCAATAAAGAGACCGAGTCTGAAGTCAATGTAAATCTAGTGAAGAG 1935
Db 1261 CAGAACCCATCCCAATAAAGAGACCGAGTCTGAAGTCAATGTAAATCTAGTGAAGAG 1320

QY 1936 ACTTGAGTCAGGACGTGAGACTGTGGGGCAGCGGGGCGAGTGGGTACTGTAAACCTT 1995
Db 1321 ACTTGAGTCAGGACGTGAGACTGTGGGGCAGCGGGGCGAGTGGGTAANTGTAAACCTT 1380
QY 1996 TAAAGATGTTAATTCAT 2013
Db 1381 TAAAGATGTTAATTCAT 1398
RESULT 9
ADA56425
ID ADA56425 standard; DNA; 1412 BP.
XX
AC ADA56425;
XX
DT 20-NOV-2003 (first entry)
XX
DE Gene encoding human secreted protein #32.
XX
KW immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;
KW cytosolic; cerebroprotective; neuroprotective; nootropic;
KW cardiovascular; antiarteriosclerotic; gene therapy;
KW human secreted protein; immune disorder; inflammation;
KW respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;
KW inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;
KW multiple sclerosis; ischaemic brain injury; Parkinson's disease;
KW Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;
KW triple helix formation; antisense gene therapy; forensic biology; ds;
KW gene.
XX
OS Homo sapiens.
XX
XX WO2002102994-A2.
PN
XX
PD 27-DEC-2002.
XX
PF 19-MAR-2002; 2002WO-US008278.
XX
PR 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
XX WPI: 2003-167512/16.
DR P-PSDB; ADA57321.
XX
XX
XX
PT New human secreted polypeptides and polynucleotides, useful for
PT diagnosing, treating or preventing e.g. immune disorders, inflammatory
PT conditions, respiratory disorders, cancers, CNS disorders, or
PT neurodegenerative disorders.
XX
PS Claim 21; SEQ ID NO 614; 1754bp; English.
XX
XX The invention relates to 592 new human secreted polypeptides useful for
XX diagnosing, treating or preventing e.g. immune disorders, inflammatory
XX conditions, respiratory disorders, cancers, CNS disorders, or
XX neurodegenerative disorders, or polypeptides comprising an amino acid
XX sequence at least 95% identical to the new sequences. The polypeptides,
XX antibodies or antibody fragments that bind to the polypeptides, nucleic
XX acids encoding the polypeptides, agonists or antagonists that binds to
XX the polypeptide, are useful in preparing diagnostic or pharmaceutical
XX compositions for diagnosing, treating or preventing an e.g. immune
XX disorders, inflammatory conditions (e.g. inflammatory bowel disease,
XX nephritis or Crohn's disease), respiratory disorders (e.g. asthma and
XX allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders
XX (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative
XX disorders (e.g. Parkinson's disease or Alzheimer's disease), and
XX cardiovascular disorders (e.g. atherosclerosis or myocarditis). The
XX polynucleotides are useful for chromosome identification, chromosome

CC mapping, for controlling gene expression through triple helix formation
CC or antisense DNA or RNA, in gene therapy, for identifying individuals
CC from minute biological samples, in forensic biology, and as hybridization
CC probes. The polypeptides are useful for as molecular weight markers on
CC sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)
CC gels, to raise antibodies, for testing biological activities, and for
CC treating or preventing neural disorders, immune system disorders,
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
CC renal, proliferative and/or cancerous diseases. This sequence corresponds
CC to a gene encoding one of the polypeptide of the invention. Note: The
CC sequence data for this patent did form part of the printed specification,
CC but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX

Sequence 1412 BP; 439 A; 310 C; 310 G; 348 T; 0 U; 5 Other;

Query Match 50.6%; Score 1369.4; DB 10; Length 1412;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1384; Conservative 2; Mismatches 11; Indels 1; Gaps 1;

QY 616 CCTTCATCTGCGTTGCCAGAACCCCTGTACAGAAACTTCTCAAGCCCCATCCTTGCCA 675
DB 2 CCTTCATCTGCGTTGCCAGAACCCCTGTACAGAAACTTCTCAAGCCCCATCCTTGCCA 61
QY 676 GGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCATGCTCTCTGTCTCC 735
DB 62 GGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCATGCTCTCTGTCTCC 121
QY 736 TGTGTGCCCCCTCTCTGCTCAGTCTCTTGTACTGGGGCTATTCTTTGGTTTCTGAAGA 795
DB 122 TGTGTGCCCCCTCTCTGCTCAGTCTCTTGTACTGGGGCTATTCTTTGGTTTCTGAAGA 181
QY 796 GAGAGAGACAAGAGAGTACATTGAAGAAGAAGAGAGTGAACATTTGTCGGAAATC 855
DB 182 GAGAGAGACAAGAGAGTACATTGAAGAAGAAGAGAGTGAACATTTGTCGGAAATC 241
QY 856 CTAACATATGCCCCCATTTCTGGAGAGAACACAGAGTACGACACATCCCTCACACTAATA 915
DB 242 CTAACATATGCCCCCATTTCTGGAGAGAACACAGAGTACGACACATCCCTCACACTAATA 301
QY 916 GAACAATCTTAAAGGAAGATCCAGCAATAACGGTTTACTCCACTGTGAAATACCGAAA 975
DB 302 GAACAATCTTAAAGGAAGATCCAGCAATAACGGTTTACTCCACTGTGAAATACCGAAA 361
QY 976 AGATGAAAAATCCCACTCACTGCTACGATGCCAGACACACCAAGCTATTGCGCTATG 1035
DB 362 AGATGAAAAATCCCACTCACTGCTACGATGCCAGACACACCAAGCTATTGCGCTATG 421
QY 1036 AGAATGTATCTAGACAGCAGTGCATCCCTAAGTCTCTGCTCAAAAAAACAATTC 1095
DB 422 AGAATGTATCTAGACAGCAGTGCATCCCTAAGTCTCTGCTCAAAAAAACAATTC 481
QY 1096 TCGGCCCAAGAAAAACATCAGAGAATTCACCTGATTGACTAGAAAATCAAGAGAA 1155
DB 482 TCGGCCCAAGAAAAACATCAGAGAATTCACCTGATTGACTAGAAAATCAAGAGAA 541
QY 1156 TGAAGAACGTGACTTTTTCAGAGATAATTAATCTCTGATGCTTTTGAATTAAAGAG 1215
DB 542 TGAAGAACGTGACTTTTTCAGAGATAATTAATCTCTGATGCTTTTGAATTAAAGAG 601
QY 1216 TTCGTAATTCATCCACTGCTGAGAAATCTCTCAAAACCAGAAAGTTTAATCACTTCAT 1275
DB 602 TTCATTAATTCATCCACTGCTGAGAAATCTCTCAAAACCAGAAAGTTTAATCACTTCAT 661
QY 1276 CCCAAAAATGGGATTGTGAATGTACAGAAACATAAAAAAGTCTTAGAAGTATTCCTA 1335
DB 662 CCCAAAAATGGGATTGTGAATGTACAGAAACATAAAAAAGTCTTAGAAGTATTCCTA 721
QY 1336 TAGAAATGTAAATGCAAGGTCAACATATTAATGACAGCCTGTGTATTAATGATGGCTC 1395
DB 722 TAAAAATGTAAATGCAAGGTCAACATATTAATGACAGCCTGTGTATTAATGATGGCTC 781
QY 1396 CAGGTCAGTCTGTGAGTTTCATTCATCCAGGGCTTGATGTCAAGATTATACCAAGA 1455

DB 782 CAGGTCAGTCTGTGAGTTTCATTCATCCAGGGCTTGATGTCAAGATTATACCAAGA 841
QY 1456 GTCTTGCTACAGAGGGCAAGAAAGACCAAAACAGACAGCAAGTCCAGCAGAGCAGAT 1515
DB 842 GTCTTGCTACAGAGGGCAAGAAAGACCAAAACAGACAGCAAGTCCAGCAGAGCAGAT 901
QY 1516 GCACTGACAAAAATGATGTATTAATTGGCTCTATAAATATGTGCCAGCACTATGCT 1575
DB 902 GCACGTGACAAAAATGATGTATTAATTGGCTCTATAAATATGTGCCAGCACTATGCT 961
QY 1576 GAGCTTACACTAATTGGTCAACGCTGCTGTCTGCCCTCATGAATTTGGCTCCAAATGAAT 1635
DB 962 GAGCTTACACTAATTGGTCAACATGCTGTCTGCCCTCATGAATTTGGCTCCAAATGAAT 1021
QY 1636 GAACCTACTTTCATGAGCAGTTGTAGCAGGGCTGACCAAGATTTCCAGAGGGCCAGGTGT 1695
DB 1022 GAACCTACTTTCATGAGCAGTTGTAGCAGGGCTGACCAAGATTTCCAGAGGGCCAGGTGT 1081
QY 1696 GGAATCCACAGACTTGAAGTCAAAAGTTCACAAAAGATGAAGATCAGGGTAGCTGACCAT 1755
DB 1082 GGAATCCACAGACTTGAAGTCAAAAGTTCACAAAAGATGAAGATCAGGGTAGCTGACCAT 1141
QY 1756 GTTGGCAGATACTATAATGAGACACAGAAAGTGTGCATGGCCCAAGAGCAAGACCTCC 1815
DB 1142 GTTGGCAGATACTATAATGAGACACAGAAAGTGTGCATGGCCCAAGAGCAAGACCTCC 1201
QY 1816 AGCCAGGCTTCATTTATGCACTGTGCTGCAAAAGAAAGTCTAGGTTTAAAGCTGTGC 1875
DB 1202 AGCCAGGCTTCATTTATGCACTGTGT - CTGCAAAAAGAAAGTCTAGGTTTAAAGCTGTGC 1260
QY 1876 CAGAACCCCATCCCAATAAAGAGACCCGAGTCTGAAGTCAATTTGTAATCTAGTGTAGAG 1935
DB 1261 CAGAACCCCATCCCAATAAAGAGACCCGAGTCTGAAGTCAATTTGTAATCTAGTGTAGAG 1320
QY 1936 ACTTGAAGTCAAGCAGTGAAGTGTGTGGGGCACGGGGCCAGTGGTACTTGTAACTTT 1995
DB 1321 ACTTGAAGTCAAGCAGTGAAGTGTGTGGGGCACGGGGCCAGTGGTANTGTAACTTT 1380
QY 1996 TAAAGATGTTAATTCAT 2013
DB 1381 TAAAGATGTTAATTCAT 1398

RESULT 10
AAZ51572
ID AAZ51572 standard; cDNA; 1272 BP.
XX AAZ51572;
AC
XX
DT 21-JUN-2000 (first entry)
XX
DE Human cell surface immunomodulator-1 (CSIMM-1) encoding cDNA.
XX
KW Cell surface immunomodulator-1; CSIMM-1; cell proliferation; CD84;
KW differentialation; signal transduction; drug screening; prevention;
KW treatment; cancer; leukaemia; melanoma; immune disorder; AIDS;
KW rheumatoid arthritis; asthma; atherosclerosis; diabetes mellitus;
KW emphysema; irritable bowel syndrome; multiple sclerosis; diagnosis;
KW osteoporosis; psoriasis; microbial infections; cytosolic; antiarthritic;
KW antidiabetic; immunosuppressive; antiarteriosclerotic; anti-HIV;
KW antiproliferative; antiinflammatory; neuroprotective; osteopathic;
KW antiproliferative; antimicrobial; human; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 38..1045
FT sig_peptide /product= "Cell surface immunomodulator-1"
FT /tag= a
FT /tag= b
FT mat_peptide 104..1042

FT /*tag= c /product= "Mature cell surface immunomodulator-1"
FT m1ec_binding 542..574
FT /*tag= d /bound_molecy= "Hybridisation probe"
PN MO200011150-A1.
XX
PD 02-MAR-2000.
XX
PF 24-AUG-1999; 99WO-US019386.
XX
PR 25-AUG-1998; 98US-00155261.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Lal P, Corley NC, Gorgone GA, Guegler KJ, Patterson C, Baughn MR;
XX
DR WPI; 2000-246561/21.
DR P-PSDB; AAY70431.
XX
PT New human cell surface immunomodulatory polypeptides and polynucleotides
PT useful for diagnosis, prevention and treatment of cancer and immune
PT disorders.
XX
PS Claim 9, Page 63; 70pp; English.
XX
CC The present sequence is a cDNA identified in Incyte clone 14448, derived
CC from human promonocyte cell line (THP-1) cDNA library (THPLPB01). It
CC encodes human cell surface immunomodulator-1 (CSIMM-1), which is a
CC regulator of cell proliferation, differentiation, cell-cell communication
CC and signal transduction. It shows homology to cell surface antigen, CD84.
CC CSIMM can be used for drug screening, prevention and treatment of cancers
CC such as leukaemia and melanoma, immune disorders such as AIDS, rheumatoid
CC arthritis, asthma, atherosclerosis, diabetes mellitus, emphysema,
CC irritable bowel syndrome, multiple sclerosis, osteoporosis, psoriasis and
CC microbial infections. CSIMM polynucleotide may be used for diagnosis of
CC CSIMM-associated diseases and as source of probes useful in mapping
CC naturally occurring genomic sequences
XX
SQ Sequence 1272 BP; 362 A; 322 C; 285 G; 302 T; 0 U; 1 Other;

Query Match 46.5%; Score 1256.6; DB 3; Length 1272;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 1262; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 5 GTGGCTTCATTTGAGTGGCTGACTTCCAGAGAGCAATATGGCTGTTCCCAACATGCT 64
DB 1 GTGGCTTCATTTGAGTGGCTGACTTCCAGAGAGCAATATGGCTGTTCCCAACATGCT 60

QY 65 CACCCTCATATATCTTTGGAGCTCAGAGGTCAGAGCTCTGAGCCGCGTGAAGA 124
DB 61 CACCCTCATATATCTTTGGAGCTCAGAGGTCAGAGCTCTGAGCCGCGTGAAGA 120

QY 125 GCTGTCGTTCCGTTGGTGGGGCGGTGACTTCCCTGAAAGTCCAAAGTAAAGCAAGT 184
DB 121 GCTGTCGTTCCGTTGGTGGGGCGGTGACTTCCCTGAAAGTCCAAAGTAAAGCAAGT 180

QY 185 TGACTCTATTGTGTGGACCTTCAACACAAACCCCTTTGTCAACCATACAGCCAGAAAGGGGG 244
DB 181 TGACTCTATTGTGTGGACCTTCAACACAAACCCCTTTGTCAACCATACAGCCAGAAAGGGGG 240

QY 245 CACTATCATAGTAGACCCAAATCGTATAGGAGAGTAGACTTCCAGATGAGGCTA 304
DB 241 CACTATCATAGTAGACCCAAATCGTATAGGAGAGTAGACTTCCAGATGAGGCTA 300

QY 305 CTCCCTGAAGCTCAGCAAAGTGAAGAGATGACTCAGGATCTACTATGTGGGATATA 364
DB 301 CTCCCTGAAGCTCAGCAAAGTGAAGAGATGACTCAGGATCTACTATGTGGGATATA 360

QY 365 CAGCTCATCACTCAGAGACCCCTCCAGCCAGAGAGTAGTGTCATGTCTAGACACCT 424
DB 361 CAGCTCATCACTCAGAGACCCCTCCAGCCAGAGAGTAGTGTCATGTCTAGACACCT 420

QY 425 GTCAAGCCTTAAAGTCACCATGGGTCTGCAGAGCAATAGAATGGCACTGTGACCAA 484
DB 421 GTCAAGCCTTAAAGTCACCATGGGTCTGCAGAGCAATAGAATGGCACTGTGACCAA 480

QY 485 TCTGACATGCTGCATGGAACATGGGGAGAGAGATGTGATTATACCTGGAAGGCCCTGGG 544
DB 481 TCTGACATGCTGCATGGAACATGGGGAGAGAGATGTGATTATACCTGGAAGGCCCTGGG 540

QY 545 GCAAGCAGCCATGAGTCCCATTAATGGGTCCATCTCCCATCTCTGAGATGGGAGA 604
DB 541 GCAAGCAGCCATGAGTCCCATTAATGGGTCCATCTCCCATCTCTGAGATGGGAGA 600

QY 605 AAGTATATGACCTTCATCTGCGTTGCCAGAAACCTGTGAGCAGAAACTTCTCAAGCCC 664
DB 601 AAGTATATGACCTTCATCTGCGTTGCCAGAAACCTGTGAGCAGAAACTTCTCAAGCCC 660

QY 665 CATCCTTGCCAGAAAGCTGTGAAAGTGTCTGTATGACCCAGATTCTCCATGTCTCT 724
DB 661 CATCCTTGCCAGAAAGCTGTGAAAGTGTCTGTATGACCCAGATTCTCCATGTCTCT 720

QY 725 CCTGTGTCCTGTGTGGTGGCCCTCTGCTGATCTCTTTGTACTGGGCTATTCTTTG 784
DB 721 CCTGTGTCCTGTGTGGTGGCCCTCTGCTGATCTCTTTGTACTGGGCTATTCTTTG 780

QY 785 GTTCTGAAGAGAGAGACAAAGAGATGATGAAAGAGAAAGAGTGGACATTG 844
DB 781 GTTCTGAAGAGAGAGACAAAGAGATGATGAAAGAGAAAGAGTGGACATTG 840

QY 845 TCGGAAGCTCCTAACATATGCCCCCAATTCTGAGAGAAACACAGATGACACAATCCC 904
DB 841 TCGGAAGCTCCTAACATATGCCCCCAATTCTGAGAGAAACACAGATGACACAATCCC 900

QY 905 TCACACTAATAGAACATCTCTAAGAGAGATCCAGCAATACGGTTACTCCACTGTGGA 964
DB 901 TCACACTAATAGAACATCTCTAAGAGAGATCCAGCAATACGGTTACTCCACTGTGGA 960

QY 965 AATACCGAAGAAATGGAAGATCCCACTCACTGCTCAGATGCCAGACACCAAGGCT 1024
DB 961 AATACCGAAGAAATGGAAGATCCCACTCACTGCTCAGATGCCAGACACCAAGGCT 1020

QY 1025 ATTGCTATGAGAAATGTTATCTAGACAGAGTCACTCCCTAAGTCTGTCTCAAAA 1084
DB 1021 ATTGCTATGAGAAATGTTATCTAGACAGAGTCACTCCCTAAGTCTGTCTCAAAA 1080

QY 1085 AAAAACAATCTCGGCCCAAGAAACAATCAGAAATTCACCTGATTGACTAGAAACA 1144
DB 1081 AAAAACAATCTCGGCCCAAGAAACAATCAGAAATTCACCTGATTGACTAGAAACA 1140

QY 1145 TCAAGGAAGATGAAGACGTGACTTTTCCAGATTAATTAATCTGATGCTTCTT 1204
DB 1141 TCAAGGAAGATGAAGACGTGACTTTTCCAGATTAATTAATTAATCTGATGCTTCTT 1200

QY 1205 AGATTTAAGAGTTGTAATTCATCCACTGCTGAGAAATCTCCTCAAAACCCAGAAAGTTT 1264
DB 1201 AGATTTAAGAGTTGTAATTCATCCACTGCTGAGAAATCTCCTCAAAACCCAGAAAGTTT 1260

QY 1265 AATCACTTCATC 1276
DB 1261 AATCACTTCATC 1272

RESULT 11
ACC72129
ID ACC72129 standard; DNA; 1082 BP.
XX
AC ACC72129;
XX
DT 07-JUL-2003 (first entry)
XX
DE Human NOV27a coding sequence.
XX
KW Human; NOV; antidiabetic; anorectic; antibacterial; virucide;

RESULT 12
AAZ65040
ID AAZ65040 standard; cDNA; 1076 BP.
XX
AC AAZ65040;
XX
DT 05-APR-2000 (first entry)
XX
DE Membrane-bound protein PRO138 encoding cDNA.
XX
KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIR ligand;
KW pharmaceutical; receptor immunoadhesin; gene mapping; ss.
XX
OS Homo sapiens.
XX
PN WO9963088-A2.
XX
PD 09-DEC-1999.
PF 02-JUN-1999; 99WO-US012252.
XX
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088722P.
PR 10-JUN-1998; 98US-0088730P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088741P.
PR 10-JUN-1998; 98US-0088742P.
PR 10-JUN-1998; 98US-0088810P.
PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088825P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088863P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089090P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 19-JUN-1998; 98US-0089947P.
PR 19-JUN-1998; 98US-0089948P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.

PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
PR 23-JUN-1998; 98US-0090349P.
PR 23-JUN-1998; 98US-0090355P.
PR 24-JUN-1998; 98US-0090429P.
PR 24-JUN-1998; 98US-0090431P.
PR 24-JUN-1998; 98US-0090435P.
PR 24-JUN-1998; 98US-0090444P.
PR 24-JUN-1998; 98US-0090445P.
PR 24-JUN-1998; 98US-0090461P.
PR 24-JUN-1998; 98US-0090472P.
PR 24-JUN-1998; 98US-0090535P.
PR 24-JUN-1998; 98US-0090538P.
PR 24-JUN-1998; 98US-0090540P.
PR 24-JUN-1998; 98US-0090557P.
PR 25-JUN-1998; 98US-0090676P.
PR 25-JUN-1998; 98US-0090678P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090690P.
PR 25-JUN-1998; 98US-0090691P.
PR 25-JUN-1998; 98US-0090694P.
PR 25-JUN-1998; 98US-0090695P.
PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 01-JUL-1998; 98US-0091358P.
PR 02-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091486P.
PR 02-JUL-1998; 98US-0091519P.
PR 02-JUL-1998; 98US-0091544P.
PR 02-JUL-1998; 98US-0091626P.
PR 02-JUL-1998; 98US-0091628P.
PR 02-JUL-1998; 98US-0091633P.
PR 02-JUL-1998; 98US-0091646P.
PR 02-JUL-1998; 98US-0091673P.
PR 07-JUL-1998; 98US-0091978P.
PR 07-JUL-1998; 98US-0091982P.
PR 09-JUL-1998; 98US-0092182P.
PR 10-JUL-1998; 98US-0092472P.
PR 20-JUL-1998; 98US-0093339P.
PR 30-JUL-1998; 98US-0094651P.
PR 04-AUG-1998; 98US-0095282P.
PR 04-AUG-1998; 98US-0095285P.
PR 04-AUG-1998; 98US-0095301P.
PR 04-AUG-1998; 98US-0095302P.
PR 04-AUG-1998; 98US-0095318P.
PR 04-AUG-1998; 98US-0095321P.
PR 04-AUG-1998; 98US-0095325P.
PR 10-AUG-1998; 98US-0095916P.
PR 10-AUG-1998; 98US-0095929P.
PR 10-AUG-1998; 98US-0096012P.
PR 11-AUG-1998; 98US-0096143P.
PR 11-AUG-1998; 98US-0096146P.
PR 12-AUG-1998; 98US-0096329P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
PR 17-AUG-1998; 98US-0096768P.
PR 17-AUG-1998; 98US-0096773P.
PR 17-AUG-1998; 98US-0096791P.
PR 17-AUG-1998; 98US-0096867P.
PR 17-AUG-1998; 98US-0096891P.
PR 17-AUG-1998; 98US-0096894P.
PR 17-AUG-1998; 98US-0096895P.
PR 17-AUG-1998; 98US-0096897P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096950P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0096960P.
PR 18-AUG-1998; 98US-0097022P.
PR 19-AUG-1998; 98US-0097141P.
PR 20-AUG-1998; 98US-0097218P.
PR 24-AUG-1998; 98US-0097661P.

PR 26-AUG-1998; 98US-0097951P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
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PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0097978P.
PR 26-AUG-1998; 98US-0097979P.
PR 26-AUG-1998; 98US-0097986P.
PR 26-AUG-1998; 98US-0098014P.
PR 31-AUG-1998; 98US-0098525P.
PR 16-SEP-1998; 98US-0100634P.
PR 12-JAN-1999; 99US-0115565P.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
PI Wood WI, Yuan J;
XX
DR WPI; 2000-072883/06.
DR P-PSDB; AAY66701.
XX
PT Membrane-bound proteins and related nucleotide sequences.
XX
PS Claim 2; Fig 170; 822pp; English.
XX

CC The invention provides membrane-bound PRO polypeptides and
CC polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LDL receptors, TIE
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be
CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will
CC also be useful for the preparation of PRO polypeptides, especially by
CC recombinant techniques
XX
SQ Sequence 1076 BP; 291 A; 285 C; 255 G; 245 T; 0 U; 0 Other;

Query Match 39.8%; Score 1076; DB 3; Length 1076;
Best Local Similarity 100.0%; Pred. No. 3.8e-273;
Matches 1076; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 GTGGCTTCATTTCAAGTGGCTGACTTCCAGAGACCAATATGGCTGTTCCCAACATGCTT 64
Db 1 GTGGCTTCATTTCAAGTGGCTGACTTCCAGAGACCAATATGGCTGTTCCCAACATGCTT 60
OY 65 CACCCCTCATCTATATCTCTTTGGCAGCTCAAGGGTCAGCAGCCTTGAGCCCGTGAAGA 124
Db 61 CACCCCTCATCTATATCTCTTTGGCAGCTCAAGGGTCAGCAGCCTTGAGCCCGTGAAGA 120
OY 125 GCTGGTCGGTCCGTTGGTGGGGCCGTGACTTTCCCTGGAAGTCCAAAGTAAAGCAAGT 184
Db 121 GCTGGTCGGTCCGTTGGTGGGGCCGTGACTTTCCCTGGAAGTCCAAAGTAAAGCAAGT 180
OY 185 TGACTCTATTGTCTGGACCTTCAACACAACCCCTCTTGTCAACAATACAGCCAGAGGGGG 244
Db 181 TGACTCTATTGTCTGGACCTTCAACACAACCCCTCTTGTCAACAATACAGCCAGAGGGGG 240
OY 245 CACTATCATAGTGAACCCAAATCGTAATAGGAGAGAGTAGACTTCCAGATGAGGCTA 304
Db 241 CACTATCATAGTGAACCCAAATCGTAATAGGAGAGAGTAGACTTCCAGATGAGGCTA 300
OY 305 CTCCCTGAAGCTCAGCAAAGTGAAGAGATGACTCAGGATCTACTATGTGGGATATA 364
Db 301 CTCCCTGAAGCTCAGCAAAGTGAAGAGATGACTCAGGATCTACTATGTGGGATATA 360
OY 365 CAGCTCATCACTCCAGCAGCCCTCCAGCCAGAGTAGTGTGCTGATGTCTACGACACCT 424
Db 361 CAGCTCATCACTCCAGCAGCCCTCCAGCCAGAGTAGTGTGCTGATGTCTACGACACCT 420

OY 425 GTCAAGCCTTAAAGTCAACCATGGGTCTGCAGAGCAATTAAGATGGCACCTGTGTACCAA 484
Db 421 GTCAAGCCTTAAAGTCAACCATGGGTCTGCAGAGCAATTAAGATGGCACCTGTGTACCAA 480
OY 485 TCTGACATGCTGCATGGAACATGGGGAGAGAGATGTAATTATACCTGGAAGGCCCTGGG 544
Db 481 TCTGACATGCTGCATGGAACATGGGGAGAGAGATGTAATTATACCTGGAAGGCCCTGGG 540
OY 545 GCAAGCAGCCAATGAGTCCCATTAATGGGTCCATCTCCCATCTCTGAGATGGGAGA 604
Db 541 GCAAGCAGCCAATGAGTCCCATTAATGGGTCCATCTCCCATCTCTGAGATGGGAGA 600
OY 605 AAGTCATATGACCTTCATCTGCGCTTGCCAGGAACCCGTGACAGAACTTCTCAAGCCC 664
Db 601 AAGTCATATGACCTTCATCTGCGCTTGCCAGGAACCCGTGACAGAACTTCTCAAGCCC 660
OY 665 CATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGATGACCCAGATTCTCCATGGTCT 724
Db 661 CATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGATGACCCAGATTCTCCATGGTCT 720
OY 725 CCTGTGCTCTCTGTTGGTCCCTCTCTGCTCAGTCTCTTTGTACTGGGGCTATTCTTTG 784
Db 721 CCTGTGCTCTCTGTTGGTCCCTCTCTGCTCAGTCTCTTTGTACTGGGGCTATTCTTTG 780
OY 785 GTTCTGAAGAGAGAGACAGAAAGTACATTTGAAGAGAAAGAGAGTGAATTG 844
Db 781 GTTCTGAAGAGAGAGACAGAAAGTACATTTGAAGAGAAAGAGTGAATTG 840
OY 845 TCGGAAACTCTTAACATATGCCCATTTCTGAGAGAACACAGATGACACAAATCCC 904
Db 841 TCGGAAACTCTTAACATATGCCCATTTCTGAGAGAACACAGATGACACAAATCCC 900
OY 905 TCACACTAATAGAACAACTCTTAAGGAAGATCCAGCAATAACGGTTTACTCCACTGTGA 964
Db 901 TCACACTAATAGAACAACTCTTAAGGAAGATCCAGCAATAACGGTTTACTCCACTGTGA 960
OY 965 AATACCGAAAAAGATGAAAAATCCCACTCACTGCTCAAGATGCCAGACACACCAAGGCT 1024
Db 961 AATACCGAAAAAGATGAAAAATCCCACTCACTGCTCAAGATGCCAGACACACCAAGGCT 1020
OY 1025 ATTGCTTATGAGAAATGTAATCTAGACAGCAGTGCATCCCTAAGTCTGTGCTCA 1080
Db 1021 ATTGCTTATGAGAAATGTAATCTAGACAGCAGTGCATCCCTAAGTCTGTGCTCA 1076

RESULT 13
AAS46020
ID AAS46020 standard; cDNA; 1076 BP.
XX
AC AAS46020;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human DNA encoding PRO polypeptide sequence #96.
XX
KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
KW PCR primer.
XX
OS Homo sapiens.
XX
PN WO200168848-A2.
XX
PD 20-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US006520.
XX
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.

PR 03-MAR-2000; 2000US-0187202P.
PR 06-MAR-2000; 2000US-0186968P.
PR 14-MAR-2000; 2000US-0189320P.
PR 14-MAR-2000; 2000US-0189328P.
PR 15-MAR-2000; 2000WO-US006884.
PR 21-MAR-2000; 2000US-0190828P.
PR 21-MAR-2000; 2000US-0191007P.
PR 21-MAR-2000; 2000US-0191048P.
PR 21-MAR-2000; 2000US-0191314P.
PR 28-MAR-2000; 2000US-0192655P.
PR 29-MAR-2000; 2000US-0193032P.
PR 29-MAR-2000; 2000US-0193053P.
PR 30-MAR-2000; 2000WO-US008439.
PR 04-APR-2000; 2000US-0194449P.
PR 04-APR-2000; 2000US-0194647P.
PR 11-APR-2000; 2000US-0195975P.
PR 11-APR-2000; 2000US-0196000P.
PR 11-APR-2000; 2000US-0196187P.
PR 11-APR-2000; 2000US-0196690P.
PR 11-APR-2000; 2000US-0196820P.
PR 18-APR-2000; 2000US-0198121P.
PR 18-APR-2000; 2000US-0198585P.
PR 25-APR-2000; 2000US-0199397P.
PR 25-APR-2000; 2000US-0199550P.
PR 25-APR-2000; 2000US-0199654P.
PR 03-MAY-2000; 2000US-0201516P.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 05-JUN-2000; 2000US-0209832P.
PR 28-JUL-2000; 2000WO-US020710.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
XX
XX (GETH) GENENTECH INC.
XX
XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2001-602746/68.
DR P-PSDB; AAU29119.
XX
PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT presence of tumors, such as prostate and breast tumors, in mammals and to
PT screen for modulators of the compounds.
XX
XX
PS Claim 2; Fig 191; 774pp; English.
XX
XX Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR
CC primers for PRO polypeptides of the invention. The sequences of the
CC invention can be used to detect the presence of a tumour in a mammal by
CC comparing the level of expression of a PRO polypeptide in a test sample
CC of cells from the animal and a control sample of normal cells, whereby a
CC higher level of expression in the test sample indicates the presence of a
CC tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,
CC pigs, goats and rabbits but are preferably human. The polypeptides can be
CC used to stimulate tumour necrosis factor (TNF) alpha release from human
CC blood, when contacted with it. A specific polypeptide can be used to
CC stimulate the proliferation or differentiation of chondrocyte cells. The
CC PRO proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders
XX
SQ Sequence 1076 BP; 291 A; 285 C; 255 G; 245 T; 0 U; 0 Other;

Query Match 39.8%; Score 1076; DB 4; Length 1076;
Best Local Similarity 100.0%; Pred. No. 3.8e-273;

Matches 1076; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	5	GTGGCTTCATTTCAGTGGCTGACTTCCAGAGCAATATGCGTGTCCCAACATGCCT	64
Db	1	GTGGCTTCATTTCAGTGGCTGACTTCCAGAGCAATATGCGTGTCCCAACATGCCT	60
QY	65	CACCTCATCTATATCCTTTGGCAGCTCAGAGGTCAGCAGCCTTGACCCGTGAAGA	124
Db	61	CACCTCATCTATATCCTTTGGCAGCTCAGAGGTCAGCAGCCTTGACCCGTGAAGA	120
QY	125	GCTGGTCGGTTCCTGTGGTGGGGCCGTGACTTTCCTCCCTGAAGTCCAAGTAAAGCAAGT	184
Db	121	GCTGGTCGGTTCCTGTGGTGGGGCCGTGACTTTCCTCCCTGAAGTCCAAGTAAAGCAAGT	180
QY	185	TGACTCTATTGTCTGGACCTTCAACACAACTCTTGTTCACCATACAGCCAGAGGGGG	244
Db	181	TGACTCTATTGTCTGGACCTTCAACACAACTCTTGTTCACCATACAGCCAGAGGGGG	240
QY	245	CACATCATATAGTACCCAAATCGTAA TAGGAGAGAGTAGACTTCCAGATGAGGCTA	304
Db	241	CACATCATATAGTACCCAAATCGTAA TAGGAGAGAGTAGACTTCCAGATGAGGCTA	300
QY	305	CTCCCTGAAGCTCAGCAAACTGAAGAAGTAGCTCAGGATCTATGTGGGATATA	364
Db	301	CTCCCTGAAGCTCAGCAAACTGAAGAAGTAGCTCAGGATCTATGTGGGATATA	360
QY	365	CAGCTCATCTCCAGCAGCCCTCCACCCAGAGTAGTGTCTACGAGCACCT	424
Db	361	CAGCTCATCTCCAGCAGCCCTCCACCCAGAGTAGTGTCTACGAGCACCT	420
QY	425	GTCAAAAGCCTTAAAGTCAACCATGGGTCTGCAGAGCAATAGAATGGCACTGTGTGACCA	484
Db	421	GTCAAAAGCCTTAAAGTCAACCATGGGTCTGCAGAGCAATAGAATGGCACTGTGTGACCA	480
QY	485	TCTGACATGTGCATGGAACATGGGGAGAGAGATGTGATTATATCTGGAAGGCCCTGGG	544
Db	481	TCTGACATGTGCATGGAACATGGGGAGAGAGATGTGATTATATCTGGAAGGCCCTGGG	540
QY	545	GCAAGCAGCCATGAGTCCCATATAGGCTCATCTCCCATCTCTGAGATGGGAGA	604
Db	541	GCAAGCAGCCATGAGTCCCATATAGGCTCATCTCCCATCTCTGAGATGGGAGA	600
QY	605	AAGTATATGACCTTCATCTGCGTTGCCAGGAACCTGTCAAGCAAACTTCTCAAGCCC	664
Db	601	AAGTATATGACCTTCATCTGCGTTGCCAGGAACCTGTCAAGCAAACTTCTCAAGCCC	660
QY	665	CATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGTGATGACCCAGATTCTCCATGTGCT	724
Db	661	CATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGTGATGACCCAGATTCTCCATGTGCT	720
QY	725	CCTGTCTCTCTGTGTGGTGCCCTCTCTGCTCAGTCTCTTTGTACTGGGGCTATTCTTTG	784
Db	721	CCTGTCTCTCTGTGTGGTGCCCTCTCTGCTCAGTCTCTTTGTACTGGGGCTATTCTTTG	780
QY	785	GTTTCTGAAGAGAGAGACAAGAGATCATTTGAAGAGAGAGAGATGGACATTTG	844
Db	781	GTTTCTGAAGAGAGAGACAAGAGATCATTTGAAGAGAGAGAGATGGACATTTG	840
QY	845	TCGGAAACTCTTAACATATGCCCCCATTTCTGAGAGAAACACAGATACGACATATCCC	904
Db	841	TCGGAAACTCTTAACATATGCCCCCATTTCTGAGAGAAACACAGATACGACATATCCC	900
QY	905	TCACACTATATGAACAATCTCTAAAGAGATCCAGCAATACGGTTTACTCCACTGTGA	964
Db	901	TCACACTATATGAACAATCTCTAAAGAGATCCAGCAATACGGTTTACTCCACTGTGA	960
QY	965	AATACCGAAAAAGATGAAAAATCCCACTCACTGCTCAGCATGCGAGACACACCAAGGCT	1024
Db	961	AATACCGAAAAAGATGAAAAATCCCACTCACTGCTCAGCATGCGAGACACACCAAGGCT	1020
QY	1025	ATTGCTATGAGATGTTATCTAGACAGCAGTGCACTCCCTAAGTCTGTGCTCA	1080
Db	1021	ATTGCTATGAGATGTTATCTAGACAGCAGTGCACTCCCTAAGTCTGTGCTCA	1076

RESULT 14
AA#92080
ID AAF92080 standard; cDNA; 1076 BP.
XX
AC AAF92080;
XX
DT 15-MAY-2001 (first entry)
XX
DE Human PRO1138 cDNA.
XX
KW Human; PRO protein; mapping; ss.
XX
OS Homo sapiens.
XX
PN WO200116318-A2.
XX
PD 08-MAR-2001.
XX
PF 24-AUG-2000; 2000WO-US023328.
XX
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 07-DEC-1999; 99US-0169495P.
PR 09-DEC-1999; 99US-0170262P.
PR 11-JAN-2000; 2000US-0175481P.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 03-MAR-2000; 2000US-0187202P.
PR 21-MAR-2000; 2000US-0191007P.
PR 30-MAR-2000; 2000WO-US008439.
PR 25-APR-2000; 2000US-0199397P.
PR 22-MAY-2000; 2000WO-US014042.
PR 05-JUN-2000; 2000US-0209832P.
XX
PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2001-183260/18.
DR P-PSDB; AAB87548.
XX
PT Eighty four nucleic acids encoding PRO polypeptides, useful in molecular
PT biology, including use as hybridization probes, and in chromosome and
PT gene mapping.
XX
PS Claim 2; Fig 45; 278pp; English.
XX
CC The present sequence is the coding sequence for a human PRO polypeptide
CC (secreted and transmembrane). The PRO protein, and PRO agonists, PRO
CC antagonists or anti-PRO antibodies are useful for preparation of a
CC medicament useful in the treatment of a condition which is responsive to
CC the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO
CC protein may also be employed as molecular weight markers for protein
CC electrophoresis. The PRO coding sequence has applications in molecular
CC biology, including use as hybridisation probes, and in chromosome and
CC gene mapping
XX
SQ Sequence 1076 BP; 291 A; 285 C; 255 G; 245 T; 0 U; 0 Other;
Query Match 39.8%; Score 1076; DB 4; Length 1076;
Best Local Similarity 100.0%; Pred. No. 3.8e-273;
Matches 1076; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 61 CACCTCATCTATATCCTTGGCAGCTCACAGGGTCAGCAGCCTCTGAGCCCGTGAAGA 120
QY 125 GCTGGTCGGTTCGGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAAGCAAGT 184
Db 121 GCTGGTCGGTTCGGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAAGCAAGT 180
QY 185 TGACTCTATTGTCTGGAACCTTCAACACACCCTCTGTTCACCATACAGCCAGAGGGGG 244
Db 181 TGACTCTATTGTCTGGAACCTTCAACACACCCTCTGTTCACCATACAGCCAGAGGGGG 240
QY 245 CACTATCATAGTAGACCCCAAAATCGTAATAGGAGAGAGTAGACTTCCCAAGATGAGGCTA 304
Db 241 CACTATCATAGTAGACCCCAAAATCGTAATAGGAGAGAGTAGACTTCCCAAGATGAGGCTA 300
QY 305 CTCCTGAAGCTCAGCAAACTGAAGAAGATGACTCAGGGATCTACTATGTGGGATATA 364
Db 301 CTCCTGAAGCTCAGCAAACTGAAGAAGATGACTCAGGGATCTACTATGTGGGATATA 360
QY 365 CAGCTCATCACTCCAGCAGCCCTCCACCAGAGTAGCGTGCATGTCTACGAGCAGCT 424
Db 361 CAGCTCATCACTCCAGCAGCCCTCCACCAGAGTAGCGTGCATGTCTACGAGCAGCT 420
QY 425 GTCAAGCCTTAAGTCACCAATGGGTCTGAGAGCAATGAAGATGGCACCCTGTGACCAA 484
Db 421 GTCAAGCCTTAAGTCACCAATGGGTCTGAGAGCAATGAAGATGGCACCCTGTGACCAA 480
QY 485 TCTGACATGCTGCATGGAACATGGGGAAGAGATGTGATTTATACCTGGAAGGCCCTGGG 544
Db 481 TCTGACATGCTGCATGGAACATGGGGAAGAGATGTGATTTATACCTGGAAGGCCCTGGG 540
QY 545 GCAAGCAGCCCAATGAGTCCCATATGGGTCCATCTCTCCCATCTCTGAGATGGGGA 604
Db 541 GCAAGCAGCCCAATGAGTCCCATATGGGTCCATCTCTCCCATCTCTGAGATGGGGA 600
QY 605 AAGTATATGACCTTCATCTGCGTTGCCAGGAACCTGTGACGAGAACTTCTCAAGCCC 664
Db 601 AAGTATATGACCTTCATCTGCGTTGCCAGGAACCTGTGACGAGAACTTCTCAAGCCC 660
QY 665 CATCTTGGCCAGGAAGCTGTGAAGGTGCTGCTGATGACCCAGATTCCCTCATGTCCT 724
Db 661 CATCTTGGCCAGGAAGCTGTGAAGGTGCTGCTGATGACCCAGATTCCCTCATGTCCT 720
QY 725 CCTGTGCTCTCTGTGTGTCGCCCTCTGCTCAGTCTCTTGTACTGGGCTATTCTTTG 784
Db 721 CCTGTGCTCTCTGTGTGTCGCCCTCTGCTCAGTCTCTTGTACTGGGCTATTCTTTG 780
QY 785 GTTTCTGAAGAGAGAGACAAGAAGTACATTGAGAAGAAGAAGATGGACATTG 844
Db 781 GTTTCTGAAGAGAGAGACAAGAAGTACATTGAGAAGAAGAAGATGGACATTG 840
QY 845 TCGGGAACCTCTTAACATATGCCCCCATTTCTGGAGAACACAGAGTACGACAAATCCC 904
Db 841 TCGGGAACCTCTTAACATATGCCCCCATTTCTGGAGAACACAGAGTACGACAAATCCC 900
QY 905 TCACACTAATAGAACCAATCTTAAAGAGATCCAGCAATACGGTTACTTCACGTGGA 964
Db 901 TCACACTAATAGAACCAATCTTAAAGAGATCCAGCAATACGGTTACTTCACGTGGA 960
QY 965 AATACCGAAAAAGATGGAATCCCACTCACTGCTCAGATGCCAGACACCAAGGCT 1024
Db 961 AATACCGAAAAAGATGGAATCCCACTCACTGCTCAGATGCCAGACACCAAGGCT 1020
QY 1025 ATTGCTTATGAGATGTATCTAGACAGCAGTGCACTCCCTAAGTCTGTCTCA 1080
Db 1021 ATTGCTTATGAGATGTATCTAGACAGCAGTGCACTCCCTAAGTCTGTCTCA 1076

RESULT 15
AA#44186
ID AAF44186 standard; cDNA; 1076 BP.
XX
AC AAF44186;

XX 02-APR-2001 (first entry)
DT
XX
DE Human PRO1138 (UNQ576) nucleotide sequence SEQ ID NO:252.
XX
KW Human; secreted and transmembrane protein; PRO; cytosstatic; cell death;
KW cancer; chromosomal mapping; gene mapping; tissue typing;
KW diagnostic assay; ss.
XX
OS Homo sapiens.
XX
PN WO200073454-A1.
XX
PD 07-DEC-2000.
XX
PF 30-MAR-2000; 2000WO-US008439.
XX
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 07-JUL-1999; 99US-0143048P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145638P.
PR 28-JUL-1999; 99US-0146222P.
PR 17-AUG-1999; 99US-0149396P.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 08-OCT-1999; 99US-0158663P.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
XX
PA (GETH) GENENTECH INC.
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PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Thomas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
XX WPI; 2001-032160/04.
DR P-PSDB; AAB65224.
XX
PT PRO polynucleotides used to produce polypeptides used to target bioactive
PT molecules such as toxins, radiolabels or antibodies, to specific cells,
PT to cause targeted cell death.
XX
XX
PS Claim 2; Fig 170; 935pp; English.
XX
XX The present invention describes human secreted and transmembrane PRO
CC proteins. The PRO proteins have cytostatic activity. The PRO proteins can
CC be used for targeted delivery of bioactive molecules, such as toxins,
CC radiolabels or antibodies, that cause cell death. PRO nucleotide
CC sequences, and their fragments, can be used as hybridisation probes, in
CC chromosomal and gene mapping, and in the generation of anti-sense RNA and
CC DNA. They may also be used to produce transgenic animals which are used
CC to develop and screen therapeutically useful reagents. The PRO nucleotide
CC and protein sequence can be used for tissue typing and in treating
CC cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to
CC AAF44470 represent PCR primers and hybridisation probes used in the
CC isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to
CC AAB65300 represent human PRO polynucleotide and protein sequences given
CC in the exemplification of the present invention

XX
SQ Sequence 1076 BP; 291 A; 285 C; 255 G; 245 T; 0 U; 0 Other;
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Best Local Similarity 100.0%; Pred. No. 3.8e-273;
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 28, 2004, 07:59:30 ; Search time 1268 Seconds
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Scoring table: IDENTITY_NUC
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Searched: 3413475 seqs, 2563800928 residues

Total number of hits satisfying chosen parameters: 6826950

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1701.4	62.9	1966	14 US-10-198-846-13630	Sequence 13630, A
3	1369.4	50.6	1412	9 US-09-984-245-15	Sequence 15, Appl 1
4	1369.4	50.6	1412	10 US-09-966-262-15	Sequence 15, Appl 1
5	1369.4	50.6	1412	10 US-09-983-966-15	Sequence 15, Appl 1
6	1369.4	50.6	1412	14 US-10-059-395-15	Sequence 15, Appl 1
7	1369.4	50.6	1412	14 US-10-143-090-15	Sequence 15, Appl 1
8	1082	40.0	1082	16 US-10-262-839-109	Sequence 109, App
9	1076	39.8	1076	9 US-09-989-722-252	Sequence 252, App
10	1076	39.8	1076	9 US-09-989-723-252	Sequence 252, App
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ALIGNMENTS

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; Sequence 1, Application US/09745605
; Patent No. US20020123617A1
; GENERAL INFORMATION:
; APPLICANT: Starling, Gary C.
; TITLE OF INVENTION: NOVEL IMMUNOGLOBIN SUPERFAMILY MEMBERS APEX-1, APEX-2,
; FILE REFERENCE: DB13NP
; CURRENT APPLICATION NUMBER: US/09/745, 605
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/172, 025
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2704
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-745-605-1

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Best local Similarity 100.0%; Pred. No. 0;
Matches 2704; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinhmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13630
; LENGTH: 1966
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1, 2, 1966
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-13630

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Best Local Similarity	98.9%	Pred. No. 0		
Matches 1767	Conservative 0	Mismatches 11	Indels 9	Gaps 5
Qy	912	AATAGACAATCCTTAAAGAGATCCAGCAATACGGTTTACTCCACTGTGGAATACCG	971	
Db	133	AAGAGACAATCCTTAAAGAGATCCAGCAATACGGTTTACTCCACTGTGGAATACCG	192	
Qy	972	AAAAAGATGAAATCCCACTCACTGCTCAGATGCAGACACACCAAGGCTATTGGCC	1031	
Db	193	AAAAAGATGAAATCCCACTCACTGCTCAGATGCAGACACACCAAGGCTATTGGCC	252	
Qy	1032	TATGAGATGTTATCTAGACAGCAGTGCACTCCCTTAAGTCTTGCTCAAAAAAAAAACA	1091	

Db	253	TATGAGAAATGGGATCTAGACAGCAGTGCACCTCCCTAAAGTCTCTGCTCAAAAAAAAAAACA	312
Qy	1092	ATTCTCGGCCCCAAGAAAAACAATCAGAAGAAATTCACTGATTTGACTAG-AAACATCAAGG	1150
Db	313	ATTCTCGGCCCCAAGAAAAACAATCAGAAGAAATTCACTGATTTGACTAGAAAAACATCAAGG	372
Qy	1151	AAGAATGAAGAACGTTGACTTTTTTCCAGGATTAATTAATCTCTGATGCTTCTTTAGATTT	1210
Db	373	AAGAATGAAGAACGTTGACTTTTTTTCCAGGATTAATTAATCTCTGATGCTTCTTTAGATTT	432
Qy	1211	AAGATTGCTAATTCATCCACTGCTGAGAAATCTCCTCAAAACCAGAGGTTTAATCAC	1270
Db	433	AAGATTGCTAATTCATCCACTGCTGAGAAATCTCCTCAAAACCAGAGGTTTAATCAC	492
Qy	1271	TTCATCCCAAAAAATGGGATTGTGAAATGTCAGCAAAACCATAAAAAAGTGTAGAAATAT	1330
Db	493	TTCATCCCAAAAAATGGGATTGTGAAATGTCAGCAAAACCATAAAAAAGTGTAGAAATAT	552
Qy	1331	TCCTATAGAAATGTAAATGCAAGGTCAACATATTAATGACAGCCTGTTGTAATGAT	1390
Db	553	TCCTATAGAAATGTAAATGCAAGGTCAACATATTAATGACAGCCTGTTGTAATGAT	612
Qy	1391	GGCTCCAGGTCAGTGTCTGAGTTTCATTCCATCCCAGGGCTTGATGTGAGATTTATAC	1450
Db	613	GGCTCCAGGTCAGTGTCTGAGTTTCATTCCATCCCAGGGCTTGATGTGAGATTTATAC	672
Qy	1451	CAAGAGTCTTGCTACCAGAGGGCAAGAAAGCAAAAACAGACAGACAAGTCCAGCAGAAG	1510
Db	673	CAAGAGTCTTGCTACCAGAGGGCAAGAAAGCAAAAACAGACAGACAAGTCCAGCAGAAG	732
Qy	1511	CAGATGACCTGACAAAAATGATGTATTAATTGGCTCTATAAATATGTGCCAGCACT	1570
Db	733	CAGATGACCTGACAAAAATGATGTATTAATTGGCTCTATAAATATGTGCCAGCACT	792
Qy	1571	ATGCTGAGCTTACACTAATTTGGTCAGACGCTGCTCTGCCCTCATGAAATTTGGCTCCAA	1630
Db	793	ATGCTGAGCTTACACTAATTTGGTCAGACGCTGCTCTGCCCTCATGAAATTTGGCTCCAA	852
Qy	1631	TGAATGAATTAATTTTCATGAGCAGTTGTAGCAGGCTTGACCACAGATTCCACAGGGCCA	1690
Db	853	TGAATGAATTAATTTTCATGAGCAGTTGTAGCAGGCTTGACCACAGATTCCACAGGGCCA	912
Qy	1691	GGTGTGATTCACAGGACTTGAAGGTCAAAGTTCACAAAGATGAAGAATCAGGGTAGCTG	1750
Db	913	GGTGTGATTCACAGGACTTGAAGGTCAAAGTTCACAAAGATGAAGAATCAGGGTAGCTG	972
Qy	1751	ACCATGTTTGGCAGATACTATATATGAGACACAGAAAGTGTGCATGGCCCCAAGACAAGGA	1810
Db	973	ACCATGTTTGGCAGATACTATATATGAGACACAGAAAGTGTGCATGGCCCCAAGACAAGGA	1032
Qy	1811	CCTCCAGCCAGGCTTCATTATATGACCTTGCTGCAAAAAGAAAAAGTCTAGGTTTAAAGGC	1870
Db	1033	CCTCCAGCCAGGCTTCATTATATGACCTTGCTGCAAAAAGAAAAAGTCTAGGTTTAAAGGC	1092
Qy	1871	TGTGCCAGAACCCATCCCAATTAAGAGACCGAGTCTGAAGTCAATTTGTAATCTAGTGT	1930
Db	1093	TGTGCCAGAACCCATCCCAATTAAGAGACCGAGTCTGAAGTCAATTTGTAATCTAGTGT	1152
Qy	1931	AGGAGACTTTGGAGTCAAGGCAAGTGAAGTGTGGGGCCACGGGGGGCAGTGGGTAATTGTAA	1990
Db	1153	AGGAGACTTTGGAGTCAAGGCAAGTGAAGTGTGGGGCCACGGGGGGCAGTGGGTAATTGTAA	1212
Qy	1991	ACCTTTAAAGATGTTAATTCATTCAATAGATATTTATTAAAGAACCTTACTATGCGGCCG	2050
Db	1213	ACCTTTAAAGATGTTAATTCATTCAATAGATATTTATTAAAGAAC--CTATGCGGCCG	1269
Qy	2051	GCATGGTGGCTCACACCTGTATCCAGCACTTTGGAGGCCAAGGTGGGTGATCTCT	2110
Db	1270	GCATGGTGGCTCACACCTGTATCCAGCACTTTGGAGGCCAAGGTGGGTGATCTCT	1329
Qy	2111	GAGGTCAAGAGTTCAAGACCAAGCCTGGCCAATGTTGAACCCCATCTTACTAAAGAT	2170
Db	1330	GAGGTCAAGAGTTCAAGACCAAGCCTGGCCAATGTTGAACCCCATCTTACTAAAGAT	1389

QY 2171 --CAAAATTGCTGAGCGTGTGTGTGCACTGT-ATCCAGCTACTCGAGGCCAAG 2227
Db 1390 ACAAAAATTGCTGAGCGTGTGTGTGCACTGTATATCCAGCTACTCGAGAGGCCAAG 1449
QY 2228 GCATGAGAATCGCTTGAACCTGGAGG--TGAGGTTGCAGTGAGCTGAGATGGCACCCTG 2285
Db 1450 GCATGAGAATCGCTTGAACCTGGAGGAGGTGGAGGTTGCACTGAGCTGAGATGGCACCCTG 1509
QY 2286 CACTCCGGCCTTAGGCAACGAGAGCAAACTCCAATACAAACAACAACAACACCTGTG 2345
Db 1510 CACTCCGGCCTTAGGCAACGAGAGCAAACTCCAATACAAACAACAACAACACCTGTG 1569
QY 2346 CTAGTCAGTCTGGCAGCTAGATGAACATCCCTACCAACACAGAGCTCACCATCTCTTA 2405
Db 1570 CTAGTCAGTCTGGCAGCTAGATGAACATCCCTACCAACACAGAGCTCACCATCTCTTA 1629
QY 2406 TACTTAAGTGA AAAACATGGGGAAGGGAAGGGAATGCTGCTTTGATATGTTCCCT 2465
Db 1630 TACTTAAGTGA AAAACATGGGGAAGGGAAGGGAATGCTGCTTTGATATGTTCCCT 1689
QY 2466 GACGCATATCTTGAATGAGAGACCTCCCTACCAAGTGATGAAGGTGTA AAAAATTATA 2525
Db 1690 GACGCATATCTTGAATGAGAGACCTCCCTACCAAGTGATGAAGGTGTA AAAAATTATA 1749
QY 2526 ACAATGCTTGTGGGCAAGAATGGGATGAGATTTATCTTCTCAGAAAAGGCATTGTG 2585
Db 1750 ACAATGCTTGTGGGCAAGAATGGGATGAGATTTATCTTCTCAGAAAAGGCATTGTG 1809
QY 2586 AAGGAATTGAGCCAGATCTCTCTCCCTACTGCAAAACCCTATTGTAGTAA AAAAGTCTTC 2645
Db 1810 AAGGAATTGAGCCAGATCTCTCTCCCTACTGCAAAACCCTATTGTAGTAA AAAAGTCTTC 1869
QY 2646 TTTACTATCTTAATAAACAAGATATTTGAGATTACATTA AAAAAAAA 2692
Db 1870 TTTACTATCTTAATAAACAAGATATTTGAGATTACATTA AAAAAAAA 1916

RESULT 3

US-09-984-245-15
; Sequence 15, Application US/09984245
; Patent No. US20020165374A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: PZ004P1
; CURRENT APPLICATION NUMBER: US/09/984,245
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/154,707
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: PCT/US98/05311
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: US 60/041,277
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/042,344
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,276
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,281
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/048,094
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,350
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,188
; PRIOR FILING DATE: 1997-05-30
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; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,187
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,099

; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,352
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,186
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; PRIOR APPLICATION NUMBER: US 60/048,154
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: US 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 1412
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1362)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (1369)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (1397)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-984-245-15

Query Match 50.6%; Score 1369.4; DB 9; Length 1412;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1384; Conservative 2; Mismatches 11; Indels 1; Gaps 1;

QY 616 CCTTCATCTGCGTTGCCAGAACCTGTCTCAGAGAACTTCTCAAGCCCATCTTGCCA 675
Db 2 CCTTCATCTGCGTTGCCAGAACCTGTCTCAGAGAACTTCTCAAGCCCATCTTGCCA 61
QY 676 GGAAGCTCTGTGAAGGTGCTGTGATGACCCAGATTCTCCATGTCTCTGTCCTCC 735
Db 62 GGAAGCTCTGTGAAGGTGCTGTGATGACCCAGATTCTCCATGTCTCTGTCCTCC 121
QY 736 TGTGGTGCCTCTCTGCTCAGTCTCTTTGTACTGGGCTATTTCTTTGGTTTGAAGA 795
Db 122 TGTGGTGCCTCTCTGCTCAGTCTCTTTGTACTGGGCTATTTCTTTGGTTTGAAGA 181
QY 796 GAGAGACAAGAAGATGATTTGAAGAAGAAGAAGAGTGACATTGTGCGGAACTC 855
Db 182 GAGAGACAAGAAGATGATTTGAAGAAGAAGAAGAGTGACATTGTGCGGAACTC 241
QY 856 CTAACATATGCCCCCATTTCTGAGAGAACAACAGAGTACACAATCCCTCACACTAATA 915
Db 242 CTAACATATGCCCCCATTTCTGAGAGAACAACAGAGTACACAATCCCTCACACTAATA 301
QY 916 GAACAATCTTAAAGGAAGATCCAGCAATACGGTTTACTCACTGTGGAATACCGAAA 975
Db 302 GAACAATCTTAAAGGAAGATCCAGCAATACGGTTTACTCACTGTGGAATACCGAAA 361

; LOCATION: (1369)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc.feature
; LOCATION: (1397)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-966-262-15

Query Match 50.6%; Score 1369.4; DB 10; Length 1412;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1384; Conservative 2; Mismatches 11; Indels 1; Gaps 1;

QY 616 CCTTCATCTGCGTTGCCAGGAACCTGTGACGAGAAACTTCTCAAGCCCCATCCTTGCCA 675
DB 2 CCTTCATCTGCGTTGCCAGGAACCTGTGACGAGAAACTTCTCAAGCCCCATCCTTGCCA 61
QY 676 GGAAGCTGTGAAGGTGCTGTGATGACCCAGATTCTCCATGCTCCTGTGTCTCC 735
DB 62 GGAAGCTGTGAAGGTGCTGTGATGACCCAGATTCTCCATGCTCCTGTGTCTCC 121
QY 736 TGTGTGCCCCCTCCTGCTCAGTCTTGTACTGGGGCTATTCTTGGTTCTGAAGA 795
DB 122 TGTGTGCCCCCTCCTGCTCAGTCTTGTACTGGGGCTATTCTTGGTTCTGAAGA 181
QY 796 GAGAGACACAGAAGAGTACATTGAAGAGAAGAAGAGTGAACATTTGTCGGAACTC 855
DB 182 GAGAGACACAGAAGAGTACATTGAAGAGAAGAAGAGTGAACATTTGTCGGAACTC 241
QY 856 CTAACATATGCCCCCATTTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAATA 915
DB 242 CTAACATATGCCCCCATTTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAATA 301
QY 916 GAACAACTCTAAGGAAGATCCAGCAATAACGGTTTACTCCACTGTGGAATACCGAAAA 975
DB 302 GAACAACTCTAAGGAAGATCCAGCAATAACGGTTTACTCCACTGTGGAATACCGAAAA 361
QY 976 AGATGAAAAATCCCACACTCACTGCTACGATGCCAGACACCAAGGCTATTGGCTATG 1035
DB 362 AGATGAAAAATCCCACACTCACTGCTACGATGCCAGACACCAAGGCTATTGGCTATG 421
QY 1036 AGAATGTATCTAGACAGAGTGACTCCCCCTAAGTCTCTGCTCAAAAAACAATTC 1095
DB 422 AGAATGTATCTAGACAGAGTGACTCCCCCTAAGTCTCTGCTCAAAAAACAATTC 481
QY 1096 TCGGCCCAAGAAAAACAATCAGAGAATTCACATGATTGACTAGAAAACATCAAGGAAGA 1155
DB 482 TCGGCCCAAGAAAAACAATCAGAGAATTCACATGATTGACTAGAAAACATCAAGGAAGA 541
QY 1156 TGAAGAACGTGACTTTTTCAGGATAAATATCTCTGATGCTTCTTGAATTGAAG 1215
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QY 1216 TTCGTAAATTCATCCACTGCTGAGAAATCTCTCAAAACCCAGAGGTTTAATCACTTCAT 1275
DB 602 TTCGTAAATTCATCCACTGCTGAGAAATCTCTCAAAACCCAGAGGTTTAATCACTTCAT 661
QY 1276 CCCAAAAATGGATTGTGAATGTGCAAAACCATAAAAAAAGTCTTAGAAGTATTCCTA 1335
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QY 1336 TAGAAATGTAATGCAAGGTCAACATATTAATGACAGCCTGTGTAATTAATGATGGCTC 1395
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QY 1396 CAGGTCAGTCTGTGAGTTTCATTCATCCAGGGCTTGATGTGAGATTATACCAAGA 1455
DB 782 CAGGTCAGTCTGTGAGTTTCATTCATCCAGGGCTTGATGTGAGATTATACCAAGA 841
QY 1456 GTCTTGCTACGAGAGGGCAAGAGACAAAAACAGACAGACAAGTCCAGCAGAAAGCAGAT 1515
DB 842 GTCTTGCTACGAGAGGGCAAGAGACAAAAACAGACAGACAAGTCCAGCAGAAAGCAGAT 901
QY 1516 GCACCTGACAAAAATGATGTATTAATTGGCTCTATAAATAATGTGCCAGCACTATGCT 1575

DB 902 GCACCTGACAAAAATGATGTATTAATTGGCTCTATAAATAATGTGCCAGCAATATGCT 961
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DB 962 GAGCTTACACTAATTGGTCAGACATGCTGTGCTGCCCTCATGAAATTGGCTCCAAATGAAT 1021
QY 1636 GAACTACTTTCATGAGCAGTTGTAGCAGGGCCTGACCAAGATTCCAGAGGGCCAGGTGT 1695
DB 1022 GAACTACTTTCATGAGCAGTTGTAGCAGGGCCTGACCAAGATTCCAGAGGGCCAGGTGT 1081
QY 1696 GGAATCCACAGAGACTTGAAGTCAAAAGTTCACAAAGATGAAGATCAGGGTAGCTGACCAT 1755
DB 1082 GGAATCCACAGAGACTTGAAGTCAAAAGTTCACAAAGATGAAGATCAGGGTAGCTGACCAT 1141
QY 1756 GTTTGGCAGATACTATAATGAGACACAGAAGTGTGATGGCCCAAGACAAGACCTCC 1815
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QY 1816 AGCCAGGCTTCATTATATGCACTGTGCTGCAAAAAGAAAGTCTAGGTTTAAAGCTGTGC 1875
DB 1202 AGCCAGGCTTCATTATATGCACTGTGT - CTGCAAAAAGAAAGTCTAGGTTTAAAGCTGTGC 1260
QY 1876 CAGAACCCATCCCAATAAAGAGACCGAGTCTGAAGTCACTGTAATCTAGTGAAG 1935
DB 1261 CAGAACCCATCCCAATAAAGAGACCGAGTCTGAAGTCACTGTAATCTAGTGAAG 1320
QY 1936 ACTTGAGTCAGGACGTGAGACTGTGGGGCACGGGGGCACTGGTACTTGTAAACCTT 1995
DB 1321 ACTTGAGTCAGGACGTGAGACTGTGTGGGGCACGGGGGCACTGGTANTGTAAACCTTT 1380
QY 1996 TAAAGATGTTAATTCAT 2013
DB 1381 TAAAGATGTTAATTCAT 1398

RESULT 5
US-09-983-966-15
; Sequence 15, Application US/09983966
; Publication No. US20030060619A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1
; CURRENT APPLICATION NUMBER: US/09/983, 966
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/154, 707
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: PCT/US98/05311
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: US 60/041, 277
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/042, 344
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041, 276
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041, 281
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/048, 094
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048, 350
; PRIOR FILING DATE: 1997-05-30
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; PRIOR APPLICATION NUMBER: US 60/048, 135
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; PRIOR APPLICATION NUMBER: US 60/050, 937
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048, 187
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; PRIOR FILING DATE: 1997-05-30


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; PRIOR APPLICATION NUMBER: US 60/048,186
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,069
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,095
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,131
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; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: US 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 1412
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1362)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (1369)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (1397)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-983-966-15

Query Match      50.6%; Score 1369.4; DB 10; Length 1412;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1384; Conservative 2; Mismatches 11; Indels 1; Gaps 1;

QY      616 CCTCATCTGCGTTGCCAGGAACCTGTGACGAGAACTTCTCAAGCCCCCATCTTGCCA 675
Db      2 CCTCATCTGCGTTGCCAGGAACCTGTGACGAGAACTTCTCAAGCCCCCATCTTGCCA 61

QY      676 GGAAGCTCTGTGAGGTGCTGCTGATGACCCAGATTCTCCATGTCCTCTGTCTCC 735
Db      62 GGAAGCTCTGTGAGGTGCTGCTGATGACCCAGATTCTCCATGTCCTCTGTCTCC 121

QY      736 TGTGTGCCCCCTCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTGGTTCTGAAGA 795
Db      122 TGTGTGCCCCCTCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTGGTTCTGAAGA 181

QY      796 GAGAGAGACAAGAGAGTACATTGAAGAGAGAGAGAGAGTGGACATTTGTCGGAACTC 855
Db      182 GAGAGAGACAAGAGAGTACATTGAAGAGAGAGAGAGTGGACATTTGTCGGAACTC 241

QY      856 CTAACATATGCCCCCATTTCTGGAGAGACACAGAGTACGACACAATCCCTCACAATA 915
Db      242 CTAACATATGCCCCCATTTCTGGAGAGACACAGAGTACGACACAATCCCTCACAATA 301

QY      916 GAACAATCTTAAGAGAGATCCAGCAATAACGGTTTACTCCACTGTGAAATAACGAAA 975
Db      302 GAACAATCTTAAGAGAGATCCAGCAATAACGGTTTACTCCACTGTGAAATAACGAAA 361

QY      976 AGATGAAAATCCCACTCACTGCTCAGCATGCCAGACACACCAAGGCTATTGCTATG 1035
Db      362 AGATGAAAATCCCACTCACTGCTCAGCATGCCAGACACACCAAGGCTATTGCTATG 421
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QY      1036 AGATGTATTCTAGACAGCAGTGCACTCCCCTAAGTCTCTGCTCAAAAAAAAAACAATTC 1095
Db      422 AGATGTATTCTAGACAGCAGTGCACTCCCCTAAGTCTCTGCTCAAAAAAAAAACAATTC 481

QY      1096 TCGCCCCAAAGAAAACAATCAGAGAATTCAGTATTGACTAGAAACATCAAGGAAGA 1155
Db      482 TCGCCCCAAAGAAAACAATCAGAGAATTCAGTATTGACTAGAAACATCAAGGAAGA 541

QY      1156 TGAAGACGTGACTTTTTCAGAGATAAATTATCTGTGATGCTTCTTAGATTAAAGAG 1215
Db      542 TGAAGACGTGACTTTTTCAGAGATAAATTATCTGTGATGCTTCTTAGATTAAAGAG 601

QY      1216 TTCGTAATTCATCCACTGCTGAGAAATCTCTCAAAACCCAGAAAGTTAATCACTTCAT 1275
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Db      722 TAAAAATGTAAATGCAAGGTACACACATATTATGACAGCCTGTTGTAATTAATGATGCTC 781

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Db      782 CAGTCAGTGTCTGAGATTTCATTCCATCCAGGGCTTGAGTGCAGATTATACCAAGA 841

QY      1456 GTCTTGCTACGAGAGGGCAAGAACCAAAACAGACAGACAAAGTCCAGAGAAGCAGAT 1515
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QY      1576 GAGCTTACCTAAATTGCTCAGACGTGCTGCTGCCCTCATGAATGGCTCCAAATGAAT 1635
Db      962 GAGCTTACCTAAATTGCTCAGACATGCTGCTGCCCTCATGAATGGCTCCAAATGAAT 1021

QY      1636 GAACTACTTTCATGAGCAGTTGTAGACAGCTGACACACAGATTCAGAGGGCCAGGTGT 1695
Db      1022 GAACTACTTTCATGAGCAGTTGTAGACAGCTGACACACAGATTCAGAGGGCCAGGTGT 1081

QY      1696 GGATCCACAGACTTGAAGGTCAAAAGTTCAAAAAGATGAAGAATCAGGGTAGCTGACCAT 1755
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QY      1756 GTTGGCAGATACTAATATGAGACACAGAAGTGTGCATGGCCCAAGACAAGACCTCC 1815
Db      1142 GTTGGCAGATACTAATATGAGACACAGAAGTGTGCATGGCCCAAGACAAGACCTCC 1201

QY      1816 AGCCAGGCTTCAATTATGCACTTGTGCTGCAAAAAGAAAGTCTAGGTTTAAAGGCTGTGC 1875
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QY      1876 CAGAACCCATCCCAATAAAGAGACCGAGTCTGAAGTCACATTTGTAATCTAGTGTAGAG 1935
Db      1261 CAGAACCCATCCCAATAAAGAGACCGAGTCTGAAGTCACATTTGTAATCTAGTGTAGAG 1320

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Db      1321 ACTTGAGTCAGGCAGTGAGACTGGTGGGGCAGGGGGCAGTGGGTAANTGTAAACCTTT 1380

QY      1996 TAAAGATGTTAATTCAT 2013
Db      1381 TAAAGATGTTAATTCAT 1398

RESULT 6
US-10-059-395-15
; Sequence 15, Application US/10059395
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Publication No. US20030018180A1
: GENERAL INFORMATION:
: APPLICANT: Young et al.
: TITLE OF INVENTION: 87 Human Secreted Proteins
: FILE REFERENCE: P2004P1
: CURRENT APPLICATION NUMBER: US/10/059,395
: PRIOR FILING DATE: 2002-01-31
: PRIOR APPLICATION NUMBER: US/09/966,262
: PRIOR FILING DATE: 2001-10-01
: PRIOR APPLICATION NUMBER: US 09/154,707
: PRIOR FILING DATE: 1998-09-17
: PRIOR APPLICATION NUMBER: PCT/US98/05311
: PRIOR FILING DATE: 1998-03-19
: PRIOR APPLICATION NUMBER: US 60/041,277
: PRIOR FILING DATE: 1997-03-21
: PRIOR APPLICATION NUMBER: US 60/042,344
: PRIOR FILING DATE: 1997-03-21
: PRIOR APPLICATION NUMBER: US 60/041,276
: PRIOR FILING DATE: 1997-03-21
: PRIOR APPLICATION NUMBER: US 60/041,281
: PRIOR FILING DATE: 1997-03-21
: PRIOR APPLICATION NUMBER: US 60/048,094
: PRIOR FILING DATE: 1997-05-30
: PRIOR APPLICATION NUMBER: US 60/048,350
: PRIOR FILING DATE: 1997-05-30
: PRIOR APPLICATION NUMBER: US 60/048,188
: PRIOR FILING DATE: 1997-05-30
: PRIOR APPLICATION NUMBER: US 60/048,135
: PRIOR FILING DATE: 1997-05-30
: PRIOR APPLICATION NUMBER: US 60/050,937
: PRIOR FILING DATE: 1997-05-30
: PRIOR APPLICATION NUMBER: US 60/048,187
: PRIOR FILING DATE: 1997-05-30
: PRIOR APPLICATION NUMBER: US 60/048,099
: PRIOR FILING DATE: 1997-05-30
: PRIOR APPLICATION NUMBER: US 60/048,352
: PRIOR FILING DATE: 1997-05-30
: PRIOR APPLICATION NUMBER: US 60/048,186
: PRIOR FILING DATE: 1997-05-30
: PRIOR APPLICATION NUMBER: US 60/048,069
: PRIOR FILING DATE: 1997-05-30
: PRIOR APPLICATION NUMBER: US 60/048,095
: PRIOR FILING DATE: 1997-05-30
: PRIOR APPLICATION NUMBER: US 60/048,131
: PRIOR FILING DATE: 1997-05-30
: PRIOR APPLICATION NUMBER: US 60/048,096
: PRIOR FILING DATE: 1997-05-30
: PRIOR APPLICATION NUMBER: US 60/048,355
: PRIOR FILING DATE: 1997-05-30
: PRIOR APPLICATION NUMBER: US 60/048,160
: PRIOR FILING DATE: 1997-05-30
: PRIOR APPLICATION NUMBER: US 60/048,351
: PRIOR FILING DATE: 1997-05-30
: PRIOR APPLICATION NUMBER: US 60/048,154
: PRIOR FILING DATE: 1997-05-30
: PRIOR APPLICATION NUMBER: US 60/054,804
: PRIOR FILING DATE: 1997-08-05
: PRIOR APPLICATION NUMBER: US 60/056,370
: PRIOR FILING DATE: 1997-08-19
: PRIOR APPLICATION NUMBER: US 60/060,862
: PRIOR FILING DATE: 1997-10-02
: NUMBER OF SEQ ID NOS: 343
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 15
: LENGTH: 1412
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc feature
: LOCATION: (1362)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (1369)

: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (1397)
: OTHER INFORMATION: n equals a,t,g, or c
US-10-059-395-15
Query Match 50.6%; Score 1369.4; DB 14; Length 1412;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1384; Conservative 2; Mismatches 11; Indels 1; Gaps 1;
Qy 616 CCTTCATCTGCGTTGCCAGAACCCCTGTGACGAGAACTTCTCAAGCCCCCATCTTGCCA 675
Db 2 CCTTCATCTGCGTTGCCAGAACCCCTGTGACGAGAACTTCTCAAGCCCCCATCTTGCCA 61
Qy 676 GGAAGCTCTGTGAAGGTGCTGTGATGACCCAGATTCTCCATGCTCTCTGTCTCC 735
Db 62 GGAAGCTCTGTGAAGGTGCTGTGATGACCCAGATTCTCCATGCTCTCTGTCTCC 121
Qy 736 TGTGTGTCCTCCCTCTGCTGCTGCTCTTTGTGATCTGGGCTATTCTTGTGTTCTGAAGA 795
Db 122 TGTGTGTCCTCCCTCTGCTGCTGCTCTTTGTGATCTGGGCTATTCTTGTGTTCTGAAGA 181
Qy 796 GAGAGAGACAAGAGAGATGTAAGAGAGAGAGAGAGAGATGACATTGTCGGAACTC 855
Db 182 GAGAGAGACAAGAGAGATGTAAGAGAGAGAGAGAGATGACATTGTCGGAACTC 241
Qy 856 CTAACTATGCCCCCTCTGAGAGAGACACAGATGACACATCCCTCACACTAATA 915
Db 242 CTAACTATGCCCCCTCTGAGAGAGACACAGATGACACATCCCTCACACTAATA 301
Qy 916 GAACAATCTTAAAGAGATCCAGCAATACGTTTACTCACTGTGGAATACCGAAA 975
Db 302 GAACAATCTTAAAGAGATCCAGCAATACGTTTACTCACTGTGGAATACCGAAA 361
Qy 976 AGATGAAAATCCCCACTCACTGCTCAGCATGCCAGACACCAAGGCTATTGCTATG 1035
Db 362 AGATGAAAATCCCCACTCACTGCTCAGCATGCCAGACACCAAGGCTATTGCTATG 421
Qy 1036 AGAATGTATCTAGACAGCATGCTACCTCCCTAAGTCTCTCAAAAAAACAATTC 1095
Db 422 AGAATGTATCTAGACAGCATGCTACCTCCCTAAGTCTCTCAAAAAAACAATTC 481
Qy 1096 TCGGCCCAAGAAAACAATCAGAAAGATTCACTGATTGCTAGAAAATCAAGAGAA 1155
Db 482 TCGGCCCAAGAAAACAATCAGAAAGATTCACTGATTGCTAGAAAATCAAGAGAA 541
Qy 1156 TGAAGAAAGTTGACTTTTCCAGATAAATTATCTGTGCTCTTTAGATTTAAG 1215
Db 542 TGAAGAAAGTTGACTTTTCCAGATAAATTATCTGTGCTCTTTAGATTTAAG 601
Qy 1216 TTGCTAATTCATCCACTGCTGAGAAATCTCCTCAACCAGAAAGTTTAATCACTTCAT 1275
Db 602 TTGCTAATTCATCCACTGCTGAGAAATCTCCTCAACCAGAAAGTTTAATCACTTCAT 661
Qy 1276 CCCAAAAATGGATTGTGATGTCAAGCAAAACCATAAAAAAGTGCTTAGAAGTATTCCTA 1335
Db 662 CCCAAAAATGGATTGTGATGTCAAGCAAAACCATAAAAAAGTGCTTAGAAGTATTCCTA 721
Qy 1336 TAGAAATGTAAATGCAAGGTCAACATATTAATGACAGCTGTGTATTAATGATGCTC 1395
Db 722 TAAAAATGTAAATGCAAGGTCAACATATTAATGACAGCTGTGTATTAATGATGCTC 781
Qy 1396 CAGGTCAAGTGTGAGTTTCAATTCATCCAGGGCTGTGATGTCAGATTATACCAAGA 1455
Db 782 CAGGTCAAGTGTGAGTTTCAATTCATCCAGGGCTGTGATGTCAGATTATACCAAGA 841
Qy 1456 GTCTTCTACCAAGAGGGCAAGAACCAAAACAGACAGCAAGTCCAGCAGAGCAGAT 1515
Db 842 GTCTTCTACCAAGAGGGCAAGAACCAAAACAGACAGCAAGTCCAGCAGAGCAGAT 901
Qy 1516 GCACCTGACAAAAATGATGTATTAATTGGCTCTATAACTATGTGCCAGCATATGCT 1575
Db 902 GCACCTGACAAAAATGATGTATTAATTGGCTCTATAACTATGTGCCAGCATATGCT 961

OY	1576	GAGCTTACACTAATTGGTCAGACGCGTGCTGTGCCTCATGAATTTGGCTCCAAATGAAT	1635
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Db	962	GAGCTTACACTAATTGGTCAGACATGCTGTCTGCCCTCATGAATTTGGCTCCAAATGAAT	1021
OY	1636	GAAC TACTTT CATGAGCAGTTGTAGCAGGCGCTGACCAGATTC CAGAGGGCCAGGTGT	1695
Db	1022	GAAC TACTTT CATGAGCAGTTGTAGCAGGCGCTGACCAGATTC CAGAGGGCCAGGTGT	1081
OY	1696	GGATCCACAGGACTTGAAGGTC AAAGTTCA CAAAGATGAAGAATCAGGGTAGCTGACCAT	1755
Db	1082	GGATCCACAGGACTTGAAGGTC AAAGTTCA CAAAGATGAAGAATCAGGGTAGCTGACCAT	1141
OY	1756	GTTTGGCAGATACTAATAATGGAGACA CAGAAGTGTGCATGCCCCAAGACAAGAACCTCC	1815
Db	1142	GTTTGGCAGATACTAATAATGGAGACA CAGAAGTGTGCATGCCCCAAGACAAGAACCTCC	1201
OY	1816	AGCCAGGCTTCATTTATGCAC TTGTGCTGCAAAAAGAAAGCTAGGTTTTAAAGGCTGTC	1875
Db	1202	AGCCAGGCTTCATTTATGCAC TTGT - CTGCAAAAAGAAAGCTAGGTTTTAAAGGCTGTC	1260
OY	1876	CAGAACCCATCCCAATAAAGAGACCGAGTCTGAAGTCA CATTTGTAATCTAGGTAGGAG	1935
Db	1261	CAGAACCCATCCCAATAAAGAGACCGAGTCTGAAGTCA CATTTGTAATCTAGGTAGGAG	1320
OY	1936	ACTTGAAGTCAGGCAAGTGAGACTG GTGGGGCACGGGGGGCAGTGGGTACTTGTAAACCTT	1995
Db	1321	ACTTGAAGTCAGGCAAGTGAGACTG GTGGGGCACGGGGGGCANTGGGTANTGTAAACCTT	1380
OY	1996	TAAAGATGTTAATTCAT	2013
Db	1381	TAAAGATGTTAATTCNT	1398

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RESULT 7
US-10-143-090-15
; Sequence 15, Application US/10143090
; Publication No. US20030069406A1
; GENERAL INFORMATION:
;   APPLICANT: Young et al.
;   TITLE OF INVENTION: 87 Human Secreted Proteins
;   FILE REFERENCE: PZ004P1
;   CURRENT APPLICATION NUMBER: US/10/143,090
;   CURRENT FILING DATE: 2002-05-13
;   PRIOR APPLICATION NUMBER: 09/154,707
;   PRIOR FILING DATE: 1998-09-17
;   NUMBER OF SEQ ID NOS: 343
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 1412
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
;   NAME/KEY: misc feature
;   LOCATION: (1362)
;   OTHER INFORMATION: n equals a,t,g, or c
;   FEATURE:
;   NAME/KEY: misc feature
;   LOCATION: (1365)
;   OTHER INFORMATION: n equals a,t,g, or c
;   FEATURE:
;   NAME/KEY: misc feature
;   LOCATION: (1397)
;   OTHER INFORMATION: n equals a,t,g, or c
US-10-143-090-15

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Query Match	50.6%	Score 1369.4	DB 14	Length 1412
Best Local Similarity	99.0%	Pred. No. 0		
Matches 1384	Conservative	2	Mismatches 11	Indels 1
			Gaps	1
QY	616	CCTTCATCTGCGTTGCCAGGAACCTGTGTCAGCAGAACTTCTCAAGCCCCATCCTTGCCA	675	
Db	2	CCTTCATCTGCGTTGCCAGGAACCTGTGTCAGCAGAACTTCTCAAGCCCCATCCTTGCCA	61	

QY	676	GGAGCCTGTGTAAGGTGCTGCTGATGACCCAGATTCTCCATGGTGCTCCTGTGTCTCC	735
DB	62	GGAAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCATGGTGCTCCTGTGTCTCC	121
QY	736	TGTTGGTCCCCCTCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTCTGAAGA	795
DB	122	TGTTGGTCCCCCTCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTCTGAAGA	181
QY	796	GAGAGACAAGAAGATACATTGAAGAGAAGAAGAGTGGACATTTGTGGGAAACTC	855
DB	182	GAGAGACAAGAAGATACATTGAAGAGAAGAAGAGTGGACATTTGTGGGAAACTC	241
QY	856	CTAACATATGCCCCCATTTCTGGAGAGAACACAGAGTACGACACATCCCTCACACTATA	915
DB	242	CTAACATATGCCCCCATTTCTGGAGAGAACACAGAGTACGACACATCCCTCACACTATA	301
QY	916	GAACAATCTTAAAGAAAGATCCAGCAAAATACGGTTTACTCCACTGTGGAATACCGAAA	975
DB	302	GAACAATCTTAAAGAAAGATCCAGCAAAATACGGTTTACTCCACTGTGGAATACCGAAA	361
QY	976	AGATGAAAATCCCCACTCACTGCTCAGATGCCAGACACACCAAGGCTATTTGCCATG	1035
DB	362	AGATGAAAATCCCCACTCACTGCTCAGATGCCAGACACACCAAGGCTATTTGCCATG	421
QY	1036	AGATGTTATCTAGACAGCAGTGCACTCCCCCTAAAGTCTCTGCTCAAAAAAAAAACAATTC	1095
DB	422	AGATGTTATCTAGACAGCAGTGCACTCCCCCTAAAGTCTCTGCTCAAAAAAAAAACAATTC	481
QY	1096	TCGGCCCCAAAGAAAACAATCAGAAGAATTCACTGATTTGACTAGAAACATCAAGGAAGA	1155
DB	482	TCGGCCCCAAAGAAAACAATCAGAAGAATTCACTGATTTGACTAGAAACATCAAGGAAGA	541
QY	1156	TGAAGAACGTGACTTTTTCAGAGATAAATTACTCTGATGCTTCTTAGATTAAAG	1215
DB	542	TGAAGAACGTGACTTTTTCAGAGATAAATTACTCTGATGCTTCTTAGATTAAAG	601
QY	1216	TTCGTAATTCATCCACTGCTGAGAAATCTCCTCAAAACCAGAAGTTTAATCACTTCAT	1275
DB	602	TTCATTAATTCATCCACTGCTGAGAAATCTCCTCAAAACCAGAAGTTTAATCACTTCAT	661
QY	1276	CCCCAAAATGGGATTGTGAATGTCAGCAAAACCATAAAAAAAAGTGCTTAGAAGTATTCCTA	1335
DB	662	CCCCAAAATGGGATTGTGAATGTCAGCAAAACCATAAAAAAAAGTGCTTAGAAGTATTCCTA	721
QY	1336	TAGAAATGTAAATGCAAGGTCAACATATTAATGACAGCCTGTTGATTAATGATGGCTC	1395
DB	722	TAAAAATGTAAATGCAAGGTCAACATATTAATGACAGCCTGTTGATTAATGATGGCTC	781
QY	1396	CAGTCAGTGTGAGGTTTCATTCATCCAGGGCTTGATGTCAGGATTATACCAAGA	1455
DB	782	CAGTCAGTGTGAGGTTTCATTCATCCAGGGCTTGATGTCAGGATTATACCAAGA	841
QY	1456	GTCTTGCTACCAGAGGGGCAAGAACCAAAAACAGACAGACAAGTCCAGCAGAAGCAGAT	1515
DB	842	GTCTTGCTACCAGAGGGGCAAGAACCAAAAACAGACAGACAAGTCCAGCAGAAGCAGAT	901
QY	1516	GCACCTGACAAAAATGGATGTATTAATTGGCTCTATAAATAATGTGCCAGCACTATGCT	1575
DB	902	GCACCTGACAAAAATGGATGTATTAATTGGCTCTATAAATAATGTGCCAGCACTATGCT	961
QY	1576	GAGCTTACACTAATTGGTCAGACGTGCTGTGCCCCCTCATGAAATTTGGCTCCAAATGAAT	1635
DB	962	GAGCTTACACTAATTGGTCAGACATGCTGTGCCCCCTCATGAAATTTGGCTCCAAATGAAT	1021
QY	1636	GAACCTACTTTCAATGACAGAGTTGTAGCAGGCTGACCAACAGATTCCAGAGGGCCAGGTGT	1695
DB	1022	GAACCTACTTTCAATGACAGAGTTGTAGCAGGCTGACCAACAGATTCCAGAGGGCCAGGTGT	1081
QY	1696	GGATCCACAGACTTTGAAGGTCAAAGTTCACAAAGATGAAGAATCAGGGTAGCTGACCAT	1755
DB	1082	GGATCCACAGACTTTGAAGGTCAAAGTTCACAAAGATGAAGAATCAGGGTAGCTGACCAT	1141

Db 1022 GAACTACTTTTCATGAGCAGTTGTAGCAGGCGCTGCACACAGATTCCAGAGGGCCAGGTGT 1081

QY 1696 GGATCCACAGGACTTGAAGSTCAAACTTCACAAAGATGAAGAATCAGGGTAGCTGACCAT 1755

Db 1082 GGATCCACAGGACTTGAAGSTCAAACTTCACAAAGATGAAGAATCAGGGTAGCTGACCAT 1141

Db 781 TGGTTCTGAGAGAGAGACAAGAAGTACATTGAAGAGAAGAGTGACATT 840
QY 843 TGTGGGAACTCCTAACATATGCCCCATTCTGAGAGAACAGAGTACGACAATC 902
Db 841 TGTGGGAACTCCTAACATATGCCCCATTCTGAGAGAACAGAGTACGACAATC 900
QY 903 CCTCACACTAATAGAACATCTTAAAGAGATCCAGCAATACGGTTTACTCGACTGTG 962
Db 901 CCTCACACTAATAGAACATCTTAAAGAGATCCAGCAATACGGTTTACTCGACTGTG 960
QY 963 GAAATACCGAAAAAGATGAAAAATCCCCACTCAGTCTCAGATGCCAGACACCAAGG 1022
Db 961 GAAATACCGAAAAAGATGAAAAATCCCCACTCAGTCTCAGATGCCAGACACCAAGG 1020
QY 1023 CTATTGCTATGAGATGTTATCTAGACAGCAGTGCACTCCCTAAGTCTCTGCTCAA 1082
Db 1021 CTATTGCTATGAGATGTTATCTAGACAGCAGTGCACTCCCTAAGTCTCTGCTCAA 1080
QY 1083 AA 1084
Db 1081 AA 1082

RESULT 9

US-09-989-722-252

; Sequence 252, Application US/09989722

; Patent No. US20020072067A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerlitsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kijavlin, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2730P1C63

; CURRENT APPLICATION NUMBER: US/09/989,722

; PRIOR FILING DATE: 2001-11-19

; PRIOR APPLICATION NUMBER: 60/049787

; PRIOR FILING DATE: 1997-06-16

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/065186

; PRIOR FILING DATE: 1997-11-12

; PRIOR APPLICATION NUMBER: 60/065311

; PRIOR FILING DATE: 1997-11-13

; PRIOR APPLICATION NUMBER: 60/066770

; PRIOR FILING DATE: 1997-11-24

; PRIOR APPLICATION NUMBER: 60/075945

; PRIOR FILING DATE: 1998-02-25

; PRIOR APPLICATION NUMBER: 60/078910

; PRIOR FILING DATE: 1998-03-20

; PRIOR APPLICATION NUMBER: 60/083322

; PRIOR FILING DATE: 1998-04-28

; PRIOR APPLICATION NUMBER: 60/084600

; PRIOR FILING DATE: 1998-05-07

; PRIOR APPLICATION NUMBER: 60/087106

; PRIOR FILING DATE: 1998-05-28

; PRIOR APPLICATION NUMBER: 60/087607

; PRIOR FILING DATE: 1998-06-02

; PRIOR APPLICATION NUMBER: 60/087609

; PRIOR FILING DATE: 1998-06-02

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; PRIOR APPLICATION NUMBER: 60/087827

; PRIOR FILING DATE: 1998-06-03

; PRIOR APPLICATION NUMBER: 60/088021

; PRIOR FILING DATE: 1998-06-04

; PRIOR APPLICATION NUMBER: 60/088025

; PRIOR FILING DATE: 1998-06-04

; PRIOR APPLICATION NUMBER: 60/088026

; PRIOR FILING DATE: 1998-06-04

; PRIOR APPLICATION NUMBER: 60/088028

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; PRIOR FILING DATE: 1998-06-04

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; PRIOR FILING DATE: 1998-06-04

; PRIOR APPLICATION NUMBER: 60/088033

; PRIOR FILING DATE: 1998-06-04

; PRIOR APPLICATION NUMBER: 60/088326

; PRIOR FILING DATE: 1998-06-04

; PRIOR APPLICATION NUMBER: 60/088167

; PRIOR FILING DATE: 1998-06-05

; PRIOR APPLICATION NUMBER: 60/088202

; PRIOR FILING DATE: 1998-06-05

; PRIOR APPLICATION NUMBER: 60/088212

; PRIOR FILING DATE: 1998-06-05

; PRIOR APPLICATION NUMBER: 60/088217

; PRIOR FILING DATE: 1998-06-05

; PRIOR APPLICATION NUMBER: 60/088655

; PRIOR FILING DATE: 1998-06-09

; PRIOR APPLICATION NUMBER: 60/088734

; PRIOR FILING DATE: 1998-06-10

; PRIOR APPLICATION NUMBER: 60/088738

; PRIOR FILING DATE: 1998-06-10

; PRIOR APPLICATION NUMBER: 60/088742

; PRIOR FILING DATE: 1998-06-10

; PRIOR APPLICATION NUMBER: 60/088810

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; PRIOR FILING DATE: 1998-06-16

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; PRIOR FILING DATE: 1998-06-17

; PRIOR APPLICATION NUMBER: 60/089599

; PRIOR FILING DATE: 1998-06-17

; PRIOR APPLICATION NUMBER: 60/089600


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Db      961 AATACCGAAAAAGATGAAAAATCCCACTCACTGCTCAGATGCCAGACACCAAGGCT 1020
QY      1025 ATTTGCCTATGAGAACTTATCTAGACAGACAGTGCCTCCCTAGTCTCTGCTCA 1080
Db      1021 ATTTGCCTATGAGAACTTATCTAGACAGACAGTGCCTCCCTAGTCTCTGCTCA 1076

RESULT 10
US-09-989-723-252
; Sequence 252, Application US/09989723
; Patent No. US20020072092A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C62
; CURRENT APPLICATION NUMBER: US/09/989,723
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088858
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; PRIOR FILING DATE: 1998-07-09

Query Match 39.8%; Score 1076; DB 9; Length 1076;
Best Local Similarity 100.0%; Pred. No. 1.5e-294;
Matches 1076; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGGCTTCATTTCAGTGGCTGACTTCAGAGAGCAATATGGCTGGTTCCCCAACATGCTT 64

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QY 125 GCTGTCGGTTCCTGGTGGGGCCGTGACTTTCCTCCCTGAAGTCCAAGTAAGCAAGT 184
Db 121 GCTGTCGGTTCCTGGTGGGGCCGTGACTTTCCTCCCTGAAGTCCAAGTAAGCAAGT 180
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; Sequence 252, Application US/09989279
; Patent No. US20020072496A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyer, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
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; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC56
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RESULT 12
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; Sequence 252, Application US/09989727
; Patent No. US2002072497A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC65
CURRENT APPLICATION NUMBER: US/09/989,727
PRIOR FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 39.8%; Score 1076; DB 9; Length 1076;
Best Local Similarity 100.0%; Pred. No. 1.5e-294;
Matches 1076; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGGCTCATTTAGTGGCTGACTTCAGAGAGCAATATGGCTGCCCAACATGCTT 64
Db 1 GTGGCTCATTTAGTGGCTGACTTCAGAGAGCAATATGGCTGCCCAACATGCTT 60
QY 65 CACCCATCTATATCTTTGGCAGCTCAAGGTCAGCAGCCTTGGAACCGTGAAGA 124
Db 61 CACCCATCTATATCTTTGGCAGCTCAAGGTCAGCAGCCTTGGAACCGTGAAGA 120
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Db 121 GCTGTCGGTTCGTTGGTGGGGCCGTTGACTTTCCCCCTGAAGTCAAAAGTAAAGCAAGT 180
QY 185 TGACTCTATTGTCTGGACCTTCAACACAAACCCCTCTTGTCAACCAATACAGCCAGAAAGGGG 244
Db 181 TGACTCTATTGTCTGGACCTTCAACACAAACCCCTCTTGTCAACCAATACAGCCAGAAAGGGG 240
QY 245 CACTATCATAGTAGCCCAAAATCGTAATAGGAGAGAGTAGACTTCCAGATGAGGCTA 304
Db 241 CACTATCATAGTAGCCCAAAATCGTAATAGGAGAGAGTAGACTTCCAGATGAGGCTA 300
QY 305 CTCCCTGAAGCTCAGCAAACTGAAGAAGATGACTCAGGGATCTACTATGTGGGATATA 364
Db 301 CTCCCTGAAGCTCAGCAAACTGAAGAAGATGACTCAGGGATCTACTATGTGGGATATA 360
QY 365 CAGCTCATCACTCCAGCAGCCCTCCACCCAGGAGTAGCTGCTGATGTCTACGAGCACCCT 424

Db 361 CAGCTCATCACTCCAGCAGCCCTCCACCCAGGAGTAGCTGCTGATGTCTACGAGCACCCT 420
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QY 485 TCTGACATGCTGCATGGAACATGGGGAAGAGATGTGATTTATACCTGGAAGGCCCTGG 544
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QY 1025 ATTGCTTATGAGATGTATCTAGACAGCAGTGCATCCCTAAGTCTCTGCTCA 1080
Db 1021 ATTGCTTATGAGATGTATCTAGACAGCAGTGCATCCCTAAGTCTCTGCTCA 1076

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; Sequence 252, Application US/09989731
; Patent No. US20020103125A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Guirney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC70
CURRENT APPLICATION NUMBER: US/09/989,731
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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QY 425 GTCAAAGCTAAAGTCAACCATGGGTCTGAGAGCAATAGAATGGCACTGTGTGACCAA 484
DB 421 GTCAAAGCTAAAGTCAACCATGGGTCTGAGAGCAATAGAATGGCACTGTGTGACCAA 480
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DB 481 TCTGACATGCTGCATGGAACATGGGGAGAGAGATGTGATTTATACCTGGAAGCCCTGGG 540
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QY 785 GTTCTGAAGAGAGAGACAAAGAGTACATTGAGAGAAAGAGAGTGCACATTG 844
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; Sequence 252, Application US/09989732
; Patent No. US20020123463A1
; GENERAL INFORMATION:
; APPLICANT: Aeshkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C57
; CURRENT APPLICATION NUMBER: US/09/989,732
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
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; PRIOR FILING DATE: 1998-07-09

Query Match 39.8%; Score 1076; DB 9; Length 1076;
Best Local Similarity 100.0%; Pred. No. 1.5e-294;
Matches 1076; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 901 TCACACTAATAGAACAACTCTTAAGGAAGATCCAGCAATACGTTTACTCCACTGTGA 960
QY 965 AATACCGAAAAAGATGAAAAATCCCACTCACTGCTCAGATGCCAGACACCAAGGCT 1024
DB 961 AATACCGAAAAAGATGAAAAATCCCACTCACTGCTCAGATGCCAGACACCAAGGCT 1020
QY 1025 ATTTGCTTATGAGAAATGTTATCTAGACAGCAGTGCATCCCTAAGTCTGTCTCA 1080
DB 1021 ATTTGCTTATGAGAAATGTTATCTAGACAGCAGTGCATCCCTAAGTCTGTCTCA 1076

RESULT 15
US-09-991-073-252
; Sequence 252, Application US/09991073
; Patent No. US20020127576A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C15
; CURRENT APPLICATION NUMBER: US/09/991, 073
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING-DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322

; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091978
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/091982
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

Query Match	39.8%	Score 1076;	DB 9;	Length 1076;
Best Local Similarity	100.0%	Pred. No. 1.5e-294;		
Matches 1076; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	5	GTGGCTTCATTTTCAGTGGCTGACTTCCAGAGAGCAATATGGCTGTTCCCAACATGCTT	64
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QY	65	CACCCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGSAACCCGTGAAGA	124
Db	61	CACCCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGSAACCCGTGAAGA	120
QY	125	GCTGGTCCGTTCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAGCAAGT	184
Db	121	GCTGGTCCGTTCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAGCAAGT	180
QY	185	TGACTCTATTGTCTGGACCTTCAACACAAACCCCTTGTCAACATACAGCCAGAGGGGG	244
Db	181	TGACTCTATTGTCTGGACCTTCAACACAAACCCCTTGTCAACATACAGCCAGAGGGGG	240
QY	245	CACATATCATAGTGACCCCAAAATCGTAATAGGAGAGAGTAGACTTCCAGATGAGGCTA	304
Db	241	CACATATCATAGTGACCCCAAAATCGTAATAGGAGAGAGTAGACTTCCAGATGAGGCTA	300
QY	305	CTCCCTGGAAGCTCAGCAAACTGGAAGAAATGACTCAGGATCTACTATGTGGGATATA	364
Db	301	CTCCCTGGAAGCTCAGCAAACTGGAAGAAATGACTCAGGATCTACTATGTGGGATATA	360
QY	365	CAGCTCATCACTCCAGCAGCCCTCCACCAGAGTAGCTGTCATGTCTACGACACCT	424
Db	361	CAGCTCATCACTCCAGCAGCCCTCCACCAGAGTAGCTGTCATGTCTACGACACCT	420
QY	425	GTCAAGCCCTAAAGTCACCATGGGTCTGCAGAGCAATTAAGATGGCACCCTGTGACCAA	484
Db	421	GTCAAGCCCTAAAGTCACCATGGGTCTGCAGAGCAATTAAGATGGCACCCTGTGACCAA	480
QY	485	TCTGACATGCTGCATGGAACATGGGGAAGAGATGTGATTATACCTGGAAGCCCTGGG	544
Db	481	TCTGACATGCTGCATGGAACATGGGGAAGAGATGTGATTATACCTGGAAGCCCTGGG	540
QY	545	GCAAGCAGCCAAATGAGTCCCATTAATGGGTCCATCCTCCCATCTCTGGAGATGGGAGA	604
Db	541	GCAAGCAGCCAAATGAGTCCCATTAATGGGTCCATCCTCCCATCTCTGGAGATGGGAGA	600
QY	605	AAGTGATATGACCTTCATCTGCGTTGCCAGGAACCCCTGTCAGCAGAACTTCTCAAGCCC	664
Db	601	AAGTGATATGACCTTCATCTGCGTTGCCAGGAACCCCTGTCAGCAGAACTTCTCAAGCCC	660
QY	665	CATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTTCATGGTCTT	724
Db	661	CATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTTCATGGTCTT	720
QY	725	CCTGTGTCCTCTGTTGGTGCCCTCTGCTCAGTCTCTTGTACTGGGGCTATTCTTTG	784
Db	721	CCTGTGTCCTCTGTTGGTGCCCTCTGCTCAGTCTCTTGTACTGGGGCTATTCTTTG	780
QY	785	GTTTCTGAAGAGAGAGACAAGAAGATACATTGAAAGAGAAGAAGATGACATTG	844
Db	781	GTTTCTGAAGAGAGAGACAAGAAGATACATTGAAAGAGAAGAAGATGACATTG	840
QY	845	TCCGGAACCTCCTAACATATGCCCCCATTTCTGGAAGAACACAGATACGACACAATCCC	904
Db	841	TCCGGAACCTCCTAACATATGCCCCCATTTCTGGAAGAACACAGATACGACACAATCCC	900
QY	905	TCACACTAATAGAACAAATCCTAAAGAGAGATCCAGCAAAATACGGTTTACTCCACTGTGGA	964

Db 901 TCACACTAATAGAACATCCCTAAAGGAGATCCAGCAATACGGTTACTCCACTGTGGA 960

Qy 965 AATACCGAAAAAGATGGAATAATCCCCCACTCACTGCTCACGATGCCAGACACACCAAGCT 1024

Db 961 AATACCGAAAAAGATGGAATAATCCCCCACTCACTGCTCACGATGCCAGACACACCAAGCT 1020

Qy 1025 ATTTGCCCTATGAGAAATGTTATCTAGACAGCAGTGCATCCCCCTAAGTCTTGCTCA 1080

Db 1021 ATTTGCCCTATGAGAAATGTTATCTAGACAGCAGTGCATCCCCCTAAGTCTTGCTCA 1076

Search completed: October 28, 2004, 13:30:12
Job time : 1274 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 28, 2004, 03:57:30 ; Search time 222 Seconds
(without alignments)
8657.537 Million cell updates/sec

Title: US-09-745-605-1

Perfect score: 2704

Sequence: 1 ggaagtgctcattcattcagc.....aaaaaaaaaaaaaaaaaa 2704

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*

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- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	890.2	32.9	921	4	US-09-023-655-401
2	375.6	13.9	435	4	US-09-513-999C-21312
3	331.6	12.3	344	4	US-09-513-999C-395
4	194.4	7.2	5037	4	US-09-705-299-13
5	190.8	7.1	4773	3	US-08-884-324-9
6	190.8	7.1	4773	4	US-09-479-862-9
7	190.8	7.1	11464	3	US-08-884-324-13
8	190.8	7.1	11464	4	US-09-479-862-13
9	190.8	7.1	28994	4	US-08-884-324-14
10	190.8	7.0	114793	4	US-10-148-806-3
11	189.4	7.0	39982	4	US-09-820-924-3
12	188.4	7.0	39982	4	US-10-369-626-3
13	188.4	6.9	162450	3	US-09-345-882-1
14	187.4	6.9	319608	4	US-09-539-333D-1
15	187.4	6.9	319608	4	US-09-679-409-1
16	187.4	6.9	55298	4	US-09-491-356C-1
17	186.4	6.9	11811	3	US-09-078-294-7
18	185.4	6.8	17000	4	US-09-548-797B-7
19	185.2	6.8	9365	3	US-09-608-285A-8
20	184.8	6.8	9365	3	US-09-608-285A-8
21	184.8	6.8	9365	3	US-09-350-836B-8
22	184.8	6.8	9365	4	US-09-370-265-8
23	184.8	6.8	9365	4	US-09-557-800C-8
24	184.8	6.8	9365	4	US-09-370-625A-8
25	184.8	6.8	14747	3	US-09-608-285A-42
26	184.8	6.8	14747	4	US-09-557-800C-42
27	184.8	6.8	15977	3	US-09-608-285A-59

28	184.6	6.8	148567	4	US-09-801-876B-3	Sequence 3, Appli
29	184.6	6.8	148567	4	US-10-254-869-3	Sequence 3, Appli
30	183.4	6.8	2921	3	US-08-618-100B-4	Sequence 4, Appli
31	183.2	6.8	55298	4	US-09-491-356C-1	Sequence 1, Appli
32	183	6.8	70000	4	US-09-851-896-3	Sequence 3, Appli
33	182.6	6.8	81001	4	US-09-750-580-1	Sequence 1, Appli
34	182.4	6.7	466	4	US-09-621-976-18219	Sequence 18219, A
35	182	6.7	64467	4	US-09-803-671B-3	Sequence 3, Appli
36	181.8	6.7	41684	4	US-09-536-059-1	Sequence 1, Appli
37	181.8	6.7	80246	3	US-09-078-294-4	Sequence 4, Appli
38	181.8	6.7	80595	3	US-09-078-294-3	Sequence 3, Appli
39	181.6	6.7	489	4	US-09-621-976-17265	Sequence 17265, A
40	181.6	6.7	111282	3	US-09-754-250-3	Sequence 3, Appli
41	181	6.7	66933	4	US-09-544-398B-11	Sequence 11, Appli
42	181	6.7	66933	4	US-09-543-771-11	Sequence 11, Appli
43	181	6.7	72049	4	US-09-544-398B-9	Sequence 9, Appli
44	181	6.7	72049	4	US-09-543-771-9	Sequence 9, Appli
45	180.8	6.7	106746	4	US-09-326-402C-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-023-655-401
; Sequence 401, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 401:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 921 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: THPLBL02
; CLONE: 156352
; US-09-023-655-401

Query Match 32.9%; Score 890.2; DB 4; Length 921;

[illegible]

RESULT 2
US-09-513-999C-21312
; Sequence 21312, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:

```

; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513, 999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 21312
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-21312

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Query Match	13.9%	Score 375.6;	DB 4;	Length 435;
Best Local Similarity	97.3%;	Pred. No. 1.9e-101;		
Matches 426;	Conservative	0;	Mismatches 4;	Indels 8;
				Gaps 4;

QY	1857	CTAGTTTAAAGCGCTGTGCCAGAACCCATCCCAATAAAGAGACCGAGTCTGAAGTCAAT	1916
Db	1	CTAGTTTAAAGCGCTGTGCCAGAACCCATCCCAATAAAGAGACCGAGTCTGAAGTCAAT	60
QY	1917	TGTAAATCTAGTGTAGAGAACTTGAGTCAGGCACTGAGACTGTGGGGCACGGGGCA	1976
Db	61	TGTAAATCTAGTGTAGAGAACTTGAGTCAGGCACTGAGACTGTGGGGCACGGGGCA	120
QY	1977	GTGGTACTGTGTAACCTTTAAAGATGTTAAATTCATTCAATAGATATTATTAAGAAC	2036
Db	121	GTGGTACTGTGTAACCTTTAAAGATGTTAAATTCATTCAATAGATATTATTAAGAAC	179
QY	2037	TACTATGCGGCCCGCATGTGTGCTCACACCTGTAAATCCAGACCTTTGGAGGCCAAG	2096
Db	180	--CTATGCGGCCCGCATGTGTGCTCACACCTGTAAATCCAGACCTTTGGAGGCCAAG	237
QY	2097	TGGGTGGGTCACTGAGGTCAGAGTTCAGAGCCAGCCCTGGCCACATGGTGAACCCCA	2156
Db	238	TGGGTGGGTCACTGAGGTCAGAGTTCAGAGTTCAGAGCCAGCCCTGGCCACATGGTGAACCCCA	297
QY	2157	TCTCTACTAAAGAT--CAAAATTTGCTGAGCGGTGTGTGTGCACCTGT-ATCCCACTA	2213
Db	298	TCTCTACTAAAGATCAAAATTTGCTGAGCGGTGTGTGTGCACCTGTAAATCCCACTA	357
QY	2214	CTCGAGAGGCCCAAGGCATGAGAATCGCTTGAACCTGG--AGGTAGGTTGCAGTGAAGCTG	2271
Db	358	CTCGAGAGGCCCAAGGCATGAGAATCGCTTGAACCTGGAGGTTGAGGTTGCAGTGAAGCTG	417
QY	2272	AGATGGCACCACTGCACT 2289	
Db	418	AGATGGCACCACTGCACT 435	

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RESULT 3
; US-09-513-999C-395
; Sequence 395, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513, 999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122, 487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 395

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LENGTH: 344
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 54..344
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 54..119
OTHER INFORMATION: score 5.9
OTHER INFORMATION: seq LIVILWQLTGSAA/SG
FEATURE:
NAME/KEY: misc_feature
LOCATION: 197
OTHER INFORMATION: k=g or t
US-09-513-999C-395

Query Match 12.3%; Score 331.6; DB 4; Length 344;
Best Local Similarity 99.7%; Pred. No. 1.9e-88;
Matches 331; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGTGGCTTCATTTCACTGAGTGGCTGACTTCCAGAGAGCAATATGGCTGTTCCCAACAT 60
DB 13 GGAAGTGGCTTCATTTCACTGAGTGGCTGACTTCCAGAGAGCAATATGGCTGTTCCCAACAT 72
QY 61 GCCTCACCCTCATCTATATCTTTGGCAGCTCAGAGGCTCAGCAGCCTCTGAGCCCGTGA 120
DB 73 GCCTCACCCTCATCTATATCTTTGGCAGCTCAGAGGCTCAGCAGCCTCTGAGCCCGTGA 132
QY 121 AAGAGCTGGTGGTCCGTTGGTGGGCGCGTGACTTCCCGCTGAAGTCCAAAGTAAAGC 180
DB 133 AAGAGCTGGTGGTCCGTTGGTGGGCGCGTGACTTCCCGCTGAAGTCCAAAGTAAAGC 192
QY 181 AAGTGACTTATGTCTGGACCTTCAACACACACCCCTTGTCAACATACAGCCAGAAG 240
DB 193 AAGTGACTTATGTCTGGACCTTCAACACACACCCCTTGTCAACATACAGCCAGAAG 252
QY 241 GGGCACTATCATAGTGAACCCAAATCGTAATAGGAGAGAGTAGACTTCCAGATGGAG 300
DB 253 GGGCACTATCATAGTGAACCCAAATCGTAATAGGAGAGAGTAGACTTCCAGATGGAG 312
QY 301 GCTACTCCCTGAGCTCAGCAAACTGAAGAAG 332
DB 313 GCTACTCCCTGAGCTCAGCAAACTGAAGAAG 344

RESULT 4

US-09-705-299-13
Sequence 13, Application US/09705299
Patent No. 6440737
GENERAL INFORMATION:
APPLICANT: Lex M. Cowbert
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF CELLULAR APOPTOSIS SUSCEPTIBILITY GENE
FILE REFERENCE: RTS-0174
CURRENT APPLICATION NUMBER: US/09/705,299
CURRENT FILING DATE: 2000-11-01
NUMBER OF SEQ ID NOS: 86
SEQ ID NO 13
LENGTH: 5037
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION:
NAME/KEY: unsure
LOCATION: 801
OTHER INFORMATION: unknown
US-09-705-299-13

Query Match 7.2%; Score 194.4; DB 4; Length 5037;
Best Local Similarity 79.9%; Pred. No. 7.6e-47;
Matches 254; Conservative 0; Mismatches 61; Indels 3; Gaps 2;

QY 2028 TTAAAGACCTACTATGCGGCCCGGCGATGGTGGCTCACACCTGTATCCAGCACTTGGG 2087
DB 2892 TTTAAAACTTAACCTTTGGTCGGGCGTGGCTCACACCTGTATCCAGCACTTGGG 2951
QY 2088 AGCCCAAGGTGGTGGTCTCATCTGAGTCAAGAGTTCAAGACCAGCCTGCCCAACATGGT 2147
DB 2952 AGCCGAGGTGGCAGATCACCTGAGTCAAGAGTTCAAGACCAGCCTGCCCAACATGGC 3011
QY 2148 GAAACCCCATCTCTAATAAGATCAAAATTGCTGAGCGTGGTGTGCACTGT-ATC 2206
DB 3012 GAAACCCCGTCTCTACTAAATAATAAATTACGTGGGTGTGGCAGCGCTGTAATC 3071
QY 2207 CCAGTACTCGAGAGGCCCAAGGCATGAATCGCTTGAACCTGG--AGGTGAGCTTGCAG 2264
DB 3072 CCAGTACTCAGAGGCTGAGGCAAGGAAATCGCTTGAACCTGGGAAAGCAGAGCTTGCAG 3131
QY 2265 TGAGCTGAGATGGCAACCACTGCACTCCGGCCTAGGCAACGAGAGCAAACTCCAATACAA 2324
DB 3132 TGAGCCAAAGATCGCCCATTTGCACTTACCTTGGGCAACAGAGTGAACCTCCGTCTCAA 3191
QY 2325 ACAACCAACAACACCT 2342
DB 3192 AGAAAAAAATACTT 3209

RESULT 5

US-08-884-324-9
Sequence 9, Application US/08884324
Patent No. 6060283
GENERAL INFORMATION:
APPLICANT: Takamori OKURA
APPLICANT: Kakuji TORIGOE
APPLICANT: Masahiro KURIMOTO
TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE
OF INDUCING THE PRODUCTION OF INTERFERON-
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/884,324
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 185,305/96
FILING DATE: 27-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: OKURA=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 4773 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: human
TISSUE TYPE: placenta
FEATURE:


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; NAME/KEY: intron
; LOCATION: 1..4773
; IDENTIFICATION METHOD: E
US-08-884-324-9

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Query Match	7.1%;	Score 190.8;	DB 3;	Length 4773;
Best Local Similarity	77.9%;	Pred. No. 8.6e-46;		
Matches 268; Conservative	0;	Mismatches 72;	Indels 4;	Gaps 3;

QY	2004	GTTAATTCATTCAATAGATAATTATTAAGAACCCTACTATGCGGCCCGGCATGTGGCTCA 	2063
Db	1334	GTTTATTCAATTTTGATGCGCCCTTTAAATMAAAGAATGTGGCTGGCGTGTGGCTCA 	1393
QY	2064	CACCTGTAATCCCAGCACATTTGGGAGGCCAAGGTGGGTGCATCTGAGGTCAGAGATT 	2123
Db	1394	CACCTGTAATCCAGCACATTTGGGAGGCCGAGGGGGCGGATCACCAGTCAGAGATT 	1453
QY	2124	CAAGACCAGCCTGGCCAACATGTGTGA AACCCCATCTCTAATAAGAT - CAAAATTTGCTG 	2182
Db	1454	CAAGACCAGCCTGACCAACATGAGAA ACCCATCTCTAATAAATA CA AAATTAGCTG 	1513
QY	2183	AGCGTGTGTGTGCACTGT- ATCCAGCTACTCGAAGGCCAAGGCATGAGAATCGCT 	2241
Db	1514	GGCGTGTGTCATATGCGCTGTAATCCAGCTACTCGGAGGCTGAGGCAGAGAAATCTTT 	1573
QY	2242	TGAACCTGG-- AGGTGAGTTTGCAGTGA GCTGAGATGGCAACA CTGCACTCCGGCCTTAGG 	2299
Db	1574	TGAACCCCGGAGGCGAGAGTTGCGATGAGCCTAGATCGTGCCA TTGCACTCCAGCCTGGG 	1633
QY	2300	CAACGAGAGCAA AACTCCAAATTACA AACA AACA AACA AACA CCTG 2343 	
Db	1634	CAACAAGAGCAA AACTCGGTCTCA AAAAAAAAAAAAAA AAGTG 1677 	

RESULT 6
US-09-479-862-9
; Sequence 9, Application US/09479862

```

? GENERAL INFORMATION:
? APPLICANT: TAKAMORI OKURA
? APPLICANT: KAKUJI TORIGOE
? APPLICANT: MASASHI KURIMOTO
? TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE
? TITLE OF INVENTION: OF INDUCING THE PRODUCTION OF INTERFERON-
? NUMBER OF SEQUENCES: 35
? CORRESPONDENCE ADDRESS:
?

```

```

; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/479,862
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/ CLASSIFICATION:
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/884,324
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BROWDY, Roger L.
/ REGISTRATION NUMBER: 25,618
/ REFERENCE/DOCKET NUMBER: OKURA=1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-628-5197
/ TELEFAX: 202-737-3528
/ INFORMATION FOR SEQ ID NO: 9:
/ SEQUENCE CHARACTERISTICS:

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; LENGTH: 4773 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: human
; TISSUE TYPE: placenta
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1..4773
; IDENTIFICATION METHOD: E
US-09-479-862-9

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Query Match	7.1%;	Score 190.8;	DB 4;	Length 4773;
Best Local Similarity	77.9%;	Pred. No. 8.6e-46;		
Matches 268;	Conservative	0;	Mismatches 72;	Indels 4;
				Gaps 3;

[illegible]

RESULT 7
US-08-884-324-13
: Sequence 13, Application US/088843224

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; GENERAL INFORMATION:
; APPLICANT: Takanori OKURA
; APPLICANT: kakuji TORIGOE
; APPLICANT: Masashi KURIMOTO
; TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE
; TITLE OF INVENTION: OF INDUCING THE PRODUCTION OF INTERFERON-
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
;

```

STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/884,324
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 185,305/96
FILING DATE: 27-JUN-1996

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 185,305/96
FILING DATE: 27-JUN-1996

LOCATION: 1466..4848
IDENTIFICATION METHOD: E
NAME/KEY: leader peptide
LOCATION: 4849..4865
IDENTIFICATION METHOD: S
NAME/KEY: mat peptide
LOCATION: 4866..4983
IDENTIFICATION METHOD: S
NAME/KEY: intron
LOCATION: 4984..6317
IDENTIFICATION METHOD: E
NAME/KEY: mat peptide
LOCATION: 6318..6451
IDENTIFICATION METHOD: S
NAME/KEY: intron
LOCATION: 6452..11224
IDENTIFICATION METHOD: E
NAME/KEY: mat peptide
LOCATION: 11225..11443
IDENTIFICATION METHOD: S
NAME/KEY: 3'UTR
LOCATION: 11444..11464
IDENTIFICATION METHOD: E
US-09-479-862-13

Query Match 7.1%; Score 190.8; DB 4; Length 11464;
Best Local Similarity 77.9%; Pred. No. 1.6e-45;
Matches 268; Conservative 0; Mismatches 72; Indels 4; Gaps 3;

QY 2004 GTTAATTCATTCATAGATATTTATTAGAACCTACTATGCGCGCGCATGTGGCTCA 2063
DB 7785 GTTTATTCATTTTGTATGCGCCCTTTTAAATAAAGAATGTGGCGGTGGCTCA 7844
QY 2064 CACCTGTAATCCAGCAGCACTTTGGAGGCCAAGGTGGTGGTCACTGAGGTGAGGATT 2123
DB 7845 CACCTGTAATCCAGCAGCACTTTGGAGGCCAAGGTGGTGGTCACTGAGGTGAGGATT 7904
QY 2124 CAAGACCAGCCTGGCCACATGATGTAACCCCATCTCTACTAAAGAT-CAAAATTGCTG 2182
DB 7905 CAAGACCAGCCTGACCAATGAGAAACCCCATCTCTACTAAATAAATAAATTAGCTG 7964
QY 2183 AGCGTGTGTGTGACACTGT-ATCCAGCTACTCGAGGCCAAGGCATGAGATCGCT 2241
DB 7965 GCGGTGTGTGATATGCTGTATCCAGCTACTCGGAGGCTGAGGAGGAGATCTTT 8024
QY 2242 TGAACCTG--AGGTGAGGTGACGTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2299
DB 8025 TGAACCTG--AGGTGAGGTGACGTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 8084
QY 2300 CAACGAGAGCAAACTCCCAATACAAACAAACAAACACCTG 2343
DB 8085 CAACGAGAGCAAACTCCGCTCTCAAAAAAAGTGTG 8128

RESULT 9

US-08-884-324-14
Sequence 14, Application US/08884324
Patent No. 6060283

GENERAL INFORMATION:
APPLICANT: Takanori OKURA
APPLICANT: Kakui TORIGOE
APPLICANT: Masahi KURIMOTO
TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE
OF INDUCING THE PRODUCTION OF INTERFERON-
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/884,324
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 185,305/96
FILING DATE: 27-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: OKURA=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 28994 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: human
TISSUE TYPE: placenta
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..15606
IDENTIFICATION METHOD: E
NAME/KEY: leader peptide
LOCATION: 15607..15685
IDENTIFICATION METHOD: S
NAME/KEY: intron
LOCATION: 15686..17056
IDENTIFICATION METHOD: E
NAME/KEY: leader peptide
LOCATION: 17057..17068
IDENTIFICATION METHOD: S
NAME/KEY: intron
LOCATION: 17069..20451
IDENTIFICATION METHOD: E
NAME/KEY: leader peptide
LOCATION: 20452..20468
IDENTIFICATION METHOD: S
NAME/KEY: mat peptide
LOCATION: 20469..20586
IDENTIFICATION METHOD: S
NAME/KEY: intron
LOCATION: 20587..21920
IDENTIFICATION METHOD: E
NAME/KEY: mat peptide
LOCATION: 21921..22054
IDENTIFICATION METHOD: S
NAME/KEY: intron
LOCATION: 22055..26827
IDENTIFICATION METHOD: E
NAME/KEY: mat peptide
LOCATION: 26828..27046
IDENTIFICATION METHOD: S
NAME/KEY: 3'UTR
LOCATION: 27047..28994
IDENTIFICATION METHOD: E
US-08-884-324-14

Query Match 7.1%; Score 190.8; DB 3; Length 28994;
Best Local Similarity 77.9%; Pred. No. 2.9e-45;
Matches 268; Conservative 0; Mismatches 72; Indels 4; Gaps 3;

QY 2004 GTTAATTCATTCATAGATATTTATTAGAACCTACTATGCGCGCGCATGTGGCTCA 2063
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Db 23388 GTTATTCAATTTGATGCGCCCTTTAAATAAAGATGTGGCTGGCGGTGGCTCA 23447
QY 2064 CACCTGTATCCAGCACTTTGGAGGCCAAGGTGGTGCATCTGAGTCAGAGTT 2123
Db 23448 CACCTGTATCCAGCACTTTGGAGGCCAAGGTGGTGCATCTGAGTCAGAGTT 23507
QY 2124 CAAGACCAGCCTGGCCCAATGCTGAACCCCATCTCTACTAAAGAT-CAAAATTGCTG 2182
Db 23508 CAAGACCAGCCTGACCAATGAGAAACCCCATCTCTACTAAATATCAAAATTAGCTG 23567
QY 2183 AGCGTGTGTGTGTCACCTGT-ATCCAGCTACTGAGAGGCCAAGGCATGAGATCGCT 2241
Db 23568 GCGGTGTGTGTCATATGCTGTATCCAGCTACTGAGAGGCCAAGGCATGAGATCTTT 23627
QY 2242 TGAACCTGG--AGGTAGGTTGCACTGAGTGAAGCCCACTGCACTCCGGCCTAGG 2299
Db 23628 TGAACCCGGGAGGCAAGGTTGCGATGAGCCTAGATGTCATTGCACTCCAGCCTGGG 23687
QY 2300 CAACGAGAGCAAACTCCAAATACAAACAACAACCAACACCTG 2343
Db 23688 CAACAAGAGCAAAACTCGGTCTCAAAAAAAAAAAAAAAAAAGTG 23731
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RESULT 10

US-09-479-862-14

; Sequence 14, Application US/09479862

; Patent No. 6790442

; GENERAL INFORMATION:

; APPLICANT: Takanori OKURA

; APPLICANT: Kakuji TORIGOE

; APPLICANT: Masahiro KURIMOTO

; TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE

; TITLE OF INVENTION: OF INDUCING THE PRODUCTION OF INTERFERON-

; NUMBER OF SEQUENCES: 35

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BROWDY AND NEIMARK

; STREET: 419 Seventh Street, N.W., Suite 300

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/479,862

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/884,324

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: BROWDY, Roger L.

; REGISTRATION NUMBER: 25,618

; REFERENCE/DOCKET NUMBER: OKURA=1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-628-5197

; TELEFAX: 202-737-3528

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 28994 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: Genomic DNA

; ORIGINAL SOURCE:

; ORGANISM: human

; TISSUE TYPE: placenta

; FEATURE:

; NAME/KEY: 5'UTR

; LOCATION: 1..15606

```
IDENTIFICATION METHOD: E
NAME/KEY: leader peptide
LOCATION: 15607..15685
IDENTIFICATION METHOD: S
NAME/KEY: intron
LOCATION: 15686..17056
IDENTIFICATION METHOD: E
NAME/KEY: leader peptide
LOCATION: 17057..17068
IDENTIFICATION METHOD: S
NAME/KEY: intron
LOCATION: 17069..20451
IDENTIFICATION METHOD: E
NAME/KEY: leader peptide
LOCATION: 20452..20468
IDENTIFICATION METHOD: S
NAME/KEY: mat peptide
LOCATION: 20469..20586
IDENTIFICATION METHOD: S
NAME/KEY: intron
LOCATION: 20587..21920
IDENTIFICATION METHOD: E
NAME/KEY: mat peptide
LOCATION: 21921..22054
IDENTIFICATION METHOD: S
NAME/KEY: intron
LOCATION: 22055..26827
IDENTIFICATION METHOD: E
NAME/KEY: mat peptide
LOCATION: 26828..27046
IDENTIFICATION METHOD: S
NAME/KEY: 3'UTR
LOCATION: 27047..28994
IDENTIFICATION METHOD: E
US-09-479-862-14
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Query Match

Best Local Similarity

Matches

Conservative

0; Mismatches

72; Indels

4; Gaps

3;

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QY 2004 GTTATTCAATTTGATGAGTATTTATTAAGAACTACTATGCGCCCGCATGTGCTCA 2063
Db 23388 GTTATTCAATTTGATGAGTATTTATTAAGAACTACTATGCGCCCGCATGTGCTCA 23447
QY 2064 CACCTGTATCCAGCACTTTGGAGGCCAAGGTGGTGCATCTGAGTCAGAGTT 2123
Db 23448 CACCTGTATCCAGCACTTTGGAGGCCAAGGTGGTGCATCTGAGTCAGAGTT 23507
QY 2124 CAAGACCAGCCTGGCCCAATGCTGAACCCCATCTCTACTAAAGAT-CAAAATTGCTG 2182
Db 23508 CAAGACCAGCCTGACCAATGAGAAACCCCATCTCTACTAAATATCAAAATTAGCTG 23567
QY 2183 AGCGTGTGTGTGTCACCTGT-ATCCAGCTACTGAGAGGCCAAGGCATGAGATCGCT 2241
Db 23568 GCGGTGTGTGTCATATGCTGTATCCAGCTACTGAGAGGCCAAGGCATGAGATCTTT 23627
QY 2242 TGAACCTGG--AGGTAGGTTGCACTGAGTGAAGCCCACTGCACTCCGGCCTAGG 2299
Db 23628 TGAACCCGGGAGGCAAGGTTGCGATGAGCCTAGATGTCATTGCACTCCAGCCTGGG 23687
QY 2300 CAACGAGAGCAAACTCCAAATACAAACAACAACCAACACCTG 2343
Db 23688 CAACAAGAGCAAAACTCGGTCTCAAAAAAAAAAAAAAAAAAGTG 23731
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RESULT 11

US-10-148-806-3

; Sequence 3, Application US/10148806

; Patent No. 6762042

; GENERAL INFORMATION:

; APPLICANT: Bai, Chang

; APPLICANT: Metzger, Michael

; APPLICANT: Liu, Xiaomei

; TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN NHL, A DNA
; FILE REFERENCE: 20585P
; CURRENT APPLICATION NUMBER: US/10/148,806
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: US00/33065
; PRIOR FILING DATE: 2000-12-09
; PRIOR APPLICATION NUMBER: 60/169,970
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 114793
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-148-806-3

Query Match 7.0%; Score 189.4; DB 4; Length 114793;
Best Local Similarity 77.8%; Pred. No. 1.9e-44;
Matches 267; Conservative 0; Mismatches 71; Indels 5; Gaps 3;

QY 2007 AATTCATCATAGATATTATTAAAGAACTACTATGCGCCGCGCATGTGGCTCACAC 2066
DB 106789 ACTGCACCTAATAATTCTTTATAGTTTTCAGAGGCCAGGCACAGTGGCTCACAC 106848
QY 2067 CTGTAATCCAGCACTTTGGGAGGCCAAGGTGGGTGCTCATCTGAGTCAAGTTCAA 2126
DB 106849 CTGTAATCCAGCACTTTGGGAGGCCAAGGTGGGTGATCAGTCAAGTTCGA 106908
QY 2127 GACCAGCTGGCCACACATGTGTAACCCCATCTCTACTAAAGAT--CAAAATTGCTGAG 2184
DB 106909 GACCAGCTGGCCGACAGGAGAAACCCCATCTCTACTAAAAATACAAAAATTAGCTGGG 106968
QY 2185 CGTGGTGTGTCACCTGT-ATCCAGCTACTCGAGAGGCCAAGCATGAGAATCGCTTG 2243
DB 106969 CGTGGTGGAGGTGCTGTATCCAGCTACTCAGAGGCTGAGGCAAGAAATCGCTTG 107028
QY 2244 AACCTGG--AGTGAGGTGTCAGTGAAGTGAATGGCACCACCTCCGCGCTAGGCA 2301
DB 107029 AACCTGGAGGAGAGGTTGTCAGTGAAGTGAATGGCACCACCTCCAGCTGGGTA 107088
QY 2302 ACGAGAGCAAACTCCATATACAAACAACAACAACACCTGT 2344
DB 107089 ACAAAGCAAACTCCATCTCAAGAAAAGAAAAAGTTT 107131

RESULT 12
US-09-820-924-3
; Sequence 3, Application US/09820924
; Patent No. 655351
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, Ellen M. et al
; TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001213
; CURRENT APPLICATION NUMBER: US/09/820,924
; CURRENT FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 39982
; TYPE: DNA
; ORGANISM: Human
US-09-820-924-3

Query Match 7.0%; Score 188.4; DB 4; Length 39982;
Best Local Similarity 80.8%; Pred. No. 1.9e-44;
Matches 257; Conservative 0; Mismatches 56; Indels 5; Gaps 3;

QY 2027 ATTAAGAACTACTATGCGGCCGCGATGTGGCTCACACCTGTAAATCCAGCACTTTGG 2086
DB 19834 AATATTAATAAAGATGAGGCCAGGCGTGTGGCTCACACCTGTAAATCCAGCACTTTGG 19893

QY 2087 GAGCCCAAGTGGGTGCTATCTGAGTCAAGATTCAAGACCAGCCTGGCCAATGG 2146
DB 19894 GAAGCTGAGGTGGGTGATCACTGAAGTCAAGAAATCAAGACCAGCCTGGTCAATGG 19953
QY 2147 TGAAAACCCATCTCTACTAAAGAT--CAAAATTGCTGAGCGTGTGTGCACTGT- 2203
DB 19954 TGAAAACCCATCTCTACTAAAAATACAAACATTAGCTGGATGTGTGTGCAATGTA 20013
QY 2204 ATCCAGCTACTCGAGAGGCCAAGGCATGAGAAATCGCTTGAACCTGG--AGGTGAGTTG 2261
DB 20014 ATCCAGCTACTTGGGAGGCTAAGGCAGAGAAATGCTTGAACCCGGAGGCAGAGTTG 20073
QY 2262 CAGTGAAGTGAATGCAACCACTGCACCTCCGCGCTAGGCAACGAGCAAACTCCAATA 2321
DB 20074 TAGTGAAGCCGAGATCACACCAFTGCACCTCCAGCCTGGGCAATAAGAGTGAATTCATCT 20133
QY 2322 CAACAACAACAACAACA 2339
DB 20134 CAAAAAATAAATAAATAAATA 20151

RESULT 13
US-10-369-626-3
; Sequence 3, Application US/10369626
; Patent No. 6787344
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, Ellen M. et al
; TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001213DIV
; CURRENT APPLICATION NUMBER: US/10/369,626
; CURRENT FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 39982
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-369-626-3

Query Match 7.0%; Score 188.4; DB 4; Length 39982;
Best Local Similarity 80.8%; Pred. No. 1.9e-44;
Matches 257; Conservative 0; Mismatches 56; Indels 5; Gaps 3;

QY 2027 ATTAAGAACTACTATGCGGCCGCGCATGTGGCTCACACCTGTAAATCCAGCACTTTGG 2086
DB 19834 AATATTAATAAAGATGAGGCCAGGCGTGTGGCTCACACCTGTAAATCCAGCACTTTGG 19893
QY 2087 GAGCCCAAGTGGGTGCTATCTGAGTCAAGATTCAAGACCAGCCTGGCCAATGG 2146
DB 19894 GAAGCTGAGGTGGGTGATCACTGAAGTCAAGAAATCAAGACCAGCCTGGTCAATGG 19953
QY 2147 TGAAAACCCATCTCTACTAAAGAT--CAAAATTGCTGAGCGTGTGTGCACTGT- 2203
DB 19954 TGAAAACCCATCTCTACTAAAAATACAAACATTAGCTGGATGTGTGTGCAATGTA 20013
QY 2204 ATCCAGCTACTCGAGAGGCCAAGGCATGAGAAATCGCTTGAACCTGG--AGGTGAGTTG 2261
DB 20014 ATCCAGCTACTTGGGAGGCTAAGGCAGAGAAATGCTTGAACCCGGAGGCAGAGTTG 20073
QY 2262 CAGTGAAGTGAATGCAACCACTGCACCTCCGCGCTAGGCAACGAGCAAACTCCAATA 2321
DB 20074 TAGTGAAGCCGAGATCACACCAATGCACTCCAGCCTGGGCAATAAGAGTGAATTCATCT 20133
QY 2322 CAACAACAACAACAACA 2339
DB 20134 CAAAAAATAAATAAATAAATA 20151

RESULT 14
US-09-345-882-1/c

Sequence 1, Application US/09345882
Patent No. 6399373
GENERAL INFORMATION:
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)
TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
FILE REFERENCE: GENSET 031A
CURRENT APPLICATION NUMBER: US/09/345,882
PRIOR FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: US 60/091,315
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/111,909
NUMBER OF SEQ ID NOS: 140
SOFTWARE: Patent.pm
SEQ ID NO 1
LENGTH: 162450
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 72794
OTHER INFORMATION: 5-124-273 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 88073
OTHER INFORMATION: 5-127-261 : polymorphic base A or C
FEATURE:
NAME/KEY: allele
LOCATION: 90842
OTHER INFORMATION: 99-1437-325 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 93714
OTHER INFORMATION: 5-128-60 : polymorphic base deletion of GT
FEATURE:
NAME/KEY: allele
LOCATION: 97122
OTHER INFORMATION: 99-1442-224 : polymorphic base G or T
FEATURE:
NAME/KEY: allele
LOCATION: 97152
OTHER INFORMATION: 5-129-144 : polymorphic base deletion of T
FEATURE:
NAME/KEY: allele
LOCATION: 99098
OTHER INFORMATION: 5-130-257 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 99117
OTHER INFORMATION: 5-130-276 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 103806
OTHER INFORMATION: 5-131-395 : polymorphic base A or T
FEATURE:
NAME/KEY: allele
LOCATION: 106940
OTHER INFORMATION: 5-133-375 : polymorphic base insertion of A
FEATURE:
NAME/KEY: allele
LOCATION: 108106
OTHER INFORMATION: 5-135-155 : polymorphic base insertion of A
FEATURE:
NAME/KEY: allele
LOCATION: 108149
OTHER INFORMATION: 5-135-198 : polymorphic base insertion of GTTT
FEATURE:
NAME/KEY: allele
LOCATION: 108308
OTHER INFORMATION: 5-135-357 : polymorphic base A or G
FEATURE:
NAME/KEY: allele

LOCATION: 108471
OTHER INFORMATION: 5-136-174 : polymorphic base C or T
FEATURE:
NAME/KEY: allele
LOCATION: 134134
OTHER INFORMATION: 5-140-120 : polymorphic base C or T
FEATURE:
NAME/KEY: allele
LOCATION: 134362
OTHER INFORMATION: 5-140-348 : polymorphic base insertion of A
FEATURE:
NAME/KEY: allele
LOCATION: 134374
OTHER INFORMATION: 5-140-361 : polymorphic base insertion of CA
FEATURE:
NAME/KEY: allele
LOCATION: 146328
OTHER INFORMATION: 5-143-84 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 146345
OTHER INFORMATION: 5-143-101 : polymorphic base A or C
FEATURE:
NAME/KEY: allele
LOCATION: 150329
OTHER INFORMATION: 5-145-24 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 160031
OTHER INFORMATION: 5-148-352 : polymorphic base G or T
FEATURE:
NAME/KEY: allele
LOCATION: 72771..72817
OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID30
FEATURE:
NAME/KEY: allele
LOCATION: 72771..72817
OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID51
FEATURE:
NAME/KEY: allele
LOCATION: 88050..88096
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID31
FEATURE:
NAME/KEY: allele
LOCATION: 88050..88096
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID52
FEATURE:
NAME/KEY: allele
LOCATION: 90819..90865
OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID49
FEATURE:
NAME/KEY: allele
LOCATION: 90819..90865
OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID70
FEATURE:
NAME/KEY: allele
LOCATION: 93690..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID32
FEATURE:
NAME/KEY: allele
LOCATION: 93690..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID53
FEATURE:
NAME/KEY: allele
LOCATION: 97099..97145
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID50
FEATURE:
NAME/KEY: allele
LOCATION: 97099..97145
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID71
FEATURE:
NAME/KEY: allele
LOCATION: 97130..97177


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/ OTHER INFORMATION: exon D g35018 gene
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: 29967..30282
/ OTHER INFORMATION: exon E g35018 gene
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: 64666..64812
/ OTHER INFORMATION: exon F g35018 gene
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: 65505..65853
/ OTHER INFORMATION: exon G g35018 gene
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 65854..67854
/ OTHER INFORMATION: 3'regulatory region g35018 gene
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: 94124..94964
/ OTHER INFORMATION: exon g35017
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: 201188..201234
/ OTHER INFORMATION: exon S g35030 gene
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: 214676..214793
/ OTHER INFORMATION: exon T g35030 gene
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: 215702..215746
/ OTHER INFORMATION: exon U g35030 gene
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: 216836..216915
/ OTHER INFORMATION: exon V g35030 gene
/ FEATURE:
/ NAME/KEY: misc_feature
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/ OTHER INFORMATION: 3'regulatory region g34872 gene
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Search completed: October 28, 2004, 10:20:41
Job time : 228 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 28, 2004, 10:20:44 ; Search time 11342 Seconds
(without alignments)
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Gapop 60.0 , Gapext 60.0

Searched: 4526729 seqs, 23644849745 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 100 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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8	1076	39.8	1076	6 AX376124	AX376124 Sequence
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DEFINITION Sequence 1 from Patent WO0146260.
ACCESSION AX180364
VERSION AX180364.1 GI:15132304
KEYWORDS
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ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Starling, G.C. and Finger, J.
TITLE Novel immunoglobulin superfamily members apex-1, apex-2 and apex-3 and uses thereof
JOURNAL Patent: WO 0146260-A 1 28-JUN-2001;
Bristol-Myers Squibb Co. (US)
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DEFINITION Homo sapiens mRNA for membrane protein FOAP-12, complete cds.
ACCESSION AB027233
VERSION AB027233.1 GI:14517605
KEYWORDS membrane protein FOAP-12.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2672)
AUTHORS Fujii,Y., Takayama,K., Tsuritani,K., Yajima,Y., Amemiya,T.,
Ukai,Y., Naito,K. and Kawaguchi,A.
Homo sapiens mRNA for FOAP-12 protein, complete cds
Unpublished
TITLE 2 (bases 1 to 2672)
AUTHORS Fujii,Y., Takayama,K., Tsuritani,K., Yajima,Y., Amemiya,T.,
Ukai,Y., Naito,K. and Kawaguchi,A.
Direct Submission
Submitted (12-MAY-1999) Yasuyuki Fujii, Taisho Pharmaceutical Co.,
Ltd., Molecular Biology Laboratory; Yoshino-cho, 1-403, Ohmiya,
Saitama 3308530, Japan (E-mail:s17561@ccm.taisho.co.jp,
Tel:+81-48-663-1111, Fax:+81-48-652-7254)
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LOCUS
DEFINITION 33 human secreted proteins.
ACCESSION BD249810
VERSION BD249810.1 GI:33059580
KEYWORDS JP 2002540763-A/12.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 2774)
AUTHORS Rosen,C.A., Ruben,S.M., Ebner,R., Young,P.E., Ni,J., Soppet,D.R.,
Moore,P.A., Shi,Y., Lafleur,D.W., Olsen,H.S., Florence,K.A. and
Komatsoulis,G.
33 human secreted proteins
Patent: JP 2002540763-A 12 03-DEC-2002;
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PF 08-FEB-2000 JP 2000598519
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PI CRAIG A ROSEN,STEVEN M RUBEN,REINHARD EBNER,PAUL E YOUNG,JIAN
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PI DANIEL R SOPPET,PAUL A MOORE,YANGGU SHI,DAVID W LAFLEUR,HENRIK

PI S OLSEN,
PI KIMBERLY A FLORENCE, GEORGE KOMATSOUJIS
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ORIGIN

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SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

REFERENCE
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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1 (bases 1 to 2445)
Bloecher, H., Boecher, M., Brandt, P., Mewes, H.W., Well, B. and
Wiemann, S.

TITLE	Direct Submission
JOURNAL	Submitted (09-JUL-2002) 1, D-85764 Neuherberg, GERMANY
COMMENT	Clone from S. Wiemann, Molecular Genome Analysis, Germ

sequenced by GBF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZp667F126) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at <http://mips.gsf.de/proj/cdna/>.

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Db	869	GCTTCTTAGATTAAAGTTCATATTCATCCACTGCTGAGAAATCTCCTCAAAACCA	928
QY	1257	GAAGGTTTAATCACTTCATCCCAAAATGGGATGTGTAATGTCAGCAAAACCATAAAAAA	1316
Db	929	GAAGGTTTAATCACTTCATCCCAAAATGGGATGTGTAATGTCAGCAAAACCATAAAAAA	988
QY	1317	GTGCTTAGAAGTATTCCTATAGAAATGTAATGCAAGGTCAACATATTTAATGACAGCCT	1376
Db	989	GTGCTTAGAAGTATTCCTATAGAAATGTAATGCAAGGTCAACATATTTAATGACAGCCT	1048
QY	1377	GTTGTATTAATGATGGCTCCAGGTCAGTGTCTGAGTTTCATCCATCCCAAGGCTTGA	1436
Db	1049	GTTGTATTAATGATGGCTCCAGGTCAGTGTCTGAGTTTCATCCATCCCAAGGCTTGA	1108
QY	1437	TGTCAGGATTATACCAAGTCTTGCTACAGAGGGCAAGAAGCAAAACAGACAGAC	1496
Db	1109	TGTCAGGATTATACCAAGTCTTGCTACAGAGGGCAAGAAGCAAAACAGACAGAC	1168
QY	1497	AAGTCCAGCAGAAAGCAGATGCACCTGACAAAATGATGATTAATTGGCTCTATAACT	1556
Db	1169	AAGTCCAGCAGAAAGCAGATGCACCTGACAAAATGATGATTAATTGGCTCTATAACT	1228
QY	1557	ATGTGCCAGCAGCTATGCTGAGCTTACACTAATTGCTCAGACGTGCTGTGCTCCCTCATG	1616
Db	1229	ATGTGCCAGCAGCTATGCTGAGCTTACACTAATTGCTCAGACGTGCTGTGCTCCCTCATG	1288
QY	1617	AAATTTGGCTCCAAATGAATGAATCTACTTTTCATGAGCAGTTGTAGCAGGCTGACACAGA	1676
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QY	1677	TTCCAGAGGGCCAGGTGTGATCCACAGAGCTTGAAGTCAAAAGTTCACAAAGATGAAG	1736
Db	1349	TTCCAGAGGGCCAGGTGTGATCCACAGAGCTTGAAGTCAAAAGTTCACAAAGATGAAG	1408
QY	1737	AATCAGGCTAGCTGACCAATGTTTGGCAGATACTATAATGAGACACAGAAAGTTCATGG	1796
Db	1409	AATCAGGCTAGCTGACCAATGTTTGGCAGATACTATAATGAGACACAGAAAGTTCATGG	1468
QY	1797	CCCAAGGACAAAGACCTCCAGCCAGGCTTCATTATGCACTTGCTGCAAAAGAAAAGT	1856
Db	1469	CCCAAGGACAAAGACCTCCAGCCAGGCTTCATTATGCACTTGCTGCAAAAGAAAAGT	1528
QY	1857	CTAGGTTTAAAGCTGTGCGCAGAAACCCATCCCAATAAAGAACCGAGTCTGAAGTCAAT	1916
Db	1529	CTAGGTTTAAAGCTGTGCGCAGAAACCCATCCCAATAAAGAACCGAGTCTGAAGTCAAT	1588
QY	1917	TGTAATCTAGTGTAGAGACTTGAGTCAAGGCAAGTGAAGTGTGGGGCAGCGGGGCA	1976
Db	1589	TGTAATCTAGTGTAGAGACTTGAGTCAAGGCAAGTGAAGTGTGGGGCAGCGGGGCA	1648
QY	1977	GTGGTACTTGTAAACCTTTAAAGATGTTAATTCATTCATATAGATATTATTAAAGAAC	2036
Db	1649	GTGGTACTTGTAAACCTTTAAAGATGTTAATTCATTCATATAGATATTATTAAAGAAC	1708
QY	2037	TA 2038	
Db	1709	TA 1710	

RESULT 5
AF390894 1352 bp mRNA linear PRI 02-NOV-2001
LOCUS Homo sapiens CD2-like receptor activating cytotoxic cells mRNA,
DEFINITION complete cds.
ACCESSION AF390894
VERSION AF390894.1 GI:16589010
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1352)
AUTHORS Bouchon,A., Cella,M., Grierson,H.L., Cohen,J.I. and Colonna,M.

TITLE	Cutting Edge: Activation of NK Cell-Mediated Cytotoxicity by a				
JOURNAL	SAP-independent Receptor of the CD2 Family				
REFERENCE	J. Immunol. 167 (2001) In press				
AUTHORS	2 (bases 1 to 1352)				
TITLE	Colonna, M.				
JOURNAL	Submitted (12-JUN-2001) Basel Institute for Immunology, 487				
FEATURES	Grenzacherstrasse, Basel CH-4005, Switzerland				
SOURCE	Location/Qualifiers				
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	21..1028				
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	CD84; SAP-independent"				
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	/product="CD2-like receptor activating cytotoxic cells"				
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	YVYGIYSSLSQPSYVLYHYEHLSPKVTMGLQSNXNGCVTNLTCCMEHEEDV				
	IYTWKALGOAANESHNGSILPISWRWGESDMTFICVARNPVSRNFPSSPILARKCEGA				
	ADPDSMYLLCLLVPLLSFLVGLFLWFLKREOREYIEKKRVDICRETPNICP				
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ORIGIN					
Query Match	46.7%;	Score 1264;	DB 9;	Length 1352;	
Best Local Similarity	99.9%;	Pred. No. 0;			
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QY	22	GCTGACTTCCAGAGCAATATGCTGTTCCCAACATGCTCACCCTCATCTATATCC	81		
Db	1	GCTGACTTCCAGAGCAATATGCTGTTCCCAACATGCTCACCCTCATCTATATCC	60		
QY	82	TTTGGCAGCTCAGAGGTCAGCAGCCTCTGGAACCCGTGAAGAGCTGTCGGTTCCGTTG	141		
Db	61	TTTGGCAGCTCAGAGGTCAGCAGCCTCTGGAACCCGTGAAGAGCTGTCGGTTCCGTTG	120		
QY	142	GTGGGGCCGTGACTTTCCCTCGAAGTCCAAAGTAAAGCAAGTTGACTTATTTGCTGGA	201		
Db	121	GTGGGGCCGTGACTTTCCCTCGAAGTCCAAAGTAAAGCAAGTTGACTTATTTGCTGGA	180		
QY	202	CCTTCAACACAAACCCCTCTTGTCAACCATACAGCCAGAAAGGGGCACTATCATAGTGACCC	261		
Db	181	CCTTCAACACAAACCCCTCTTGTCAACCATACAGCCAGAAAGGGGCACTATCATAGTGACCC	240		
QY	262	AAAATCGTAATAGGAGAGAGTAGACTTCCAGATGAGGCTACTCCCTGAAGCTCAGCA	321		
Db	241	AAAATCGTAATAGGAGAGAGTAGACTTCCAGATGAGGCTACTCCCTGAAGCTCAGCA	300		
QY	322	AACTGAAGAAGATGACTCAGGATCTACTATGTGGGATATACAGCTCATCTCCAGC	381		
Db	301	AACTGAAGAAGATGACTCAGGATCTACTATGTGGGATATACAGCTCATCTCCAGC	360		
QY	382	AGCCCTCCACCCAGAGTAGCTGCTGCATGCTACGAGCAGCAGCTGTCAAAGCCTAAAGTCA	441		
Db	361	AGCCCTCCACCCAGAGTAGCTGCTGCATGCTACGAGCAGCAGCTGTCAAAGCCTAAAGTCA	420		
QY	442	CCATGGGTCTGCAGAGCAATAGAGTGAAGTGTGTGACCAATGTGACATGCTGCATGG	501		
Db	421	CCATGGGTCTGCAGAGCAATAGAGTGAAGTGTGTGACCAATGTGACATGCTGCATGG	480		
QY	502	AACATGGGGAAGAGATGTGATTATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGT	561		
Db	481	AACATGGGGAAGAGATGTGATTATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGT	540		
QY	562	CCCATATATGGGTCCATCTCCCATCTCTCTGAGATGGGAGAAAGTATATGACCTTCA	621		

Db	541	CCCCAATATGGGTCCATCCTCCCATCTCCTGAGATGGGAGAAAGTGAATGACCTTCA	600
QY	622	TCTGCGTGGCAGAACCCCTGTGACAGAACTTCTCAAGCCCCCATCTTGCAGGAAGC	681
Db	601	TCTGCGTGGCAGAAACCCCTGTGACAGAACTTCTCAAGCCCCCATCTTGCAGGAAGC	660
QY	682	TCTGTGAAGGTGCTGCTGATGAGACCCAGATTCTCCATGCTGCTCCTGCTGCTGTTGG	741
Db	661	TCTGTGAAGGTGCTGCTGATGAGACCCAGATTCTCCATGCTGCTCCTGCTGCTGTTGG	720
QY	742	TGCCCCCTCCTGCTCAGTCTCTTTGTACTGCGGCTATTCTTTGTTTCTGAAGAGAGA	801
Db	721	TGCCCCCTCCTGCTCAGTCTCTTTGTACTGCGGCTATTCTTTGTTTCTGAAGAGAGA	780
QY	802	GACAGAAGAGTACTTGAAGAAGAAGAGAGTGCACATTGTTCGGGAACTCCTAACAA	861
Db	781	GACAGAAGAGTACTTGAAGAAGAAGAGAGTGCACATTGTTCGGGAACTCCTAACAA	840
QY	862	TATGCCCCCATTTCTGAGAGAACACAGAGTACGACACATCCCTCACACTAATAGAACAA	921
Db	841	TATGCCCCCATTTCTGAGAGAACACAGAGTACGACACATCCCTCACACTAATAGAACAA	900
QY	922	TCCFAAAGAGATCCAGCAATACGGTTTACTCCACTGTGGAATACCGAATAAGATGG	981
Db	901	TCCFAAAGAGATCCAGCAATACGGTTTACTCCACTGTGGAATACCGAATAAGATGG	960
QY	982	AAAATCCCCACTGACTGCTCAGATGCCAGACACACCAAGGCTATTGGCTATGAGAAATG	1041
Db	961	AAAATCCCCACTGACTGCTCAGATGCCAGACACACCAAGGCTATTGGCTATGAGAAATG	1020
QY	1042	TTATCTAGACAGAGTGCACCTCCCTAAGTCTCTGCTCAAAAAAACAATTCTCGGCC	1101
Db	1021	TTATCTAGACAGAGTGCACCTCCCTAAGTCTCTGCTCAAAAAAACAATTCTCGGCC	1080
QY	1102	CAAGAAAAACAATCAGAAAGATTCACTGATTGACTAGAAACATCAAGGAAGATGAAGA	1161
Db	1081	CAAGAAAAACAATCAGAAAGATTCACTGATTGACTAGAAACATCAAGGAAGATGAAGA	1140
QY	1162	ACGTGACTTTTTCAGGATAAATTATCTGATGCTTCTTAGATTAAAGTTGTA	1221
Db	1141	ACGTGACTTTTTCAGGATAAATTATCTGATGCTTCTTAGATTAAAGTTGTA	1200
QY	1222	ATTCATCCACTGCTGAGAATCTCCTCAAAACCCAGAAGTTTAATCACTTCATCCCAA	1281
Db	1201	ATTCATCCACTGCTGAGAATCTCCTCAAAACCCAGAAGTTTAATCACTTCATCCCAA	1260
QY	1282	AATGGATTGTGAATGTACGCAAAACCATTAATAAAGTGCTTAGAAGTATTCCTAT	1336
Db	1261	AATGGATTGTGAATGTACGCAAAACCATTAATAAAGTGCTTAGAAGTATTCCTAT	1315

RESULT 6
AR252549 LOCUS AR252549 1076 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 252 from patent US 6478825.
ACCESSION AR252549
VERSION AR252549.1 GI:27300457
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1076)
AUTHORS Winterbottom,J.M., Shimp,L., Boyce,T.M. and Kaes,D.
TITLE Implant, method of making same and use of the implant for the
treatment of bone defects
JOURNAL Patent: US 6478825-A 252 12-NOV-2002;
FEATURES Location/Qualifiers
source 1..1076
/organism="unknown"
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QY	65	CACCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGAGCCTCTGGAACCGTGAAGA	124
Db	61	CACCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGAGCCTCTGGAACCGTGAAGA	120
QY	125	GCTGTCGGTTCCGTTGGTGGGCGGTGACTTTCCCTGAAGTCCAAAGTAAAGCAAGT	184
Db	121	GCTGTCGGTTCCGTTGGTGGGCGGTGACTTTCCCTGAAGTCCAAAGTAAAGCAAGT	180
QY	185	TGACTTATTTGTCTGGAACCTTCAACACACCCTCTTGTTCACCATACAGCCAGAAGGGG	244
Db	181	TGACTTATTTGTCTGGAACCTTCAACACACCCTCTTGTTCACCATACAGCCAGAAGGGG	240
QY	245	CACTATCATAGTGACCCCAAAATCGTAATAGGAGAGAGTACCTTCCAGATGAGGCTTA	304
Db	241	CACTATCATAGTGACCCCAAAATCGTAATAGGAGAGAGTACCTTCCAGATGAGGCTTA	300
QY	305	CTCCCTGAAGCTCAGCAAACTGAAGAAGATGACTCAGGGATCTACTATGTGGGATATA	364
Db	301	CTCCCTGAAGCTCAGCAAACTGAAGAAGATGACTCAGGGATCTACTATGTGGGATATA	360
QY	365	CAGCTCATCACTCCAGCAGCCCTCCACCAGAGTACGTGCTCATGTCTACGAGCACCCT	424
Db	361	CAGCTCATCACTCCAGCAGCCCTCCACCAGAGTACGTGCTCATGTCTACGAGCACCCT	420
QY	425	GTCAAGCCTTAAAGTCAACCATGGGCTGACAGAGCAATAGAATGGCACCTGTGTACCAA	484
Db	421	GTCAAGCCTTAAAGTCAACCATGGGCTGACAGAGCAATAGAATGGCACCTGTGTACCAA	480
QY	485	TCTGACATGCTGTCATGGAACATGGGGGAAGAGATGTGATTTTATACCTGGAAGGCCCTGGG	544
Db	481	TCTGACATGCTGTCATGGAACATGGGGGAAGAGATGTGATTTTATACCTGGAAGGCCCTGGG	540
QY	545	GCAAGCAGCCAATGAGTCCCAATATGGGTCCATCTCCCATCTCTGAGATGGGAGAA	604
Db	541	GCAAGCAGCCAATGAGTCCCAATATGGGTCCATCTCCCATCTCTGAGATGGGAGAA	600
QY	605	AAGTGATATGACCTTCATCTGGGTTGCCAGGAACCTGTCAAGCAAACTTCTCAAGCCC	664
Db	601	AAGTGATATGACCTTCATCTGGGTTGCCAGGAACCTGTCAAGCAAACTTCTCAAGCCC	660
QY	665	CATCCTTGCCAGGAAGCTGTGAAAGGTGCTGCTGATGACCCAGATTCTCCATGCTCT	724
Db	661	CATCCTTGCCAGGAAGCTGTGAAAGGTGCTGCTGATGACCCAGATTCTCCATGCTCT	720
QY	725	CCTGTCTCTCCTGTTGTGTCCTCTCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTG	784
Db	721	CCTGTCTCTCCTGTTGTGTCCTCTCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTG	780
QY	785	GTTTCTGAAGAGAGAGACAAAGAGTACATTGAAAGAAAGAGAGTGGACATTTG	844
Db	781	GTTTCTGAAGAGAGAGACAAAGAGTACATTGAAAGAAAGAGAGTGGACATTTG	840
QY	845	TCGGGAAACTCCTAACATATGCCCCCATTTCTGAGAGAACACAGAGTACGACAAATCCC	904
Db	841	TCGGGAAACTCCTAACATATGCCCCCATTTCTGAGAGAACACAGAGTACGACAAATCCC	900
QY	905	TCACACTAATAGAACAAATCCTTAAAGAAAGATCCAGCAAAATACGTTTACTCCACTGTGA	964
Db	901	TCACACTAATAGAACAAATCCTTAAAGAAAGATCCAGCAAAATACGTTTACTCCACTGTGA	960
QY	965	AATACGAAAAAAGATGAAAAATCCCCACTCACTGCTCAGAGTCCAGACACACCAAGGCT	1024
Db	961	AATACGAAAAAAGATGAAAAATCCCCACTCACTGCTCAGAGTCCAGACACACCAAGGCT	1020
QY	1025	ATTGCTTATGAGATGTTATCTAGACAGAGTGCATCTCCCTAAGTCTCTGCTCA	1080

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|||||

RESULT 7
AX092314

LOCUS 1076 bp DNA linear PAT 21-MAR-2001

AX092314

DEFINITION Sequence 45 from Patent WO0116318.

AX092314

ACCESSION AX092314

VERSION AX092314.1 GI:13444471

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE

1

Autors

Baton, D.L., Filvaroff, B., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Grimaldi, C.J., Gurney, A.L., Watanabe, C.K. and
Wood, W.I.

Secretd and transmembrane polypeptides and nucleic acids encoding
the same

Patent: WO 0116318-A 45 08-MAR-2001;

Genentech, Inc. (US)

Location/Qualifiers

1. 1076

/organism="Homo sapiens"
/mol_type="unassigned DNA"
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FEATURES

Source

ORIGIN

Query Match	39.8%	Score 1076;	DB 6;	Length 1076;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 1076; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

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OY		65	CACCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAGA	124
Db		61	CACCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAGA	120
OY		125	GCTGTCGGTTCGGTTGGTGGGGCCGTGACTTTCCCTGTAAGTCCAAAGTAAAGCAAGT	184
Db		121	GCTGTCGGTTCGGTTGGTGGGGCCGTGACTTTCCCTGTAAGTCCAAAGTAAAGCAAGT	180
OY		185	TGACTCTATTGTCCTGGACCTTCAACACAACCCCTCTTGTCAACCATACAGCCAGAAAGGGG	244
Db		181	TGACTCTATTGTCCTGGACCTTCAACACAACCCCTCTTGTCAACCATACAGCCAGAAAGGGG	240
OY		245	CACATCATAGTAGACCCCAAATCGTAATAGGAGAGAGTAGACTTCCAGATGAGGCTA	304
Db		241	CACATCATAGTAGACCCCAAATCGTAATAGGAGAGAGTAGACTTCCAGATGAGGCTA	300
OY		305	CTCCCTGAAGCTCAGCAAACCTGAAGAAGATGACTCAGGGAATCTATATGTGGGGATATA	364
Db		301	CTCCCTGAAGCTCAGCAAACCTGAAGAAGATGACTCAGGGAATCTATATGTGGGGATATA	360
OY		365	CAGCTCATCACTCCAGCAGCCCTCCACCAGAGTAGTGTGCTGCATGTCTACGAGCACT	424
Db		361	CAGCTCATCACTCCAGCAGCCCTCCACCAGAGTAGTGTGCTGCATGTCTACGAGCACT	420
OY		425	GTCAAAGCCTAAAGTCACCAATGGGCTCTGCAGAGCAATTAAGATGGCACCCTGTGTGACAA	484
Db		421	GTCAAAGCCTAAAGTCACCAATGGGCTCTGCAGAGCAATTAAGATGGCACCCTGTGTGACAA	480
OY		485	TCTGACATGCTGCATGGAACAATGGGGAAGAGATGTGATTTATACTGGAAGGCCCTGGG	544
Db		481	TCTGACATGCTGCATGGAACAATGGGGAAGAGATGTGATTTATACTGGAAGGCCCTGGG	540
OY		545	GCAAGCAGCCAAATGAGTCCCAATAATGGGTCATCTCCCAATCTCTGGAGATGGGGAGA	604
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OY	605	AAGTATATGACCTTCATCTCGGTGCCAGGAACCCTGTCAAGAACTCTCAAGCCC	664
Db	601	AAGTGATATGACTTCATCTCGGTGCCAGGAACCCTGTCAAGAACTCTCAAGCCC	660
OY	665	CATCCTTGCCAGGAAGCTCTGTGAAGGTCTGTGATGACCCAGATTCTCCATGGTCTT	724
Db	661	CATCCTTGCCAGGAAGCTCTGTGAAGGTCTGTGATGACCCAGATTCTCCATGGTCTT	720
OY	725	CCTGTGTCCTCTGTGGTGGTCCCCCTCTGCTCAGTCTCTTTGTACTGGGGCTAATTTCTTTG	784
Db	721	CCTGTGTCCTCTGTGGTGGTCCCCCTCTGCTCAGTCTCTTTGTACTGGGGCTAATTTCTTTG	780
OY	785	GTTTCTGAAGAGAGAGACAAGAAGATCATTTGAAGAGAAGAAGAGATGGACATTTG	844
Db	781	GTTTCTGAAGAGAGAGACAAGAAGATCATTTGAAGAGAAGAAGAGATGGACATTTG	840
OY	845	TCCGGAACCTCCTAACATATGCCCCCATTTCTGAGAGAACAAGATGACGACAATCCC	904
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Db	961	AATACCGAAAAAGATGGAAAATCCCCCACTCACTGCTTCACGATGCCAGACACCAAGGCT	1020
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Db	1021	ATTGCCTATGAGATGTTATCTAGACAGCAGTGCACTCCCCTAAGTCTGTGCTCA	1076

RESULT 8				
AX376124				
LOCUS	AX376124	1076 bp	DNA	linear
DEFINITION	Sequence 191 from Patent WO0168848.			PAT 01-MAR-2002
ACCESSION	AX376124			
VERSION	AX376124.1	GI:19170454		
KEYWORDS				
SOURCE				
ORGANISM	Homo sapiens (human)			
	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	1			
AUTHORS	Baker, K.P., Chen, J., Desnoyers, L., Goddard, A., Godowski, P.J.,			
	Gurney, A.L., Pan, J., Smith, V., Watanabe, C.K., Wood, W.I. and			
	Zhang, Z.			
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding			
	the same			
JOURNAL	Patent: WO 0168848-A 191 20-SEP-2001;			
	Genentech, Inc. (US)			
FEATURES	Location/Qualifiers			
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	Query Match	39.8%;	Score 1076;	DB 6;	Length 1076;	
	Best Local Similarity	100.0%;	Pred. No. 0;	Mismatches 0;	Indels 0;	Gaps 0;
	Matches 1076;	Conservative	0;	Mismatches	0;	Indels
Oy	5 GTGGCTTCATTTCAGTGGCTGACTTCCAGAGACCAATATGTGGCTGTTCCCCAACATGCGCT					
Db	1 GTGGCTTCATTTCAGTGGCTGACTTCCAGAGACCAATATGTGGCTGTTCCCCAACATGCGCT					
Oy	65 CACCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCGCTTGGAACCCGTGAAGA					
Db	61 CACCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCGCTTGGAACCCGTGAAGA					
Oy	125 GCTGGTCCGTTCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAGTAAGCAAGT					


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Db      121 GCTGTCGTTCCGTTGGTGGGGCCGTGACTTCCCCCTGAAGTCCAAAGTAAGCAGT 180
QY      185 TGACTCTATGTGTGACCTTCAACACAAACCCCTTTGTCCACCATACAGCCAGAAGGGG 244
Db      181 TGACTCTATGTGTGACCTTCAACACAAACCCCTTTGTCCACCATACAGCCAGAAGGGG 240
QY      245 CACTATCATAGTGACCCAAATCGTAATAGGGAGAGTAGACTTCCAGATGGAGGCTA 304
Db      241 CACTATCATAGTGACCCAAATCGTAATAGGGAGAGTAGACTTCCAGATGGAGGCTA 300
QY      305 CTCCCTGAAGCTCAGCAAACTGAAGAAGATGACTCAGGGATCTACTATGTGGGATATA 364
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QY      365 CAGCTCATCTCCAGCAGCCCTCCACCAGAGTACGTGCTGCAITGCTACGAGCACCT 424
Db      361 CAGCTCATCTCCAGCAGCCCTCCACCAGAGTACGTGCTGCAITGCTACGAGCACCT 420
QY      425 GTCAAAGCCTAAAGTCAACCATGGGTCTGACAGCAATAAGAATGCACCTGTGACCAA 484
Db      421 GTCAAAGCCTAAAGTCAACCATGGGTCTGACAGCAATAAGAATGCACCTGTGACCAA 480
QY      485 TCTGACATGCTGCATGGAACATGGGGAAGAGATGTGATTATACCTGGAAGCCCTGGG 544
Db      481 TCTGACATGCTGCATGGAACATGGGGAAGAGATGTGATTATACCTGGAAGCCCTGGG 540
QY      545 GCAAGCAGCCAAATGAGTCCCATAATGGGTCCATCTCCCATCTCCTTGAGATGGGGAGA 604
Db      541 GCAAGCAGCCAAATGAGTCCCATAATGGGTCCATCTCCCATCTCCTTGAGATGGGGAGA 600
QY      605 AAGTGATATGACCTTTCATCTGCGTTGCCAGGAACCTGTGAGCAGAAACTTCTCAAGCCC 664
Db      601 AAGTGATATGACCTTTCATCTGCGTTGCCAGGAACCTGTGAGCAGAAACTTCTCAAGCCC 660
QY      665 CATCCTTGCCAGGAGCTCTGTGAAGGTGCTGATGACCCAGATTCCTCATGTGTCCT 724
Db      661 CATCCTTGCCAGGAGCTCTGTGAAGGTGCTGATGACCCAGATTCCTCATGTGTCCT 720
QY      725 CCTGTGTCCTGTTGGTGGCCCCCTCCGTCGAGTCTCTTTGTACTGGGGCTATTTCTTTG 784
Db      721 CCTGTGTCCTGTTGGTGGCCCCCTCCGTCGAGTCTCTTTGTACTGGGGCTATTTCTTTG 780
QY      785 GTTCTGAAGAGAGAGACAAGAAGATGACTTGAAGAGAGAGAGAGAGAGATTTG 844
Db      781 GTTCTGAAGAGAGAGACAAGAAGATGACTTGAAGAGAGAGAGAGAGATTTG 840
QY      845 TCGGGAACCTCCTAACATATGCCCCCATTTGTGAGAGAGAACACAGAGTAGACACAATCCC 904
Db      841 TCGGGAACCTCCTAACATATGCCCCCATTTGTGAGAGAGAACACAGAGTAGACACAATCCC 900
QY      905 TCACACTAATATGAACAATCCTAAAGGAAGATCCAGCAAAATACGGTTTACTCCACTGTGGA 964
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LOCUS      AX403365
DEFINITION      Sequence 252 from Patent WO0073454.
ACCESSION      AX403365
VERSION      AX403365.1  GI:21436903
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
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REFERENCE
AUTHORS      1 Ashkenazi,A.J., Baker,K.P., Botstein,D., Desnoyers,L., Eaton,D.,
Ferrara,N., Gerber,H., Gjeritsen,M., Goddard,A., Godowski,P.,
Grimaldi,C.J., Gurney,A.L., Kljavin,I., Napier,M.A., Pan,J.,
Paoni,N.F., Roy,M., Stewart,T.A., Tumas,D., Watanabe,C.K.,
Williams,P., Wood,W.I. and Zhang,Z.
TITLE      Secretd and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL      Patent: WO 0073454-A 252 07-DEC-2000;
Genentech Inc. (US)
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LOCUS Homo sapiens clone DNA58850 19A (UNQ576) mRNA, complete cds.
ACCESSION AY358512
VERSION AY358512.1 GI:37182146
KEYWORDS FLI_CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1076)
Clark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J.,

TITLE
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment
JOURNAL Genome Res. 13 (10), 2265-2270 (2003)
PUBMED 12975309
REFERENCE 2 (bases 1 to 1076)
AUTHORS Clark, H.F.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA

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Best Local Similarity 100.0%; Pred. No. 0;
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ACCESSION	AL713801		
VERSION	AL713801.1	GI:19584564	
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ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 3532)		
TITLE	Duesterhoeft,A., Lauber,J., Mewes,H.W., Weil,B. and Wiemann,S.		
JOURNAL	Submitted (12-MAR-2002) MIPS, Am Klopferspitz 18a, D-82152 Martinsried, GERMANY		
COMMENT	Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@kfz-heidelberg.de; sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZp667N1110) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/cdna/.		
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DEFINITION	Sequence 254 from patent US 6478825.		
ACCESSION	AR252550		
VERSION	AR252550.1	GI:27300458	
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SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 1053)		
AUTHORS	Winterbottom,J.M., Shimp,L., Boyce,T.M. and Kaes,D.		
TITLE	Implant, method of making same and use of the implant for the treatment of bone defects		
JOURNAL	Patent: US 6478825-A 254 12-NOV-2002;		

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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;
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DEFINITION Sequence 254 from Patent WO0073454.
ACCESSION AX403367
VERSION AX403367.1 GI:21436904
KEYWORDS
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
1 Ashkenazi, A.J., Baker, K.P., Botstein, D., Desnoyers, L., Eaton, D., Ferrara, N., Gerber, H., Gertlesen, M., Goddard, A., Godowski, P., Grimaldi, C.J., Gurney, A.L., Kijavlin, I., Napier, M.A., Pan, J., Paoni, N.F., Roy, M., Stewart, T.A., Tumas, D., Watanabe, C.K., Williams, P., Wood, W.I. and Zheng, Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same
JOURNAL Patent: WO 0073454-A 254 07-DEC-2000;
Genentech Inc. (US)

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ORIGIN

Query Match 38.6%; Score 1044; DB 6; Length 1053;
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QY 46 CTGTTCCCAACATGCTCAACCTCATCTATATCTTTGGCAGCTCAGAGGTCAACAG 105
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DB 301 TCTACTATGTGGGATATACAGCTCATCTCAGCAGGCCCTCCACCAGAGTACGTGC 360
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DB 421 ATGGACCTGTGTGAACCAATCTGACATGCTGATGGAACATGGGAAGAGATGTGATTT 480

QY 526 ATACCTGGAAGGCCCTGGGGCAAGCAGCCCAATGAGTCCCATATGGGTCATCCTCCCA 585
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Db 481 ATACCTGGAAGGCCCTGGGGCAAGCAGCCCAATGAGTCCCATATGGGTCATCCTCCCA 540
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QY 826 AGAAGAGATGACATTTGTGCGGAACCTCTAATCATATGCCCCCATCTCGAGAGACA 885
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Db 781 AGAAGAGATGACATTTGTGCGGAACCTCTAATCATATGCCCCCATCTCGAGAGACA 840
QY 886 CAGAGTACGACACAATCCCTCACACTAATAGAACCAATCCTAAAGGAAGATCCAGCAATA 945
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Db 841 CAGAGTACGACACAATCCCTCACACTAATAGAACCAATCCTAAAGGAAGATCCAGCAATA 900
QY 946 CGGTTTACTCCACTGTGGAATATCCGAAAAAGATGAAAAATCCCACTCACTGCTCAGCA 1005
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Db 901 CGGTTTACTCCACTGTGGAATATCCGAAAAAGATGAAAAATCCCACTCACTGCTCAGCA 960
QY 1006 TGCCAGACACACCAAGGCTATTGCTATGAGAAATGTTATCTAGACAGAGTGCACTCCC 1065
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Db 961 TGCCAGACACACCAAGGCTATTGCTATGAGAAATGTTATCTAGACAGAGTGCACTCCC 1020
QY 1066 CTAAGTCTCTGCTCAAAAAAAA 1089
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Db 1021 CTAAGTCTCTGCTCAAAAAAAA 1044

RESULT 14
BD249841 2780 bp DNA linear PAT 17-JUL-2003
LOCUS 33 human secreted proteins.
DEFINITION
ACCESSION BD249841
VERSION BD249841.1 GI:33059611
KEYWORDS JP 2002540763-A/43.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
AUTHORS Rosen,C.A., Ruben,S.M., Ebner,R., Young,P.E., Ni,J., Soppet,D.R.,
Moore,P.A., Shi,Y., Lafleur,D.W., Olsen,H.S., Florence,K.A. and
Komatsoulis,G.
TITLE 33 human secreted proteins
JOURNAL Patent: JP 2002540763-A 43 03-DEC-2002;
HUMAN GENOME SCIENCES INC
COMMENT OS Homo sapiens (human)
PN JP 2002540763-A/43
PD 03-DEC-2002
PF 08-FEB-2000 JP 2000598519
PR 10-FEB-1999 US 60/119468
PI CRAIG A ROSEN,STEVEN W RUBEN,REINHARD EBNER,PAUL E YOUNG,JIAN
NI,
PI DANIEL R SOPPET,PAUL A MOORE,YANGGU SHI,DAVID W LAFLEUR,HENRIK
PI S OLSEN,
PI KIMBERLY A FLORENCE,GEORGE KOMATSOULIS
PC C12N15/09,A61K31/7115,A61K38/00,A61K48/00,A61P1/00,A61P1/04,
PC A61P1/16,

PC A61P3/12,A61P5/10,A61P7/00,A61P7/04,A61P7/06,A61P9/00,A61P9/10, PC
A61P11/06,
PC A61P13/12,A61P15/00,A61P15/16,A61P17/00,A61P17/02,A61P17/06,
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PC A61P19/02,A61P19/04,A61P19/08,A61P21/00,A61P25/00,A61P25/14,
PC A61P25/16,
PC A61P25/18,A61P25/24,A61P25/28,A61P27/02,A61P31/04,A61P31/18,
PC A61P35/00,
PC A61P35/02,A61P37/00,A61P37/02,A61P37/06,A61P37/08,A61P43/00,
PC A61P43/00,
PC C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/10 PC
,C12P21/02,C12Q1/02,
PC C12Q1/68,G01N33/15,G01N33/50,G01N33/53,G01N33/56,
PC C12N15/00,
PC A61K37/02,C12N5/00
CC 33 human secreted proteins
FH Key location/Qualifiers
FT source 1..2780
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FEATURES
source 1..2780
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 38.4%; Score 1039; DB 6; Length 2780;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1089; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 950 TTACTCCACTGTGGAATATCCGAAAAAGATGAAAAATCCCACTGCTCAGCATGCC 1009
|||
Db 1026 TTACTCCACTGTGGAATATCCGAAAAAGATGAAAAATCCCACTGCTCAGCATGCC 1085
QY 1010 AGACACCAAGGCTATTGCTATGAGATGTTATCTAGACAGAGTGCACTCCCTAA 1069
|||
Db 1086 AGACACCAAGGCTATTGCTATGAGATGTTATCTAGACAGAGTGCACTCCCTAA 1145
QY 1070 GTCTGCTCAAAAAAAAAAACAATTTCTGGCCCAAGAAAAACAATCAGAAGAAATTCAGT 1129
|||
Db 1146 GTCTGCTCAAAAAAAAAAACAATTTCTGGCCCAAGAAAAACAATCAGAAGAAATTCAGT 1205
QY 1130 ATTTGACTAGAAACATCAAGGAGAAATGAAGAACGTTGACTTTTTCAGGATAAATTAT 1189
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Db 1206 ATTTGACTAGAAACATCAAGGAGAAATGAAGAACGTTGACTTTTTCAGGATAAATTAT 1265
QY 1190 CTCTGATGCTTTTATGATTAAAGTTCGTAATTCATCCACTGCTGAGAAATCTCCTC 1249
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Db 1266 CTCTGATGCTTTTATGATTAAAGTTCATTAATTCATCCACTGCTGAGAAATCTCCTC 1325
QY 1250 AAACCCAGAAAGTTTAATCACTTCATCCAAAAATGGGATTGTGAATGTCAGCAAAACAT 1309
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Db 1326 AAACCCAGAAAGTTTAATCACTTCATCCAAAAATGGGATTGTGAATGTCAGCAAAACAT 1385
QY 1310 AAAAAAGTGCTTAGAAGTATCTATAGAAATGTAATGCAAGTCCACACATATTAAATG 1369
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Db 1386 AAAAAAGTGCTTAGAAGTATCTATAGAAATGTAATGCAAGTCCACACATATTAAATG 1445
QY 1370 ACAGCTGTGTATTAATGATGGCTCCAGTCAAGTCAAGTGTCTGAGATTTCATTCACCCAGG 1429
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Db 1446 ACAGCTGTGTATTAATGATGGCTCCAGTCAAGTCAAGTGTCTGAGATTTCATTCACCCAGG 1505
QY 1430 GCTTGATGTCAAGATTATACCAAGAGTCTTGCTACCCAGAGGGCAAGAACCAAAACA 1489
|||
Db 1506 GCTTGATGTCAAGATTATACCAAGAGTCTTGCTACCCAGAGGGCAAGAACCAAAACA 1565
QY 1490 GACAGCAAGTCCAGCAGAGAGATGCACCTGCACCAAAAAATGATGTATTATGGCTCT 1549
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Db 1566 GACAGCAAGTCCAGCAGAGAGATGCACCTGCACCAAAAAATGATGTATTATGGCTCT 1625
QY 1550 ATAACTATGTGCCAGCAGCTATGCTGAGCTTACACTAAATGGTCAAGCGTGTCTGC 1609
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Db 1626 ATAACTATGTGCCAGCACTATGCTGAGCTTACACTAATTGCTCAGACGTCGTCTGTC 1685

QY 1610 CCTCATGAATTGGCTCCAAATGAATGAAGTACTTTCATGAGCAGTGTAGACGGCCTGA 1669

Db 1686 CCTCATGAATTGGCTCCAAATGAATGAAGTACTTTCATGAGCAGTGTAGACGGCCTGA 1745

QY 1670 CCACAGATTCACAGAGGGCCAGGTGTGATCCACAGACTTGAAGGTCAAAGTTCACAAA 1729

Db 1746 CCACAGATTCACAGAGGGCCAGGTGTGATCCACAGACTTGAAGGTCAAAGTTCACAAA 1805

QY 1730 GATGAAGATCAGGGTAGCTGACCATGTTTGGCAGATCTAATATGAGACAGAAAGTG 1789

Db 1806 GATGAAGATCAGGGTAGCTGACCATGTTTGGCAGATCTAATATGAGACAGAAAGTG 1865

QY 1790 TGCATGCCCCAAGACAGAGACTCCAGCAGGCTTCATTATGCACTTGTGCTCAAAA 1849

Db 1866 TGCATGCCCCAAGACAGAGACTCCAGCAGGCTTCATTATGCACTTGTGCTCAAAA 1925

QY 1850 GAAAAGTCTAGTTTAAAGCTGTGCCAGAACCCATCCCAATAAAGAGACCGAGTCTGAA 1909

Db 1926 GAAAAGTCTAGTTTAAAGCTGTGCCAGAACCCATCCCAATAAAGAGACCGAGTCTGAA 1985

QY 1910 GTCACATTGTAATCTAGTGTAGAGACTTGGAGTCAGCAGTGAAGTGGGGCAGC 1969

Db 1986 GTCACATTGTAATCTAGTGTAGAGACTTGGAGTCAGCAGTGAAGTGGGGCAGC 2045

QY 1970 GGGGGCAGTGGGTACTTGTAAACCTTTAAAGATGTTAATTCATTCAATAGATATTTATT 2029

Db 2046 GGGGGCAGTGGGTACTTGTAAACCTTTAAAGATGTTAATTCATTCAATAGATATTTATT 2105

QY 2030 AAGAACCTAC 2039

Db 2106 AAGAACCTAC 2115

RESULT 15

AF291815 1083 bp mRNA linear PRI 13-NOV-2001

LOCUS AF291815 Homo sapiens NK cell receptor (CS1) mRNA, complete cds.

DEFINITION AF291815 AF291815

ACCESSION AF291815.1 GI:13021809

VERSION AF291815.1

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1083)

AUTHORS Boles,K.S. and Mathew,P.A.

TITLE Molecular cloning of CS1, a novel human natural killer cell receptor belonging to the CD2 subset of the immunoglobulin superfamily

JOURNAL Immunogenetics 52 (3-4), 302-307 (2001)

MEDLINE 2115149

PUBMED 11220635

REFERENCE 2 (bases 1 to 1083)

AUTHORS Boles,K.S. and Mathew,P.A. Sr.

TITLE Direct Submission

JOURNAL Submitted (01-AUG-2000) Molecular Biology and Immunology, UNT Health Science Center, 3500 Camp Bowie Blvd, Fort Worth, TX 76107, USA

FEATURES

source

1..1083 Location/Qualifiers

/organism="Homo sapiens"

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/chromosome="1"

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12..1019

CDS

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/db_xref="GI:13021810"

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ORIGIN

Query Match 38.2%; Score 1032; DB 9; Length 1083;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 CAGAGGCAATATGGCTGGTTCGCCCAACATGCTCACCCTCATATATCCTTGGCAGC 90

Db 1 CAGAGGCAATATGGCTGGTTCGCCCAACATGCTCACCCTCATATATCCTTGGCAGC 60

QY 91 TCACAGGGTCAGAGCCCTCTGAGACCCGTGAAGAAGCTGGTCCGTTGGTGGGCCG 150

Db 61 TCACAGGGTCAGAGCCCTCTGAGACCCGTGAAGAAGCTGGTCCGTTGGTGGGCCG 120

QY 151 TGACTTCCCCCTGAAGTCCAAAGTAAGCAAGTGAAGTCTATGTCGAGCCTTCAACA 210

Db 121 TGACTTCCCCCTGAAGTCCAAAGTAAGCAAGTGAAGTCTATGTCGAGCCTTCAACA 180

QY 211 CAACCCCTTGTACACATACAGCCAGAGGGGCCACTATCATAGTAGCCAAATCGTA 270

Db 181 CAACCCCTTGTACACATACAGCCAGAGGGGCCACTATCATAGTAGCCAAATCGTA 240

QY 271 ATAGGAGAGAGTAGACTTCCCAAGATGAGGCTACTCCCTGAAGCTCAGCAAATGAGA 330

Db 241 ATAGGAGAGAGTAGACTTCCCAAGATGAGGCTACTCCCTGAAGCTCAGCAAATGAGA 300

QY 331 AGAATGACTCAGGATCTACTATGTGGGATATACAGCTCATCACTCCAGACCCCTCCA 390

Db 301 AGAATGACTCAGGATCTACTATGTGGGATATACAGCTCATCACTCCAGACCCCTCCA 360

QY 391 CCCAGAGTAGCTGCTGCATGTCTACGAGCAGCTGTCAAAGCCTAAAGTCAACATGGGTC 450

Db 361 CCCAGAGTAGCTGCTGCATGTCTACGAGCAGCTGTCAAAGCCTAAAGTCAACATGGGTC 420

QY 451 TGCAGAGCAATAGAATGGCACCTGTGTGACCAATCTGACATGCTGCAATGGAATGGGG 510

Db 421 TGCAGAGCAATAGAATGGCACCTGTGTGACCAATCTGACATGCTGCAATGGAATGGGG 480

QY 511 AAGAGATGTATTATACCTGGAAGGCCCTGGGGCAAGCAGCAATGAGTCCCATATATG 570

Db 481 AAGAGATGTATTATACCTGGAAGGCCCTGGGGCAAGCAGCAATGAGTCCCATATATG 540

QY 571 GGTCCATCTCCCATCTCTCTGAGATGGGAGAAAGTGATATGACCTTCATCTGCGTTG 630

Db 541 GGTCCATCTCCCATCTCTCTGAGATGGGAGAAAGTGATATGACCTTCATCTGCGTTG 600

QY 631 CCAGGAACCTGTGACGAGAAACTTCTCAAGCCCCCATCTTGGCCAGAGCTGTGGAAG 690

Db 601 CCAGGAACCTGTGACGAGAAACTTCTCAAGCCCCCATCTTGGCCAGAGCTGTGGAAG 660

QY 691 GTGCTGTGATGACCCAGATTCTCTCAGTGTCTCTGTGTCTCTGTGTGTCGCCCTCC 750

Db 661 GTGCTGTGATGACCCAGATTCTCTCAGTGTCTCTGTGTCTCTGTGTGTCGCCCTCC 720

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Db 721 TGCTCAGTCTCTTGTACTGGGGCTATTTCTTGGTTCTGAAGAGAGAGACAAGAAG 780

QY 811 AGTACATTGAAGAGAGAGAGAGAGAGATGACATTTGTCCGGAACCTCTTAACATATGCCCCC 870

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QY 991 ACTCACTGCTCAGATGCCAGACACACCAAGCTATTGCTATGAGATGTTATCTAGA 1050

Db 961 ACTCACTGCTCAGATGCCAGACACACCAAGCTATTGCTATGAGATGTTATCTAGA 1020

QY 1051 CAGCAGTGCACT 1062

Db 1021 CAGCAGTGCACT 1032

RESULT 16

AC068728

LOCUS 166345 bp DNA linear HTG 01-MAR-2001

DEFINITION Homo sapiens chromosome 1 clone RP11-8D14, WORKING DRAFT SEQUENCE, 5 unordered pieces.

AC068728

AC068728.7 GI:13174202

VERSION HTG, HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLLTOP.

KEYWORDS HTG, HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLLTOP.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

AUTHORS 1 (bases 1 to 166345)

Abola,A.P., Bruno,D., Conn,L., Dela Rosa,M., Faulkner,D., Federespiel,N., Glukhov,S., Hansen,N., Herman,Z.S., Hyman,R., Mao,J., Marathe,R., Morehouse,A.J., Oefner,P., Palm,C.J., Ramirez,D., Wilhelm,J., Yu,S. and Davis,R.W.

Unpublished

2 (bases 1 to 166345)

Abola,A.P., Bruno,D., Conn,L., Dela Rosa,M., Faulkner,D., Federespiel,N., Glukhov,S., Hansen,N., Herman,Z.S., Hyman,R., Mao,J., Marathe,R., Morehouse,A.J., Oefner,P., Palm,C.J., Ramirez,D., Wilhelm,J., Yu,S. and Davis,R.W.

Direct Submission

Submitted (08-MAY-2000) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA

On Mar 1, 2001 this sequence version replaced gi:11878529.

----- Genome Center

Center: Stanford DNA Sequencing and Technology Development Center

Center code: SDSTDC

Web site: http://sequence-www.stanford.edu/group/human/

Contact: hum-info@sequence.stanford.edu

----- Project Information

Center project name: 922

Center clone name: RP11-8D14

----- Summary Statistics

Sequencing Vector: M13mp18; X02513

Chemistry: Dye-primer; 0% of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 160988 bases at least Q40

Consensus quality: 161717 bases at least Q30

Consensus quality: 161956 bases at least Q20

Insert size: 164605; agarose-fp

Insert size: 165945; sum-of-contigs

Quality coverage: 9.0x in Q20 bases; agarose-fp

Quality coverage: 8.9x in Q20 bases; sum-of-contigs.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 5 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

* 1 1866: contig of 1866 bp in length

* 1867 1966: gap of unknown length

* 1967 3797: contig of 1831 bp in length

* 3798 3897: gap of unknown length

* 3898 23083: contig of 19186 bp in length

* 23084 23183: gap of unknown length

* 23184 62924: contig of 39741 bp in length

* 62925 63024: gap of unknown length

* 63025 166345: contig of 103321 bp in length.

FEATURES

location/Qualifiers

source

1. 166345

/organism="Homo sapiens"

/mol_type="genomic DNA"

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/chromosome="1"

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/clone_lib="RPCT human BAC library 11"

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3898. 23083

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clone_end:Sp6"

23184. 62924

/note="assembly_name:Contig23"

63025. 166345

/note="assembly_name:Contig24

clone_end:T7"

ORIGIN

Query Match 37.5%; Score 1013; DB 2; Length 166345;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1063; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 976 AGATGAAAAATCCCACTACTGCTCAGATGCCAGACACCAAGCTATTGGCTATG 1035

Db 127990 AGATGAAAAATCCCACTACTGCTCAGATGCCAGACACCAAGCTATTGGCTATG 128049

QY 1036 AGATGTTATCTAGACAGAGTGCACTCCCTAAGTCTGCTCAAAAAACAATTC 1095

Db 128050 AGATGTTATCTAGACAGAGTGCACTCCCTAAGTCTGCTCAAAAAACAATTC 128109

QY 1096 TCGGCCCAAGAAAAACAATTCAGAAAGATTGACTAGAAACATCAAGGAAGA 1155

Db 128110 TCGGCCCAAGAAAAACAATTCAGAAAGATTGACTAGAAACATCAAGGAAGA 128169

QY 1156 TGAAGAACGTTGACTTTTTCAGAGATAATATCTGATGCTTCTTAGATTTAAGAG 1215

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Db 128230 TTCGTAATTCATCCACTGCTGAGAAATCTCCTCAAAACCAGAAAGTTTAATCACTTCAT 128289

QY 1276 CCAAAAAATGGATTGTGAATGTCAAGCAAAACCATAAAAAAAGTGCTTAGAAGTATTCCTA 1335

Db 128290 CCAAAAAATGGATTGTGAATGTCAAGCAAAACCATAAAAAAAGTGCTTAGAAGTATTCCTA 128349

QY 1336 TAGAAATGTAATGCAAGGTCAACATATTAATGACAGCCTGTGTATTAATGATGGCTC 1395

Db 128350 TAGAAATGTAATGCAAGGTCAACATATTAATGACAGCCTGTGTATTAATGATGGCTC 128409

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Db 128410 CAGGTCAAGTGTCTGAGTTTCATTCATCCCAAGGCTTGATGTCAGAGTTATACCAAGA 128469

QY 1456 GTCCTGTACCAGAGGGCAAGAACCAAAACAGACAGCAAGTCCAGCAGAAAGCAGAT 1515

Db 128470 GTCCTGTACCAGAGGGCAAGAACCAAAACAGACAGCAAGTCCAGCAGAAAGCAGAT 128529

QY 1516 GCACCTGACAAAAATGATGTATTAATTGGCTCTATAAATACTATGTGCCAGCACTATGCT 1575

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Db 128590 GAGCTTACACTAATTTGGTCAGACGTGCTGTCTGCCCTCATGAATTTGGCTCCAAATGAAT 128649
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QY 1696 GGATCCACAGGACTTGAAGGTCAAAGTTCACAAAGATGAAGAATCAGGGTAGCTGACCAT 1755
Db 128710 GGATCCACAGGACTTGAAGGTCAAAGTTCACAAAGATGAAGAATCAGGGTAGCTGACCAT 128769
QY 1756 GTTTGGCAGATACTATAATGAGACACAGAAGTGTGCATGGCCCAAGACAGACCTCC 1815
Db 128770 GTTTGGCAGATACTATAATGAGACACAGAAGTGTGCATGGCCCAAGACAGACCTCC 128829
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Db 128890 CAGAACCCATCCCAATAAAGAGACCGAGTCTGAAGTCAATTTGTAATCTAGTGTAGAG 128949
QY 1936 ACTTGAGTCAGGCGAGTGAAGTGTGGGGGCGACGGGGGCGAGTGGTACTTTGTAACCTT 1995
Db 128950 ACTTGAGTCAGGCGAGTGAAGTGTGGGGGCGACGGGGGCGAGTGGTACTTTGTAACCTT 129009
QY 1996 TAAAGATGTTAATTCATTCAATAGATATTATTAAAGAACCTTAC 2039
Db 129010 TAAAGATGTTAATTCATTCAATAGATATTATTAAAGAACCTTAC 129053

RESULT 17
BD249842
LOCUS BD249842 1412 bp DNA linear PAT 17-JUL-2003
DEFINITION 33 human secreted proteins.
ACCESSION BD249842
VERSION BD249842.1 GI:33059612
KEYWORDS JP 2002540763-A/44.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1412)
AUTHORS Rosen,C.A., Ruben,S.M., Ebner,R., Young,P.E., Ni,J., Soppet,D.R.,
Moore,P.A., Shi,Y., Lafleur,D.W., Olsen,H.S., Florence,K.A. and
Komatsoulis,G.
33 human secreted proteins
Patent: JP 2002540763-A 44 03-DEC-2002;
HUMAN GENOME SCIENCES INC
OS Homo sapiens (human)
PN JP 2002540763-A/44
PD 03-DEC-2002
PF 08-FEB-2000 JP 2000598519
PR 10-FEB-1999 US 60/119468
PI CRAIG A ROSEN,STEVEN M RUBEN,REINHARD EBNER,PAUL E YOUNG,JIAN
NI,
PI DANIEL R SOPPET,PAUL A MOORE,YANGSU SHI,DAVID W LAFLEUR,HENRIK
TITLE
JOURNAL
COMMENT
PI S OLSEN,
PI KIMBERLY A FLORENCE,GEORGE KOMATSOUKIS
PC C12N15/09,A61K31/7115,A61K38/00,A61K48/00,A61P1/00,A61P1/04,
PC A61P1/16,
PC A61P3/12,A61P5/10,A61P7/00,A61P7/04,A61P7/06,A61P9/00,A61P9/10, PC
A61P11/06,
PC A61P13/12,A61P15/00,A61P15/16,A61P17/00,A61P17/02,A61P17/06,
PC A61P17/10,
PC A61P19/02,A61P19/04,A61P19/08,A61P21/00,A61P25/00,A61P25/14,
PC A61P25/16,

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LOCUS 87 human secreted proteins.
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ACCESSION BD082372.1 GI:22627982
VERSION JP 200152239-A/14.
KEYWORDS Mastadenovirus
SOURCE Mastadenovirus
ORGANISM Viruses; dsDNA viruses, no RNA stage; Adenoviridae.
REFERENCE 1 (bases 1 to 1412)
AUTHORS Young,P., Greene,J.M., Ferrie,A.M., Ruben,S.M., Rosen,C.A.,
Duan,R.D., Hu,J.S., Florence,K.A., Olsen,H.S., Ebner,R.,
Brewer,L.A., Moore,P.A., Shi,Y., Lafleur,D.W. and Ni,J.
TITLE 87 human secreted proteins
JOURNAL Patent: JP 200152239-A 14 13-NOV-2001;
HUMAN GENOME SCIENCES INC SECRETARY OF THE DEPARTMENT OF HEALTH
HUMAN SERVICES
PN JP 200152239-A/14
PD 13-NOV-2001
PF 19-MAR-1998 JP 1998542119
PR 21-MAR-1997 US 60/041281,21-MAR-1997 US 60/041276 PR
21-MAR-1997 US 60/042344,21-MAR-1997 US 60/041277 PR
30-MAY-1997 US 60/048355,30-MAY-1997 US 60/048096 PR
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30-MAY-1997 US 60/048188,30-MAY-1997 US 60/048094 PR
30-MAY-1997 US 60/048350,05-AUG-1997 US 60/054804 PR
19-AUG-1997 US 60/056370,02-OCT-1997 US 60/060862 PI PAUL
YOUNG,JOHN M GREENE,ANN M FERRIE,STEVEN M RUBEN,CRAIG A PI
ROSEN,
PI ROXANNE D DUAN,JING SHAN HU,KIMBERLY A FLORENCE,HENRIK S
OLSEN,
PI REINHARD EBNER,LAURIE A BREWER,PAUL A MOORE,YANGGU SHI,DAVID W
PI LAFLEUR,
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REFERENCE	1 Murphy, J.J. and Norton, J.D.		
AUTHORS	Murphy, J.J. and Norton, J.D.		
TITLE	Cell type specific early response gene expression during		
JOURNAL	Plasmacytoid differentiation of human B lymphocytic leukaemia cells		
REFERENCE	2 Biochim. Biophys. Acta 1049, 262-271 (1990)		
AUTHORS	Murphy, J.J., Hobby, P., Vilarino-Varela, J., Bishop, B.,		
JOURNAL	Jordanidou, P., Sutton, B.J. and Norton, J.D.		
REFERENCE	A novel immunoglobulin superfamily receptor (19A) related to CD2 is		
AUTHORS	expressed on activated lymphocytes and promotes homotypic B-cell		
JOURNAL	adhesion. J. 361 (Pt 3), 431-436 (2002)		
MEDLINE	21611458		

PUBMED	11802771
REFERENCE	3
AUTHORS	Murphy, J.J.
TITLE	Direct Submission
JOURNAL	Submitted (17-MAR-2000) Murphy J.J., Division of Life Sciences, King's College London, 150 Stamford Street. London, SE1 8WA, UNITED KINGDOM
REMARK	revised by [3]
REFERENCE	4 (bases 1 to 1111)
AUTHORS	Murphy, J.J.
TITLE	Direct Submission
JOURNAL	Submitted (21-JAN-2001) Murphy J.J., Division of Life Sciences, King's College London, Franklin-Wilkins Building, 150 Stamford Street. London, SE1 9NN, UNITED KINGDOM
COMMENT	On Jan 30, 2001 this sequence version replaced gi:7320862.
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VERSION BC027867.1 GI:20380756
KEYWORDS MGC.
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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1 (bases 1 to 2658)
REFERENCE
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
Schnersch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
12477932
2 (bases 1 to 2658)
Strausberg,R.
Direct Submission
Submitted (08-APR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK
COMMENT
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayale,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
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Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
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Best Local Similarity 99.6%; Pred. No. 0;
Matches 1120; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 1995 TTAAGATGGTTAATTCATTCAATAGATATTATTAGAACCTA 2038
Db 1861 TTAAGATGGTTAATTCATTCAATAGATATTATTAGAACCTA 1904
RESULT 21
HSA404F10
LOCUS
DEFINITION
HSA404F10 195976 bp DNA linear PRI 29-JUL-2000
Human DNA sequence from clone RP11-404F10 on chromosome
1q23.1-24.1. Contains the 5' end of the SLAM gene for signaling
lymphocytic activation molecule, a SET (SET translocation (myeloid
leukemia-associated)) protein pseudogene, the CD48 gene for CD48
antigen (B-cell membrane protein), the gene for a novel LY9
(lymphocyte antigen 9) like protein and the 5' end of the LY9 gene.
Contains ESTs, STSs and GSSs, complete sequence.
ALI21985
ALI21985.13 GI:7161187
HTG; CD48; LY9; SET; SLAM.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 195976)
Bates,K.
Direct Submission
Submitted (04-APR-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Mar 6, 2000 this sequence version replaced gi:6983370.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
feature key.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr1
RP11-404F10 is from the library RPCI-11.2 constructed at the
Roswell Park Cancer Institute by the group of Pieter de Jong. For
further details see http://bacpac.med.buffalo.edu/
VECTOR: pBACe3.6
This sequence is the entire insert of clone RP11-404F10.
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Query Match 33.7%; Score 910; DB 9; Length 195976;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1060; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1156 TGAAGAACGTTGACTTTTTCAGGATAAATTATCTGATGCTTCTTAGATTAAAGAG 1215
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QY 1216 TTCGTAATTCATCCACTGCTGAGAAATCTCCTCAACCCAGAAAGTTTAATCACTTCAT 1275
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Db 141398 TAAAGATGTTAATTCATTCATATAGATATTTATTAAGAACCTA 141440

RESULT 22
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LOCUS AX405882
DEFINITION Sequence 297 from Patent WO02222660.
ACCESSION AX405882
VERSION AX405882.1 GI:21439203
KEYWORDS

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1
Tang, Y.T., Liu, C., Zhou, P., Asundi, V., Zhang, J., Zhao, Q.A., Ren, F., Xue, A.J., Yang, Y., Wehrman, T. and Drmanac, R.T.
TITLE Novel nucleic acids and polypeptides
JOURNAL Patent: WO 0222660-A 297 21-MAR-2002;
HYSEQ, INC. (US)
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 811; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GAAGTGGCTTCATTTCAAGTGGCTGACTTCAGAGACCAATATGCTGTTCCCAACATG 61
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QY 242 GGGCACTATCATAGTGAACCCAAATCGTAATAGGGAGAGAGTAGACTTCCAGATGAGG 301
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QY	722	CCTCCTGTGTCTCCTGTGTGGTGCCCCCTCTGCTCAGTCTCTTTGTACTGGGGCTATTCT	781
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QY	782	TTGGTTTCTGAAGAGAGAGACACAAGAGAG	812
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DEFINITION	Homo sapiens mRNA for 19A24 protein (19A24 gene).		
ACCESSION	AJ271869		
VERSION	AJ271869.1	GI:7161174	
KEYWORDS	19A24 gene.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
AUTHORS	1 Murphy,J.J., Norton,J.D., Hobby,P. and Sutton,B.J.		
TITLE	An early response gene that encodes an immunoglobulin superfamily member with structural similarity to CD2		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 1074)		
AUTHORS	Murphy,J.J.		
TITLE	Direct Submission		
JOURNAL	Submitted (01-FEB-2000) Murphy J.J., Immunology Research Group, Division of Life Sciences, King's College London, 150 Stamford Street, London, SE1 8WA, UNITED KINGDOM		
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Best local Similarity	100.0%;	Pred. No. 0;	
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QY	91	TCACAGGGGTACGACGCTCTGGACCCCGTGAAGAAGCTGTGGTTCGTTGGTGGGCCG	150
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QY	151	TGACTTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTTATGTCTGGAACCTTCAACA	210
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QY	511	AAGAGGATGTGATTATATCTTGGAAGGCCCTGGGGCAAGCAACCAATGAGTCCCATATG	570
Db	503	AAGAGGATGTGATTATATCTTGGAAGGCCCTGGGGCAAGCAACCAATGAGTCCCATATG	562
QY	571	GGTCCATCTCTCCCATCTCTGAGATGGGAGAAAGTATAGCCTTCATCTGCGTTG	630
Db	563	GGTCCATCTCTCCCATCTCTGAGATGGGAGAAAGTATAGCCTTCATCTGCGTTG	622
QY	631	CCAGGAAACCTGTGACGAGAACTTCTCAAGCCCCCATCTTGCCAGGAAGCTGTGAAG	690
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QY	691	GTGCTGCTGATGACCCAGATTCTCCATGTCCTCTGTCCTGTTGTTGTCGCCCTCC	750
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Db	743	TGCTCAGTCTCTTGTACTGGGGCTATTCTTGTGTTCTGAAGAGAGAGACAAGAAG	802
QY	811	AG 812	
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DEFINITION	Sequence 401 from patent US 6607879.		
ACCESSION	AR379856		
VERSION	AR379856.1	GI:40087490	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 921)		
AUTHORS	Cocks,B.G., Stuart,S.G. and Seilhamer,J.J.		
TITLE	Compositions for the detection of blood cell and immunological response gene expression		
JOURNAL	Patent: US 6607879-A 401 19-AUG-2003;		
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TITLE Direct Submission
JOURNAL Submitted (09-JUL-2002) 1, D-85764 Neuberberg, GERMANY
COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by EMBL (European Molecular Biology Laboratories, Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project.
This clone (DKFZp666F188) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/cDNA/.
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Db 121 TATGCTGAGCTTACACTAATTGTCAGACGTGCTGCTGCCCTCATGAATTGGCTCAA 180
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QY 1990 AACCTTTAAAGATGTTAATTCATTCATAGATATTATTAAAGACCTA 2038
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LOCUS CQ723314 1350 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 9248 from Patent WO02068579.
ACCESSION CQ723314
VERSION CQ723314.1 GI:42284171
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof
JOURNAL Patent: WO 02068579-A 9248 06-SEP-2002;
PE Corporation (NY) (US)
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LOCUS CQ071439 522 bp DNA linear PAT 20-JAN-2004
DEFINITION Sequence 7239 from Patent WO0157278.
ACCESSION CQ071439
VERSION CQ071439.1 GI:41041308
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human hela cells or other human cervical epithelialcells

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VERSION	CQ176644.1	GI:41171383		
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SOURCE	Homo sapiens (human)			
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REFERENCE	1			
AUTHORS	Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.			
TITLE	Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human heart			
JOURNAL	Patent: WO 0157274-A 8040 09-AUG-2001;			
FEATURES	Aeomica, Inc. (US)			
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VERSION	CQ224251.1	GI:41206669		
KEYWORDS				
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	1			
AUTHORS	Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.			
TITLE	HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130> PB 0004 WO			

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VERSION	CQ262264.1	GI:41234744									
KEYWORDS	Homo sapiens (human)										
SOURCE	Homo sapiens										
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REFERENCE	1 Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.										
AUTHORS	Human genome-derived single exon nucleic acid probes useful for										
TITLE	analysis of gene expression in human fetal liver										
JOURNAL	Patent: WO 0157277-A 10525 09-AUG-2001;										
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ORIGIN											

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

Sims, S.
Direct Submission
Submitted (12-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 21, 2000 this sequence version replaced gi:9230972.

----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk
----- Project Information
Center project name: bA167A1
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 146348 bases at least Q40
Consensus quality: 156528 bases at least Q30
Consensus quality: 162553 bases at least Q20
Insert size: 169515; sum-of-contigs
Insert size: 156873; 10.5% error; agarose-fp
Quality coverage: 2.18x in Q20 bases; sum-of-contigs Quality coverage: 3.50x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 48 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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QY 335 TGACTCAGGGATCTACTATGTGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCA 394
Db 87644 TGACTCAGGGATCTACTATGTGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCA 87703

QY 395 GGAGTAGCTGTCATGTCTACG 417
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Db 87704 GGAGTAGCTGTCATGTCTACG 87726

RESULT 37
AX884532 344 bp DNA linear PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 395 from Patent EP1033401.
ACCESSION AX884532
VERSION AX884532.1 GI:40039787
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y.
TITLE Expressed sequence tags and encoded human proteins
JOURNAL Patent: EP 1033401-A 395 06-SEP-2000;
Genset (FR)
FEATURES
source 1..344
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/mol_type="unassigned DNA"
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54..>344
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/translation="MAGSPFTCLILYILWQLTGSAAAGPYKELVGSVGAVTFPLKSK
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ORIGIN

Query Match 10.4%; Score 281; DB 6; Length 344;
Best Local Similarity 99.7%; Pred.No. 3.9e-155;
Matches 331; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGTGGCTTCATTTTCAGTGGCTGACTTCCAGAGACAATATGGCTGCCCAACAT 60
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QY 61 GCCTCACCCTCATCTATATCTCTTGGCAGCTCAAGGGTCAGCAGCCTCTGACCCGTGA 120
Db 73 GCCTCACCCTCATCTATATCTCTTGGCAGCTCAAGGGTCAGCAGCCTCTGACCCGTGA 132

QY 121 AAGAGCTGGTCGTTCCGTTGGTGGGGCCGTGACTTCCCCCTGAAGTCCAAAGTAAAGC 180
Db 133 AAGAGCTGGTCGTTCCGTTGGTGGGGCCGTGACTTCCCCCTGAAGTCCAAAGTAAAGC 192

QY 181 AAGTGACTCTAATTGCTGGAACCTTCAACAACACCCCTCTGTGCACATACAGCCAGAAG 240
Db 193 AAGTGACTCTAATTGCTGGAACCTTCAACAACACCCCTCTGTGCACATACAGCCAGAAG 252

QY 241 GGGCACTATCATAGTGACCCAAATCGTAATAGGAGAGAGAGTAGACTTCCAGATGAG 300
Db 253 GGGCACTATCATAGTGACCCAAATCGTAATAGGAGAGAGAGTAGACTTCCAGATGAG 312

QY 301 GCTACTCCCTGAAGCTCAGCAAACTGAAGAAG 332
Db 313 GCTACTCCCTGAAGCTCAGCAAACTGAAGAAG 344

RESULT 38
BD024142 344 bp DNA linear PAT 27-AUG-2002
LOCUS
DEFINITION Sequence tag and encoded human protein.
ACCESSION BD024142
VERSION BD024142.1 GI:22565365
KEYWORDS UP 2001269182-A/388.
SOURCE Homo sapiens (human)
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ORGANISM      Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE          1 (bases 1 to 344)
JOURNAL        Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.
               Sequence tag and encoded human protein
               Patent: JP 2001269182-A 388 02-OCT-2001;
               GENSET
COMMENT        OS Homo sapiens (human)
               PN JP 2001269182-A/388
               PD 02-OCT-2001
               PF 24-FEB-2000 JP 2000118773
               PR 26-FEB-1999 US 60/122487
               PI JEAN BAPTISTE DUMAS MILNE EDWARDS,EIMERIC DUCLAIR,JEAN YVES
               PI JORDAN
               PC C12N15/09,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N1/21,PC
               PC C12N5/10,
               PC C12P21/02,C12P21/08,C12Q1/68//G06F17/30,C12N15/00,C12N5/00,PC
               G06F15/40
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Query Match 10.4%; Score 281; DB 6; Length 344;
Best Local Similarity 99.7%; Pred. No. 3.9e-155;
Matches 331; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGTGGCTTCATTTTCAGTGGCTGACTTCAGAGAGCAATATGGCTGCCCAACAT 60
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Db 13 GGAAGTGGCTTCATTTTCAGTGGCTGACTTCAGAGAGCAATATGGCTGCCCAACAT 72

QY 61 GCCTCACCCTCATCTATATCCTTTGGCAGCTCACAGGTCAGAGCCTCTGACCCGTGA 120
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QY 121 AAGAGCTGGTGGTCCGTTGGTGGGGCCGTGACTTCCCCCTGAAGTCCAAAGTAAGC 180
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QY 181 AAGTGACTCTATTGTCTGGACCTTCAACACAAACCCCTTGTGTCAACCATACAGCCAGAAG 240
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Db 193 AAGTGACTCTATTGTCTGGACCTTCAACACAAACCCCTTGTGTCAACCATACAGCCAGAAG 252

QY 241 GGGGCACTATCATAGTGACCCCAAAATCGTAATAGGAGAGAGTAGACTTCCCAGATGAG 300
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Db 253 GGGGCACTATCATAGTGACCCCAAAATCGTAATAGGAGAGAGTAGACTTCCCAGATGAG 312

QY 301 GCTACTCCCTGAAGCTCAGCAAACTGAAGAAG 332
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Db 313 GCTACTCCCTGAAGCTCAGCAAACTGAAGAAG 344

RESULT 39
BD076035 347 bp DNA linear PAT 27-AUG-2002
LOCUS      5' EST of secretory protein expressed in endoblast.
ACCESSION BD076035
VERSION    BD076035.1 GI:22621638
KEYWORDS   JP 2001512005-A/161.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE    1 (bases 1 to 347)
AUTHORS      Edwards,J.B.D.M., Duclert,A. and Lacroix,B.
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TITLE          5' EST of secretory protein expressed in endoblast
JOURNAL        Patent: JP 2001512005-A 161 21-AUG-2001;
COMMENT        OS Homo sapiens (human)
               PN JP 2001512005-A/161
               PD 21-AUG-2001
               PF 31-JUL-1998 JP 2000505194
               PR 01-AUG-1997 US 08/904468
               PI JEAN BAPTISTE DUMAS MILNE EDWARDS,AYMERIC DUCLEERT,BRUNO PI
               PI LACROIX
               PC C12N15/09,C07K19/00,C12M1/00,C12N1/15,C12N1/19,C12N1/21,C12N5/
               PC 10,C12Q1/68,
               PC C12N15/00,C12N5/00
               CC blastn
               CC identity 98
               CC region 18..301
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               CC est
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               CC region 1..61
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               CC est
               CC Von Heijne matrix
               CC score 5.9
               CC seq LIVINGMQLTGSAA/SG
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               FT misc feature 49..109
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                   /db_xref="taxon:9606"

ORIGIN
Query Match 10.4%; Score 281; DB 6; Length 347;
Best Local Similarity 99.7%; Pred. No. 3.9e-155;
Matches 331; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGTGGCTTCATTTTCAGTGGCTGACTTCAGAGAGCAATATGGCTGTTCCCAACAT 60
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Db 13 GGAAGTGGCTTCATTTTCAGTGGCTGACTTCAGAGAGCAATATGGCTGTTCCCAACAT 72

QY 61 GCCTCACCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGACCCCTGAGCCCGTGA 120
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QY 121 AAGAGCTGGTGGTCCGTTGGTGGGGCCGTGACTTCCCCCTGAAGTCCAAAGTAAGC 180
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QY 181 AAGTGACTCTATTGTCTGGACCTTCAACACAAACCCCTTGTGTCAACCATACAGCCAGAAG 240
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QY 241 GGGGCACTATCATAGTGACCCCAAAATCGTAATAGGAGAGAGTAGACTTCCCAGATGAG 300
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Db 253 GGGGCACTATCATAGTGACCCCAAAATCGTAATAGGAGAGAGTAGACTTCCCAGATGAG 312

QY 301 GCTACTCCCTGAAGCTCAGCAAACTGAAGAAG 332
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Db 313 GCTACTCCCTGAAGCTCAGCAAACTGAAGAAG 344

RESULT 40
BD248091 401 bp DNA linear PAT 17-JUL-2003
LOCUS      5' ESTs for secreted proteins expressed in various tissues.
ACCESSION BD248091
VERSION    BD248091.1 GI:33057861
KEYWORDS   JP 2002525024-A/156.
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 401)
AUTHORS Edwards,J.B.D.M., Duclert,A. and Lacroix,B.
TITLE 5' ESTs for secreted proteins expressed in various tissues
JOURNAL Patent: JP 2002525024-A 156 13-AUG-2002;
GENSET
COMMENT OS Homo sapiens (human)
PN JP 2002525024-A/156
PD 13-AUG-2002
PF 31-JUL-1998 JP 2000505294
PR 01-AUG-1997 US 08/905051
PI JEAN BAPTISTE DUMAS MILNE EDWARDS,AYMERIC DUCLEERT,BRUNO PI
LACROIX
PC C12N15/09,C12N15/09,C07K14/47,C12M1/00,C12P21/02,C12N15/00, PC
C12N15/00
CC blastn
CC identity 98
CC region 18. .317
CC id H73135
CC est
CC blastn
CC identity 93
CC region 318. .366
CC id H73135
CC est
CC blastn
CC identity 100
CC region 1. .61
CC id AA251602
CC est
CC Von Heijne matrix
CC score 5.9
CC seq livilmqltgsaa/sg
CC n=a, g, c or t
FH Key Location/Qualifiers
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FT misc_feature 336. .384
FT misc_feature 25. .85
FT sig_peptide 30. .95
FT misc_feature 332.
FEATURES Location/Qualifiers
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Best Local Similarity 99.7%; Pred. No. 6.1e-154;
Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 121 GTTCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTCTA 180
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Db 181 TTGTCCTGACCTTCAACACAACCCCTCTTGTACCAATACAGCCAGAAAGGGGGCAHTATCA 240
OY 253 TAGTGACCCAAATCGTAATAGGAGAGAGATAGACTTCCCAAGATGAGGCTACTCCCTGA 312
Db 241 TAGTGACCCAAATCGTAATAGGAGAGAGATAGACTTCCCAAGATGAGGCTACTCCCTGA 300

OY 313 AGCTCAGCAACTGAAGAAGATGACTCAG 342
Db 301 AGCTCAGCAACTGAAGAAGATGACTCAG 330
RESULT 41
CQ772054 401 bp DNA linear PAT 04-MAR-2004
LOCUS
DEFINITION Sequence 162 from Patent EP1375514.
ACCESSION CQ772054
VERSION CQ772054.1 GI:45126015
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
Dumas Milne Edwards,J.B., Duclert,A. and Lacroix,B.
TITLE 5'ESTs for secreted proteins expressed in various tissues
JOURNAL Patent: EP 1375514-A 162 02-JAN-2004;
GENSET (FR)
FEATURES Location/Qualifiers
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Best Local Similarity 99.7%; Pred. No. 6.1e-154;
Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 13 ATTCAGTGGCTGACTTCAGAGACAATATGGCTGTTCCCAACATGCTCACCCTCA 72
Db 1 ATTCAGTGGCTGACTTCAGAGACAATATGGCTGTTCCCAACATGCTCACCCTCA 60
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Db 61 TCTATATCCTTTGGCAGCTCACAGGCTCAGCAGCCTCTGGAACCCGTGAAGAAGCTGTGCG 120
OY 133 GTTCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTCTA 192
Db 121 GTTCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTCTA 180
OY 193 TTGTCCTGACCTTCAACACAACCCCTCTTGTACCAATACAGCCAGAAAGGGGGCACTATCA 252
Db 181 TTGTCCTGACCTTCAACACAACCCCTCTTGTACCAATACAGCCAGAAAGGGGGCAHTATCA 240
OY 253 TAGTGACCCAAATCGTAATAGGAGAGAGATAGACTTCCCAAGATGAGGCTACTCCCTGA 312
Db 241 TAGTGACCCAAATCGTAATAGGAGAGAGATAGACTTCCCAAGATGAGGCTACTCCCTGA 300
OY 313 AGCTCAGCAACTGAAGAAGATGACTCAG 342
Db 301 AGCTCAGCAACTGAAGAAGATGACTCAG 330
RESULT 42
CQ080659 275 bp DNA linear PAT 20-JAN-2004
LOCUS
DEFINITION Sequence 16459 from Patent WO0157278.
ACCESSION CQ080659
VERSION CQ080659.1 GI:41050528
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1

AUTHORS Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human hela cells or other human
cervical epithelialcells
JOURNAL Patent: WO 0157278-A 16459 09-AUG-2001;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
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QY 203 CTTCAACACAAACCCCTCTGTGCACCATACAGCCAGAAAGGGGGCACTATCATAGTGACCCA 262
Db 61 CTTCAACACAAACCCCTCTGTGCACCATACAGCCAGAAAGGGGGCACTATCATAGTGACCCA 120
QY 263 AAATCGTAATAGGAGAGAGATGAGTACTTCCAGATGAGGCTACTCCCTGAAGCTCAGCAA 322
Db 121 AAATCGTAATAGGAGAGAGATGAGTACTTCCAGATGAGGCTACTCCCTGAAGCTCAGCAA 180
QY 323 ACTGAAGAAGATGACTCAGGGATCTACTATGTGGGATATACAGCTCATCTCCAGCA 382
Db 181 ACTGAAGAAGATGACTCAGGGATCTACTATGTGGGATATACAGCTCATCTCCAGCA 240
QY 383 GCCCTCCACCCAGAGTACGTGCTGCATGTCTACG 417
Db 241 GCCCTCCACCCAGAGTACGTGCTGCATGTCTACG 275
RESULT 43
CQ15107 275 bp DNA linear PAT 21-JAN-2004
LOCUS Sequence 23966 from Patent WO0157272.
ACCESSION CQ15107
VERSION CQ15107.1 GI:41084977
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human placenta
JOURNAL Patent: WO 0157272-A 23966 09-AUG-2001;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.5e-151;
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 203 CTTCAACACAAACCCCTCTGTGCACCATACAGCCAGAAAGGGGGCACTATCATAGTGACCCA 262
Db 61 CTTCAACACAAACCCCTCTGTGCACCATACAGCCAGAAAGGGGGCACTATCATAGTGACCCA 120
QY 263 AAATCGTAATAGGAGAGAGATGAGTACTTCCAGATGAGGCTACTCCCTGAAGCTCAGCAA 322
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QY 323 ACTGAAGAAGATGACTCAGGGATCTACTATGTGGGATATACAGCTCATCTCCAGCA 382
Db 181 ACTGAAGAAGATGACTCAGGGATCTACTATGTGGGATATACAGCTCATCTCCAGCA 240
QY 383 GCCCTCCACCCAGAGTACGTGCTGCATGTCTACG 417
Db 241 GCCCTCCACCCAGAGTACGTGCTGCATGTCTACG 275
RESULT 44
CQ153950 275 bp DNA linear PAT 21-JAN-2004
LOCUS Sequence 23972 from Patent WO0157276.
ACCESSION CQ153950
VERSION CQ153950.1 GI:41161302
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human bone marrow
JOURNAL Patent: WO 0157276-A 23972 09-AUG-2001;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
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Query Match 10.2%; Score 275; DB 6; Length 275;
Best Local Similarity 100.0%; Pred. No. 1.5e-151;
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 143 TGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAGCAAGTTGACTTATTGTCTGGAC 202
Db 1 TGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAGCAAGTTGACTTATTGTCTGGAC 60
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QY 263 AAATCGTAATAGGAGAGAGATGAGTACTTCCAGATGAGGCTACTCCCTGAAGCTCAGCAA 322
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QY 323 ACTGAAGAAGATGACTCAGGGATCTACTATGTGGGATATACAGCTCATCTCCAGCA 382
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QY 383 GCCCTCCACCCAGAGTACGTGCTGCATGTCTACG 417
Db 241 GCCCTCCACCCAGAGTACGTGCTGCATGTCTACG 275
RESULT 45

CQ186535 LOCUS CQ186535 275 bp DNA linear PAT 21-JAN-2004
DEFINITION Sequence 17931 from Patent WO0157274.
ACCESSION CQ186535
VERSION CQ186535.1 GI:41181549
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS 1 Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human heart
JOURNAL Patent: WO 0157274-A 17931 09-AUG-2001;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
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ORIGIN
Query Match 10.2%; Score 275; DB 6; Length 275;
Best Local Similarity 100.0%; Pred. No. 1.5e-151;
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 143 TGGGGCCGTGACTTTCCCTGAGTCCAAAGTAAGCAAGTTGACTCTATTGTCTGAC 202
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DB 1 TGGGGCCGTGACTTTCCCTGAGTCCAAAGTAAGCAAGTTGACTCTATTGTCTGAC 60
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OY 203 CTTCACACACACCCCTCTTGTTCACCATACAGCCAGAGGGGGCACTATCATAGTGACCCA 262
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DB 61 CTTCACACACACCCCTCTTGTTCACCATACAGCCAGAGGGGGCACTATCATAGTGACCCA 120
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OY 263 AAATCGTAATAGGAGAGAGTAGACTTCCACAGATGAGGCTACTCCCTGAAGCTCAGCAA 322
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OY 323 ACTGAAGAAGATGACTCAGGATCTACTATGTGGGATATACAGCTCATCACTCCAGCA 382
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DB 181 ACTGAAGAAGATGACTCAGGATCTACTATGTGGGATATACAGCTCATCACTCCAGCA 240
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OY 383 GCCCTCCACCCAGAGTAGCTGCTGCTGCTACG 417
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DB 241 GCCCTCCACCCAGAGTAGCTGCTGCTGCTACG 275
|||||

RESULT 46
LOCUS CQ237182 275 bp DNA linear PAT 21-JAN-2004
DEFINITION Sequence 24021 from Patent WO0157273.
ACCESSION CQ237182
VERSION CQ237182.1 GI:41220462
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS 1 Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130> PB 0004 WO
3<150> US 60/180,312<151> 04 February 2000 (04.02.00)<150> US
60/207,456<151> 26 May 2000 (26.05.00)<150> US 09/632,366<151> 03
August 2000 (03.08.00)<150> GB 24263.6<151> 03 October 2000
(03.10.00)<150> US 60/236,359<151> 27 September 2000
(27.09.00)<150> US 60/234,687<151> 21 September 2000
(21.09.00)<150> US 09/608,408<151> 30 June 2000 (30.06.00)<170>
Molecular Dynamics Sequence Listing Engine

JOURNAL Patent: WO 0157273-A 24021 09-AUG-2001;
Aeomica, Inc. (US)
FEATURES
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL121985.13-EXPRESSED IN ADULT LIVER, SIGNAL
= 6.5-NT HIT: AJ271869.1, EVALUE 0.00e+00-EST_HUMAN HIT:
AW963563.1, EVALUE 0.00e+00"

ORIGIN
Query Match 10.2%; Score 275; DB 6; Length 275;
Best Local Similarity 100.0%; Pred. No. 1.5e-151;
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 143 TGGGGCCGTGACTTTCCCTGAGTCCAAAGTAAGCAAGTTGACTCTATTGTCTGAC 202
|||||
DB 1 TGGGGCCGTGACTTTCCCTGAGTCCAAAGTAAGCAAGTTGACTCTATTGTCTGAC 60
|||||

OY 203 CTTCACACACACCCCTCTTGTTCACCATACAGCCAGAGGGGGCACTATCATAGTGACCCA 262
|||||
DB 61 CTTCACACACACCCCTCTTGTTCACCATACAGCCAGAGGGGGCACTATCATAGTGACCCA 120
|||||

OY 263 AAATCGTAATAGGAGAGAGTAGACTTCCACAGATGAGGCTACTCCCTGAAGCTCAGCAA 322
|||||
DB 121 AAATCGTAATAGGAGAGAGTAGACTTCCACAGATGAGGCTACTCCCTGAAGCTCAGCAA 180
|||||

OY 323 ACTGAAGAAGATGACTCAGGATCTACTATGTGGGATATACAGCTCATCACTCCAGCA 382
|||||
DB 181 ACTGAAGAAGATGACTCAGGATCTACTATGTGGGATATACAGCTCATCACTCCAGCA 240
|||||

OY 383 GCCCTCCACCCAGAGTAGCTGCTGCTGCTACG 417
|||||
DB 241 GCCCTCCACCCAGAGTAGCTGCTGCTGCTACG 275
|||||

RESULT 47
LOCUS CQ274801 275 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 23062 from Patent WO0157277.
ACCESSION CQ274801
VERSION CQ274801.1 GI:41247405
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS 1 Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human fetal liver
JOURNAL Patent: WO 0157277-A 23062 09-AUG-2001;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
1..275
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL121985.13-EXPRESSED IN FETAL LIVER, SIGNAL
= 7.5-NT HIT: AJ271869.1, EVALUE 0.00e+00-EST_HUMAN HIT:
AW963563.1, EVALUE 0.00e+00"

ORIGIN
Query Match 10.2%; Score 275; DB 6; Length 275;
Best Local Similarity 100.0%; Pred. No. 1.5e-151;
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 143 TGGGGCCGTGACTTTCCCTGAGTCCAAAGTAAGCAAGTTGACTCTATTGTCTGAC 202
|||||
DB 1 TGGGGCCGTGACTTTCCCTGAGTCCAAAGTAAGCAAGTTGACTCTATTGTCTGAC 60
|||||

OY 203 CTTCACACACACCCCTCTTGTTCACCATACAGCCAGAGGGGGCACTATCATAGTGACCCA 262
|||||

Db 61 CTTCAACACACACCCCTCTGTGCACCATATACAGACCAGAGGGGGCAGTATCATAGTGACCCA 120

QY 263 AAATCGTAATAGGGAGAGAGTAGACTTCCCGATGGAGGCTACTCCCTGAAGCTCAGCAA 322

Db 121 AAATCGTAATAGGGAGAGAGTAGACTTCCCGATGGAGGCTACTCCCTGAAGCTCAGCAA 180

QY 323 ACTGAAGAAGATGACTCAGGGATCTACTATGTGGGATATACAGTCTCATCTCCAGCA 382

Db 181 ACTGAAGAAGATGACTCAGGGATCTACTATGTGGGATATACAGTCTCATCTCCAGCA 240

QY 383 GCCCTCCACCCAGAGTAGCGTGTGCTGATGTCTACG 417

Db 241 GCCCTCCACCCAGAGTAGCGTGTGCTGATGTCTACG 275

RESULT 48

LOCUS CQ311787 275 bp DNA linear PAT 23-JAN-2004

DEFINITION Sequence 22892 from Patent WO0186003.

ACCESSION CQ311787

VERSION CQ311787.1 GI:41272364

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R. Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human lung Patent: WO 0186003-A 22892 15-NOV-2001; Aeomica, Inc. (US)

JOURNAL Location/Qualifiers

FEATURES

source 1..275

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

/note="MAP TO AL121985.13-EXPRESSED IN LUNG, SIGNAL = 5.9-NT HIT: AJ271869.1, EVALUE 0.00e+00~EST_HUMAN HIT: AW963563.1, EVALUE 0.00e+00"

ORIGIN

Query Match 10.2%; Score 275; DB 6; Length 275;

Best Local Similarity 100.0%; Pred. No. 1.5e-151;

Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 143 TGGGGCCGTGACTTTCCCGCTGAAGTCCAAGTAAAGCAAGTTGACTTATGTCTGAC 202

Db 1 TGGGGCCGTGACTTTCCCGCTGAAGTCCAAGTAAAGCAAGTTGACTTATGTCTGAC 60

QY 203 CTTCAACACACACCCCTCTGTGCACCATATACAGCCAGAGGGGGCAGTATCATAGTGACCCA 262

Db 61 CTTCAACACACACCCCTCTGTGCACCATATACAGCCAGAGGGGGCAGTATCATAGTGACCCA 120

QY 263 AAATCGTAATAGGGAGAGAGTAGACTTCCCGATGGAGGCTACTCCCTGAAGCTCAGCAA 322

Db 121 AAATCGTAATAGGGAGAGAGTAGACTTCCCGATGGAGGCTACTCCCTGAAGCTCAGCAA 180

QY 323 ACTGAAGAAGATGACTCAGGGATCTACTATGTGGGATATACAGTCTCATCTCCAGCA 382

Db 181 ACTGAAGAAGATGACTCAGGGATCTACTATGTGGGATATACAGTCTCATCTCCAGCA 240

QY 383 GCCCTCCACCCAGAGTAGCGTGTGCTGATGTCTACG 417

Db 241 GCCCTCCACCCAGAGTAGCGTGTGCTGATGTCTACG 275

RESULT 49

LOCUS CQ349144 275 bp DNA linear PAT 23-JAN-2004

DEFINITION Sequence 23238 from Patent WO0157275.

ACCESSION CQ349144

VERSION CQ349144.1 GI:41298215

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human brain Patent: WO 0157275-A 23238 09-AUG-2001; Aeomica, Inc. (US)

JOURNAL Location/Qualifiers

FEATURES

source 1..275

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

/note="MAP TO AL121985.13-EXPRESSED IN BRAIN, SIGNAL = 7-NT HIT: AJ271869.1, EVALUE 0.00e+00~EST_HUMAN HIT: AW963563.1, EVALUE 0.00e+00"

ORIGIN

Query Match 10.2%; Score 275; DB 6; Length 275;

Best Local Similarity 100.0%; Pred. No. 1.5e-151;

Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 143 TGGGGCCGTGACTTTCCCGCTGAAGTCCAAGTAAAGCAAGTTGACTTATGTCTGAC 202

Db 1 TGGGGCCGTGACTTTCCCGCTGAAGTCCAAGTAAAGCAAGTTGACTTATGTCTGAC 60

QY 203 CTTCAACACACACCCCTCTGTGCACCATATACAGCCAGAGGGGGCAGTATCATAGTGACCCA 262

Db 61 CTTCAACACACACCCCTCTGTGCACCATATACAGCCAGAGGGGGCAGTATCATAGTGACCCA 120

QY 263 AAATCGTAATAGGGAGAGAGTAGACTTCCCGATGGAGGCTACTCCCTGAAGCTCAGCAA 322

Db 121 AAATCGTAATAGGGAGAGAGTAGACTTCCCGATGGAGGCTACTCCCTGAAGCTCAGCAA 180

QY 323 ACTGAAGAAGATGACTCAGGGATCTACTATGTGGGATATACAGTCTCATCTCCAGCA 382

Db 181 ACTGAAGAAGATGACTCAGGGATCTACTATGTGGGATATACAGTCTCATCTCCAGCA 240

QY 383 GCCCTCCACCCAGAGTAGCGTGTGCTGATGTCTACG 417

Db 241 GCCCTCCACCCAGAGTAGCGTGTGCTGATGTCTACG 275

RESULT 50

LOCUS AX905449 435 bp DNA linear PAT 18-DEC-2003

DEFINITION Sequence 21312 from Patent EP1033401.

ACCESSION AX905449

VERSION AX905449.1 GI:40060406

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Dumas Milne Edwards, J.B., Duclert, A. and Giordano, J.Y. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. Expressed sequence tags and encoded human proteins Patent: EP 1033401-A 21312 06-SEP-2000; Genset (FR)

JOURNAL Location/Qualifiers

FEATURES

source 1..435

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 6.7%; Score 182; DB 6; Length 435;

Best Local Similarity 100.0%; Pred. No. 5e-96;

Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1857	CTAGGTTTTAAGGCTGTG	CCAGAACCCATCCCAATAAAGAGACCGAGTCTGAAGTCACAT	1916
Db	1	CTAGGTTTTAAGGCTGTG <th>CCAGAACCCATCCCAATAAAGAGACCGAGTCTGAAGTCACAT</th> <td>60</td>	CCAGAACCCATCCCAATAAAGAGACCGAGTCTGAAGTCACAT	60
QY	1917	TGTAATCTAGTGTAGAGACTTGAGT <th>CAGGCAGTGAGACTGTGGGGCAGCGGGGGCA</th> <td>1976</td>	CAGGCAGTGAGACTGTGGGGCAGCGGGGGCA	1976
Db	61	TGTAATCTAGTGTAGAGACTTGAGT <th>CAGGCAGTGAGACTGTGGGGCAGCGGGGGCA</th> <td>120</td>	CAGGCAGTGAGACTGTGGGGCAGCGGGGGCA	120
QY	1977	GTGGGTACTTGTAAACCTTTAAAGATGTTAATTCATTCAATAGATATTATTAAAGACC		2036
Db	121	GTGGGTACTTGTAAACCTTTAAAGATGTTAATTCATTCAATAGATATTATTAAAGACC		180
QY	2037	TA	2038	
Db	181	TA	182	
RESULT	51			
LOCUS	BD040982		435 bp	DNA linear PAT 27-AUG-2002
DEFINITION				
ACCESSION	BD040982			
VERSION	BD040982.1	GI:22582724		
KEYWORDS	JP 2001269182-A/17228.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				

COMMENT	OS Homo sapiens (human)
	PN JP 2001269182-A/17228
	PD 02-OCT-2001
	PF 24-FEB-2000 JP 2000118773
	PR 26-FEB-1999 US 60/122487
	PI JEAN BAPTISTE DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
	PI JORDAN
	PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
	C12N5/10,
	PC C12P21/02, C12P21/08, C12Q1/68//G06F17/30, C12N15/00, C12N5/00, PC
	G06F15/40
FEATURES	CC
source	Key Location/Qualifiers.
	1. .435
	/organism="Homo sapiens"
	/mol_type="genomic DNA"
	/db_xref="taxon:9606"
ORIGIN	
Query Match	6.7%; Score 182; DB 6; Length 435;
Best Local Similarity	100.0%; Pred. No. 5e-96;
Matches 182; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY 1857 CTAGGTTTAAAGCGCTGTGCCAGAACCCATCCCAATAAAGAGACCAGAGTCTGAAGTCACAT	1916
DB 1 CTAGGTTTAAAGCGCTGTGCCAGAACCCATCCCAATAAAGAGACCAGAGTCTGAAGTCACAT	60
QY 1917 TGTAAATCTAGGTAGAGACTTGAGTCAGGCAGTCAGACTGTGGGGCACGGGGGCA	1976
DB 61 TGTAAATCTAGGTAGAGACTTGAGTCAGGCAGTCAGACTGTGGGGCACGGGGGCA	120
QY 1977 GTGGGACTTGTAAACCTTAAAGATGTTAATTCATTCATAGATATTATTAAAGACC	2036
DB 121 GTGGGACTTGTAAACCTTAAAGATGTTAATTCATTCATAGATATTATTAAAGACC	180
QY 2037 TA 2038	
DB 181 TA 182	

RESULT	52			
LOCUS	CQ432314			
DEFINITION	Sequence 17348 from Patent WO0151628.	392 bp	DNA	linear
ACCESSION	CQ432314			
VERSION	CQ432314.1	GI:41384543		
KEYWORDS				
SOURCE				
ORGANISM	Homo sapiens (human)			
	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
REFERENCE	1			
AUTHORS	Illie,J., Xu,Y., Wang,Y. and Steinmann,K.			
TITLE	Novel genes, compositions, kits, and methods for identification, assessment, prevention, and therapy of breast cancer			
JOURNAL	Patent: WO 0151628-A 17348 19-JUL-2001; Millennium Pharmaceuticals, Inc. (US)			
FEATURES				
source	Location/Qualifiers			
	1..392			
	/organism="Homo sapiens"			
	/mol_type="unassigned DNA"			
	/db_xref="taxon:9606"			
ORIGIN				

Query Match	Best Local Similarity	Score	DB	Length
Matches 221; Conservative	99.5%;	171;	6;	392;
		Pred. No. 1.8e-89;		
		Mismatches 0;	Indels 1;	Gaps 0;

Query	1656	TGTAGCAGG	CTTGACCA	CAGATTCC	CCAGAGG	CCAGGTGT	GGATCC	CACAGACT	TGTAAG	1715
Db	36	TGTAGCAGG <td>CTTGACCA <th>CAGATTCC</th> <th>CCAGAGG</th> <th>CCAGGTGT</th> <th>GGATCC</th> <th>CACAGACT</th> <th>TGTAAG</th> <td>95</td> </td>	CTTGACCA <th>CAGATTCC</th> <th>CCAGAGG</th> <th>CCAGGTGT</th> <th>GGATCC</th> <th>CACAGACT</th> <th>TGTAAG</th> <td>95</td>	CAGATTCC	CCAGAGG	CCAGGTGT	GGATCC	CACAGACT	TGTAAG	95
QY	1716	TCAAAGTT	CAAAAGAT	TGAAGAT	CAGGGTAG	CTGACCAT	GTTTGG	CAGATACT	ATAATG	1775
Db	96	TCAAAGTT	CAAAAGAT	TGAAGAT	CAGGGTAG	CTGACCAT	GTTTGG	CAGATACT	ATAATG	155
QY	1776	GAGACAC	AGAAGTGT	GCATGG	CCCCAAG	ACAAGAC	CTCCAG	CCAGCTTC	ATTATG	CA
Db	156	GAGACAC	AGAAGTGT	GCATGG	CCCCAAG	ACAAGAC	CTCCAG	CCAGCTTC	ATTATG	CA
QY	1836	CTTGTGCT	GCAAAAG	AAAGTCT	AGGTTT	TAAGGCT	GTGCCA			1877
Db	216	CTTGTGCT	GCAAAAG	AAAGTCT	AGGTTT	TAAGGCT	GTGCCA			257

RESULT 53.	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	ORIGIN
CQ423465	CQ423465	Sequence 8499 from Patent WO0151628.	CQ423465	CQ423465.1	GI:41375694		Homo sapiens (human)	1	Lillie, J., Xu, Y., Wang, Y. and Steinmann, K.	Novel genes, compositions, kits, and methods for identification, assessment, prevention, and therapy of breast cancer	Patent: WO 0151628-A 8499 19-JUL-2001; Millennium Pharmaceuticals, Inc. (US)	Location/Qualifiers 1..329 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"	Query Match Best Local Similarity
		329 bp	DNA	linear	PAT 28-JAN-2004								4.8%; Score 129; DB 6; Length 329; 100.0%; Pred. No. 2.2e-64;

Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Oy	1656 TGTAGCAGGCTGACCCACAGATTCCAGAGGGCCAGGTGTGATCCACAGACTTGAAGG 1715
Db	90 TGTAGCAGGCTGACCCACAGATTCCAGAGGGCCAGGTGTGATCCACAGACTTGAAGG 149
Oy	1716 TCAAGTTCAAAAGATGAAGAATCAGGCTAGCTGACCATTGTTGGCAGATACTATAATG 1775
Db	150 TCAAGTTCAAAAGATGAAGAATCAGGCTAGCTGACCATTGTTGGCAGATACTATAATG 209
Oy	1776 GAGACACAG 1784
Db	210 GAGACACAG 218

RESULT 54
AC013435/c
LOCUS AC013435 116283 bp DNA linear PRI 21-FEB-2002
DEFINITION Homo sapiens BAC clone RP11-52C8 from 2, complete sequence.
ACCESSION AC013435
VERSION AC013435.7 GI:18140107
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Sulston, J.E. and Waterston, R.
TITLE 1 (bases 1 to 116283)
JOURNAL Toward a complete human genome sequence
MEDLINE Genome Res. 8 (11), 1097-1108 (1998)
9847074

REFERENCE
AUTHORS Tomlinson, C., Kozlowski, A. and Spalding, L.
TITLE 2 (bases 1 to 116283)
JOURNAL The sequence of Homo sapiens BAC clone RP11-52C8
REFERENCE Unpublished (2001)
AUTHORS 3 (bases 1 to 116283)
TITLE Waterston, R.H.
JOURNAL Direct Submission
Submitted (11-NOV-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA

REFERENCE
AUTHORS 4 (bases 1 to 116283)
TITLE Waterston, R.H.
JOURNAL Direct Submission
Submitted (13-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA

REFERENCE
AUTHORS 5 (bases 1 to 116283)
TITLE Waterston, R.
JOURNAL Direct Submission
Submitted (21-FEB-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Jan 13, 2002 this sequence version replaced gi:17647042.

----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu/gsc>
Contact: sapiens@watson.wustl.edu
----- Summary Statistics
Center project name: H_NH0052C08

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence

from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:
The RPc1-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanesse, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>
VECTOR: pBACE3.6

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-690I21, 2000 bp overlap.
Actual end of this clone is at base position 116283 of RP11-52C8.

FEATURES	
Source	
location/Qualifiers	
1..116283	/organism="Homo sapiens"
	/mol_type="genomic DNA"
	/db_xref="taxon:9606"
	/chromosome="2"
	/map="2"
	/clone="RP11-52C8"
	/clone_1ib="RPc1-11"
3..301	/rpt_family="Alu"
446..478	/rpt_family="Alu"
	/rpt_family="Alu"
862..1291	/rpt_family="Alu"
1286..1321	/rpt_family="Alu"
	/rpt_family="Alu"
1301..1604	/rpt_family="Alu"
1613..1904	/rpt_family="Alu"
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2072..2115	/rpt_family="Alu"
2122..2209	/rpt_family="Alu"
	/rpt_family="Alu"
3549..3654	/rpt_family="Alu"
3656..3921	/rpt_family="Alu"
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4042..4204	/rpt_family="Alu"
4212..4246	/rpt_family="Alu"
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4320..4592	/rpt_family="Alu"
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4567..4592	/rpt_family="Alu"
4593..4883	/rpt_family="Alu"
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4884..5139	/rpt_family="Alu"
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5140..5319	/rpt_family="Alu"
5309..5347	/rpt_family="Alu"
	/rpt_family="Alu"
5320..5496	/rpt_family="Alu"
	/rpt_family="Alu"
5497..5789	/rpt_family="Alu"
	/rpt_family="Alu"
5790..5934	/rpt_family="Alu"
	/rpt_family="Alu"

repeat_region 5935. .6069 /rpt_family="Alu"
repeat_region 6071. .6267 /rpt_family="MER2_type"
repeat_region 6269. .6616 /rpt_family="MALR"
repeat_region 6638. .6689 /rpt_family="MIR"
repeat_region 7142. .7431 /rpt_family="Alu"
repeat_region 7450. .7748 /rpt_family="Alu"
repeat_region 8170. .8263 /rpt_family="MALR"
repeat_region 8438. .8682 /rpt_family="MALR"
repeat_region 8689. .9295 /rpt_family="MALR"
repeat_region 9934. .9995 /rpt_family="AT_rich"
repeat_region 9996. .10287 /rpt_family="Alu"
repeat_region 10284. .10320 /rpt_family="AT_rich"
repeat_region 10414. .10539 /rpt_family="L1"
repeat_region 10554. .10811 /rpt_family="Alu"
repeat_region 10818. .11183 /rpt_family="L1"
repeat_region 11357. .11689 /rpt_family="L1"
repeat_region 11690. .11991 /rpt_family="Alu"
repeat_region 11992. .12185 /rpt_family="L1"
repeat_region 12240. .12532 /rpt_family="Alu"
repeat_region 12541. .12594 /rpt_family="ERV1"
repeat_region 12638. .12976 /rpt_family="L1"
repeat_region 13195. .13390 /rpt_family="L1"
repeat_region 13391. .13620 /rpt_family="Alu"
repeat_region 13593. .13620 /rpt_family="AT_rich"
repeat_region 13621. .14281 /rpt_family="L1"
repeat_region 14282. .14577 /rpt_family="Alu"
repeat_region 14578. .14882 /rpt_family="L1"
repeat_region 15349. .15492 /rpt_family="Alu"
repeat_region 15492. .15536 /rpt_family="T-rich"
repeat_region 15781. .16078 /rpt_family="Alu"
repeat_region 16059. .16078 /rpt_family="CAA)n"
repeat_region 16478. .16797 /rpt_family="Alu"
repeat_region 16598. .16620 /rpt_family="AT_rich"
repeat_region 16768. .16800 /rpt_family="(GAAA)n"
repeat_region 17267. .17479 /rpt_family="CT-rich"
repeat_region 17497. .17590

Query Match 2.8%; Score 76; DB 9; Length 116283;

Best Local Similarity 100.0%; Pred. No. 1.1e-32;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2066 CCTGTAATCCAGCACTTTGGAGAGCCAGCTGGGTGATCATCTGAGTCAGAGTCA 2125
Db 68814 CCTGTAATCCAGCACTTTGGAGAGCCAGCTGGGTGATCATCTGAGTCAGAGTCA 68755
Qy 2126 AGACCAGCTGCCAA 2141
Db 68754 AGACCAGCTGCCAA 68739

RESULT 55
AC068218 117432 bp DNA linear HTG 23-SEP-2000
LOCUS Homo sapiens chromosome 2 clone RP11-105A13 map 2, *** SEQUENCING
DEFINITION IN PROGRESS ***, 32 unordered pieces.
AC068218 AC068218.2 GI:10280755
VERSION HTG; HTGS_PHASE1.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 117432)
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
TITLE Homo sapiens chromosome 2, clone RP11-105A13
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 117432)
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,
Boguslavskiy, L., Boukhgalter, B., Brown, A., Burkett, G.,
Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S.,
Collamore, A., Cooke, P., Deareliano, K., Dewar, K., Diaz, J.S.,
Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D.,
Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczy, J.,
Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,
McCarthy, M., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J.,
Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J.,
Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
O'Neil, D., Oliver, T.M., Oliver, J., Peterson, K., Pierre, N.,
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
Strange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Testfaye, S., Theodore, J., Turrell, A., Travers, M., Trigilio, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
Young, G., Zainoun, J., Zimmer, A. and Zody, M.

TITLE
JOURNAL
COMMENT
Submitted (30-APR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Sep 23, 2000 this sequence version replaced gi:7671278.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: W1BR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Project information
Center project name: L10125
Center clone name: 105_A_13

***** NOTE: This is a 'working draft' sequence. It currently
* consists of 32 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will

* be preserved.
* 1 637: contig of 637 bp in length
* 638 737: gap of 100 bp
* 738 1740: contig of 1003 bp in length
* 1741 1840: gap of 100 bp
* 1841 3127: contig of 1287 bp in length
* 3128 3227: gap of 100 bp
* 3228 4542: contig of 1315 bp in length
* 4543 4642: gap of 100 bp
* 4643 6297: contig of 1655 bp in length
* 6298 6397: gap of 100 bp
* 6398 8080: contig of 1683 bp in length
* 8081 8180: gap of 100 bp
* 8181 10438: contig of 2258 bp in length
* 10439 10538: gap of 100 bp
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* 12440 12539: gap of 100 bp
* 12540 15004: contig of 2465 bp in length
* 15005 15104: gap of 100 bp
* 15105 17541: contig of 2437 bp in length
* 17542 17641: gap of 100 bp
* 17642 19304: contig of 1663 bp in length
* 19305 19404: gap of 100 bp
* 19405 21237: contig of 1833 bp in length
* 21238 21337: gap of 100 bp
* 21338 22932: contig of 1595 bp in length
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* 30703 34245: contig of 3543 bp in length
* 34246 34345: gap of 100 bp
* 34346 36988: contig of 2643 bp in length
* 36989 37088: gap of 100 bp
* 37089 40052: contig of 2964 bp in length
* 40053 40152: gap of 100 bp
* 40153 43222: contig of 3070 bp in length
* 43223 43322: gap of 100 bp
* 43323 47008: contig of 3686 bp in length
* 47009 47108: gap of 100 bp
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* 50281 50380: gap of 100 bp
* 50381 55078: contig of 4698 bp in length
* 55079 55178: gap of 100 bp
* 55179 60366: contig of 5188 bp in length
* 60367 60466: gap of 100 bp
* 60467 63933: contig of 3467 bp in length
* 63934 64033: gap of 100 bp
* 64034 68186: contig of 4153 bp in length
* 68187 68286: gap of 100 bp
* 68287 73579: contig of 5293 bp in length
* 73580 73679: gap of 100 bp
* 73680 80613: contig of 6934 bp in length
* 80614 80713: gap of 100 bp
* 80714 99197: contig of 18484 bp in length
* 99198 99297: gap of 100 bp
* 99298 108271: contig of 8974 bp in length
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Best Local Similarity 100.0%; Pred. No. 1.1e-32;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2066 CCTGTAATCCAGCACTTGGAGGCCAAGTGGTGGTCATCTGAGTCAGAGTTCA 2125
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Db 8768 CCTGTAATCCAGCACTTGGAGGCCAAGTGGTGGTCATCTGAGTCAGAGTTCA 8827
OY 2126 AGACCAGCTGGCCAA 2141
|||||
Db 8828 AGACCAGCTGGCCAA 8843

RESULT 56
AC023445/c
LOCUS
DEFINITION Homo sapiens chromosome 5 clone RP11-715K1 map 5, LOW-PASS SEQUENCE
SAMPLING.
AC023445 156886 bp DNA linear HTG 11-APR-2000
AC023445.2 GI:7533994
VERSION AC023445.2 GI:7533994
KEYWORDS HTG; HTGS PHASE0.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 156886)
AUTHORS Birren,B., Linton,L., Nuebaum,C. and Lander,E.
TITLE Homo sapiens chromosome 5, clone RP11-715K1
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 156886)
Birren,B., Linton,L., Nuebaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Beda,F., Boguslavsky,L.,
Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A.,
Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
Dearellano,K., Dewar,K., Dodge,S., Domino,M., Doyle,M.,
Fenster,J., Ferreira,P., FitzHugh,W., Forrest,C., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., Landers,T., Largocque,K., Lehoczy,J., Levine,R.,
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Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J., Naylor,J.,
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Olivar,T.M.,
Peterson,K., Pierre,N., Pisanic,C., Pollara,V., Raymond,C.,
Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S.,
Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A.,
Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B.,
Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and
Zody,M.

TITLE Direct Submission
JOURNAL Submitted (14-FEB-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT On Apr 11, 2000 this sequence version replaced gi:6970665.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L6374
Center clone name: 715_K_1

* NOTE: This record contains 173 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will

* be preserved.
* 1 777: contig of 777 bp in length
* 778 877: gap of 100 bp
* 878 1659: contig of 782 bp in length
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* 2683 3485: contig of 803 bp in length
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* 3586 4344: contig of 759 bp in length
* 4345 4444: gap of 100 bp
* 4445 5237: contig of 793 bp in length
* 5238 5337: gap of 100 bp
* 5338 6133: contig of 796 bp in length
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* 6234 7042: contig of 809 bp in length
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*	50014	50113: gap of 100 bp
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*	51027	51833: contig of 807 bp in length
*	51834	51933: gap of 100 bp
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*	55532	56309: contig of 778 bp in length
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*	58082	58181: gap of 100 bp
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*	58878	58977: gap of 100 bp
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*	59785	59884: gap of 100 bp
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*	60788	61588: contig of 801 bp in length

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Best Local Similarity 100.0%; Pred. No. 6.5e-28;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2103 GGTGATCTGAGGTCAGAGTTCAAGACCAGCTGGCCACATGTTGAACCCCATCTCTA 2162
Db 15945 GGTGATCTGAGGTCAGAGTTCAAGACCAGCTGGCCACATGTTGAACCCCATCTCTA 15886

Qy 2163 CTAAGAT 2170
Db 15885 CTAAGAT 15878

RESULT 57
AC010598 174551 bp DNA linear PRI 22-MAR-2003
LOCUS Homo sapiens chromosome 5 clone CTC-56009, complete sequence.
DEFINITION AC010598
AC010598
AC010598.6 GI:9558579
VERSION HTG.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Unpublished
2 (bases 1 to 174551)

REFERENCE
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (16-SEP-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 174551)

REFERENCE
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Submitted (28-JUL-2000) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 174551)

REFERENCE
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Submitted (22-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jul 28, 2000 this sequence version replaced gi:7711473.

COMMENT
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu

Quality: Phrap Quality >=40 99.4% of Sequence;
Estimated Total Number of Errors is 2.1.
STS Content:
WI-9707 G22840.

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ORIGIN

Query Match 2.5%; Score 68; DB 9; Length 174551;
Best Local Similarity 100.0%; Pred. No. 6.5e-28;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2103 GGTGATCTGAGGTCAGAGTTCAAGACCAGCTGGCCACATGTTGAACCCCATCTCTA 2162
Db 134800 GGTGATCTGAGGTCAGAGTTCAAGACCAGCTGGCCACATGTTGAACCCCATCTCTA 134859

Qy 2163 CTAAGAT 2170
Db 134860 CTAAGAT 134867

RESULT 58
LOCUS CQ695774 330 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 40700 from Patent WO02070737.
ACCESSION CQ695774
VERSION CQ695774.1 GI:42243043

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Liew,C.C., Marshall,W.E. and Zhang,H.
TITLE Compositions and methods relating to osteoarthritis
JOURNAL Patent: WO 02070737-A 40700 12-SEP-2002;
Chondrogene Inc. (CA)
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source location/Qualifiers
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QY 2165 AAA 2167
Db 173 AAA 175
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CQ414086 CQ414086 976 bp DNA linear PAT 23-JAN-2004
LOCUS Sequence 21157 from Patent WO0170979.
DEFINITION CQ414086
ACCESSION CQ414086
VERSION CQ414086.1 GI:41321867
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Lee,J. and Lillie,J.
TITLE Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 21157 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
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Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2105 TCATCTGAGGTCAAGAGTTCAGACCGCTGGCCACATGTTGAACCCCATCTTACT 2164
Db 767 TCATCTGAGGTCAAGAGTTCAGACCGCTGGCCACATGTTGAACCCCATCTTACT 826
QY 2165 AAA 2167
Db 827 AAA 829
RESULT 60
HSA131341 HSA131341 9507 bp DNA linear PRI 01-FEB-1999
LOCUS Homo sapiens ogg1 gene, exons 1-7.
DEFINITION AJ131341
ACCESSION AJ131341
VERSION AJ131341.1 GI:4210713

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Dhenaut,A., Boiteux,S. and Radicella,J.
TITLE Genomic structure and promoter characterization of the human 8-OH-guanine glycosylase gene (OGG1) gene
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 9507)
AUTHORS Radicella,J.
TITLE Direct Submission
JOURNAL Submitted (05-DEC-1998) Radicella J., Departement de Radiobiologie et Radiopathologie, Commissariat a l' Energie Atomique, 60 Avenue du general Leclerc, Fontenay aux Roses, F 92265, FRANCE
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/protein_id="CAA10351.1"
/db_xref="GI:4210714"
/db_xref="GOA:O15527"
/db_xref="Swiss-Prot:O15527"
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intron
exon
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intron

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exon											
ORIGIN											
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QY	2165	AAA	2167								
Db	4872	AAA	4874								
RESULT 61											
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DEFINITION	AF521807	Homo sapiens 8-oxoguanine DNA glycosylase (OGG1) gene, complete cds.									
ACCESSION	AF521807										
VERSION	AF521807.1	GI:21668117									
KEYWORDS											
SOURCE		Homo sapiens (human)									
ORGANISM		Homo sapiens									
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
AUTHORS		1 (bases 1 to 10461) Rieder,M.J., Livingston,R.J., Braun,A.C., Montoya,M.A., Chung,M.-W., Miyamoto,K.E., Nguyen,C.P., Nguyen,D.A., Poel,C.L., Robertson,P.D., Schackwitz,W.S., Sherwood,J.K., Witrak,L.A. and Nickerson,D.A.									
TITLE		Direct Submission									
JOURNAL		Submitted (14-JUN-2002) Genome Sciences, University of Washington, 1705 NE Pacific, Seattle, WA 98195, USA									
COMMENT		To cite this work please use: NIEHS-SNPs, Environmental Genome Project, NIEHS ES15478, Department of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).									
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		/frequency="0.01"									
variation		870									
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variation		888									
		/frequency="0.03"									
variation		923..1214									
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repeat_region	2736. .2921 /rpt_family="Alu" /rpt_type=dispersed 2812 /gene="OGG1" /frequency="0.91" /replace="n" 2828 /gene="OGG1" /frequency="0.01" /replace="t" 3320. .3478 /rpt_family="MIR" /rpt_type=dispersed 3413 /gene="OGG1" /frequency="0.01" /replace="g" 3551. .3651 /rpt_family="L2" /rpt_type=dispersed 4288. .4519 /rpt_family="MIR" /rpt_type=dispersed 4591. .4647 /rpt_family="Alu" /rpt_type=dispersed 4611 /gene="OGG1" /frequency="0.01" /replace="t"
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Best Local Similarity 100.0%; Pred. No. 6e-25;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 2165 AAA 2167
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Db 4984 AAA 4986
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DEFINITION Homo sapiens chromosome 16, cosmid clone 306E5 (LANL), complete
sequence.
AC004224
VERSION AC004224.1 GI:2911722
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 41495)
Ricke,D.O. and Wagner,R.P.
TITLE Large Scale Sequence Analysis and Annotation with the Sequence
Comparison Analysis (SCAN) System
JOURNAL
REFERENCE 2 (bases 1 to 41495)
AUTHORS Ricke,D.O., Bruce,D., Mundt,M., Doggett,N., Munk,C., Saunders,E.,
Robinson,D., Jones,M., Buckingham,J., Chasteen,L., Thompson,S.,
Goodwin,L., Bryant,J., Tesmer,J., Meincke,L., Longmire,J.,
White,S., Ueng,S., Tatum,O., Campbell,C., Fawcett,J., Maltbie,M.,
Misra,M. and Deaven,L.
TITLE Sequencing of Human Chromosome 16p13.3
JOURNAL
REFERENCE 3 (bases 1 to 41495)
AUTHORS Ricke,D.O., Bruce,D., Mundt,M., Doggett,N., Munk,C., Saunders,E.,
Robinson,D., Jones,M., Buckingham,J., Chasteen,L., Thompson,S.,
Goodwin,L., Bryant,J., Tesmer,J., Meincke,L., Longmire,J.,
White,S., Ueng,S., Tatum,O., Campbell,C., Fawcett,J., Maltbie,M.,
Misra,M. and Deaven,L.
TITLE Direct Submision
JOURNAL Submitted (26-FEB-1998) Center for Human Genome Studies, DOE Joint
Genome Institute, Los Alamos National Laboratory, MS M888, Los
Alamos, NM 87545, USA
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repeat_region 3062..3558
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Best Local Similarity 100.0%; Pred. No. 6.1e-25;
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Db      40311 TCATCTGAGTCAGAGTCAAGACCCTGGCCACATGTGAACCCCATCTCTACT 40252

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Db      40251 AAA 40249

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ACCESSION      AL138915
VERSION      AL138915
KEYWORDS      HTG.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
              1 (bases 1 to 42569)
REFERENCE      Almeida,J.
AUTHORS      Direct Submission
TITLE      Submitted (31-OCT-2000) Sanger Centre, Hinxton, Cambridgeshire,
JOURNAL      CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
              requests: clonerequest@sanger.ac.uk
              On Nov 8, 2000 this sequence version replaced gi:10800462.
COMMENT      During sequence assembly data is compared from overlapping clones.
              Where differences are found these are annotated as variations
              together with a note of the overlapping clone name. Note that the
              variation annotation may not be found in the sequence submission
              corresponding to the overlapping clone, as we submit sequences with
              only a small overlap as described above.
              This sequence has been finished according to sequence map criteria
              as follows. An attempt is made to resolve all sequencing problems,
              such as compressions and repeats, but not necessarily within known
              annotated human repeat sequence elements (e.g. Alu). Where the
              sequence is ambiguous, there is an annotation using the 'unsure'
              feature key.
              The following abbreviations are used to associate primary accession
              numbers given in the feature table with their source databases:
              Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
              on the WORMPEP database can be found at
              http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
              was generated from part of bacterial clone contigs of human
              chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
              Group. Further information can be found at
              http://www.sanger.ac.uk/HGP/Chr6
              RP11-288K24 is from the library RPCI-11.1 constructed at the
              Roswell Park Cancer Institute by the group of Pieter de Jong. For
              further details see http://bacpac.med.buffalo.edu/
              VECTOR: pBACe3.6
              IMPORTANT: This sequence is not the entire insert of clone
              RP11-288K24. It may be shorter because we sequence overlapping
              sections only once, except for a 100 base overlap.
              The true right end of clone RP11-288K24 is at 42569 in this
              sequence. The true left end of clone RP11-440J4 is at 4198 in this
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5443. .5585
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5696. .5997
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9729. .10019
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11256. .11303
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14516. .14822
/note="AluSx repeat: matches 3. .311 of consensus"
14823. .15068
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16512. .16969
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misc_feature 26491. .27075 /note="match: GSS: Em:AQ351931"
repeat_region 26735. .26822 /note="L22 copies 4 mer atag 84% conserved"
repeat_region 26855. .27598 /note="L1ME1 repeat: matches 5376. .6159 of consensus"
repeat_region 27599. .27905 /note="AluSx repeat: matches 3. .308 of consensus"
repeat_region 27906. .27927 /note="L1ME1 repeat: matches 5356. .5376 of consensus"
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repeat_region 31609. .31644 /note="9 copies 4 mer agat 83% conserved"
repeat_region 31645. .31704 /note="15 copies 4 mer gata 70% conserved"
repeat_region 31774. .32115 /note="L1MEC repeat: matches 1514. .1853 of consensus"
repeat_region 32128. .32183 /note="14 copies 4 mer tata 73% conserved"
repeat_region 32130. .32183 /note="27 copies 2 mer ta 75% conserved"
repeat_region 32221. .32712 /note="L1ME repeat: matches 5012. .5465 of consensus"
repeat_region 32638. .33046 /note="L1ME3 repeat: matches 5789. .6155 of consensus"
repeat_region 33361. .33565 /note="MIR repeat: matches 61. .256 of consensus"
repeat_region 33568. .33627 /note="L2 repeat: matches 2691. .2749 of consensus"
repeat_region 33824. .33945 /note="L2 repeat: matches 2560. .2710 of consensus"
repeat_region 34491. .34588 /note="MER5A repeat: matches 9. .106 of consensus"
repeat_region 34928. .35088 /note="L2 repeat: matches 2572. .2744 of consensus"
misc_feature complement(35669. .36001)
repeat_region /note="match: GSS: Em:AQ217519"
repeat_region 37561. .37630 /note="L2 repeat: matches 2679. .2748 of consensus"
repeat_region 37976. .38226 /note="MIR repeat: matches 2. .243 of consensus"
repeat_region 38728. .39043

repeat_region /note="AluUb repeat: matches 5. .292 of consensus"
39906. .40158 /note="MLT1J repeat: matches 238. .512 of consensus"
Query Match 2.3%; Score 63; DB 9; Length 42569;
Best Local Similarity 100.0%; Pred. No. 6.1e-25;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2105 TCATCTGAGTCAAGATTCAAGACCCTGGCCACATGTGAAACCCCATCTTACT 2164
DB 28224 TCATCTGAGTCAAGAGTTCAAGACCCTGGCCACATGTGAAACCCCATCTTACT 28165
QY 2165 AAA 2167
DB 28164 AAA 28162
RESULT 64
AC073932/c 48217 bp DNA linear PRI 10-JAN-2002
LOCUS AC073932
DEFINITION Homo sapiens BAC clone RP11-242J7 from 4, complete sequence.
ACCESSION AC073932
VERSION AC073932.4 GI:18042387
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 48217)
AUTHORS Sulston,J.E. and Waterston,R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE 99063792
PUBMED 9847074
REFERENCE 2 (bases 1 to 48217)
AUTHORS Tranf,L., Cotton,M. and Creason,K.
TITLE The sequence of Homo sapiens BAC clone RP11-242J7
JOURNAL Unpublished (2002)
REFERENCE 3 (bases 1 to 48217)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (05-JUL-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 4 (bases 1 to 48217)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (03-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 5 (bases 1 to 48217)
AUTHORS Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (10-JAN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Jan 3, 2002 this sequence version replaced gi:17976485.
COMMENT ----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: saplens@watson.wustl.edu
----- Summary Statistics
Center project name: H_NH0242J07

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >=

30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanesse, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-326111, 2000 bp overlap; the clone sequenced to the right is RP11-36716, 2000 bp overlap.

Data from AC084049 was used to finish this clone AC073932. Polymorphisms exist between AC079257 and AC073932.

FEATURES

Source

Location/Qualifiers
1. .48217
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="4"
/map="4"
/clone="RP11-242J7"
/clone_lib="RPCI-11"
1. .129
/rpt_family="MaLR"
1701. .2054
/rpt_family="MaLR"
2055. .2344
/rpt_family="L1"
2376. .2590
/rpt_family="L1"
2733. .2769
/rpt_family="AT_rich"
2740. .3043
/rpt_family="Alu"
3079. .3464
/rpt_family="MaLR"
4731. .4994
/rpt_family="Alu"
5110. .5407
/rpt_family="Alu"
5111. .5130
/rpt_family="(TTTGTG)n"
5544. .5932
/rpt_family="MER1_type"
6062. .6083
/rpt_family="(T)n"
6540. .6869
/rpt_family="Alu"
6843. .6884
/rpt_family="(TAAA)n"
6926. .6949
/rpt_family="(T)n"
6947. .7258
/note="match to EST AW515568 (NID:g7153650) xu73c09.x1"
7018. .7051
/rpt_family="T-rich"
7891. .8258
/rpt_family="L1"
8279. .8325

repeat_region 8447. .9075 /rpt_family="MER1_type"
repeat_region 9636. .9782 /rpt_family="L1"
repeat_region 9783. .10076 /rpt_family="Alu"
repeat_region 10077. .10240 /rpt_family="Alu"
repeat_region 10533. .10588 /rpt_family="Alu"
repeat_region 10918. .11458 /rpt_family="MIR"
repeat_region 11612. .11703 /rpt_family="MaLR"
repeat_region 11743. .12665 /rpt_family="Alu"
repeat_region 12019. .12047 /rpt_family="ERV1"
repeat_region 12666. .12742 /rpt_family="GC_rich"
repeat_region 12743. .12953 /rpt_family="ERV1"
repeat_region 12966. .13082 /rpt_family="ERV1"
repeat_region 13267. .13469 /rpt_family="MaLR"
repeat_region 13921. .13988 /rpt_family="MIR"
repeat_region 13989. .14282 /rpt_family="MER2_type"
repeat_region 14283. .14653 /rpt_family="Alu"
repeat_region 14665. .14975 /rpt_family="MER2_type"
repeat_region 14976. .15273 /rpt_family="MaLR"
repeat_region 15274. .15343 /rpt_family="Alu"
repeat_region 15422. .15664 /rpt_family="MaLR"
repeat_region 15755. .16046 /rpt_family="L1"
repeat_region 16368. .16592 /rpt_family="Alu"
repeat_region 17444. .17745 /rpt_family="MIR"
repeat_region 17758. .18056 /rpt_family="Alu"
repeat_region 18906. .19512 /rpt_family="Alu"
repeat_region 19611. .20260 /rpt_family="ERV1"
repeat_region 23473. .23781 /rpt_family="ERV1"
repeat_region 24100. .24400 /rpt_family="Alu"
repeat_region 24484. .24997 /rpt_family="Alu"
repeat_region 27975. .28257 /rpt_family="ERVK"
repeat_region 28294. .28360 /rpt_family="Alu"
repeat_region 28438. .28484 /rpt_family="ERV1"
repeat_region 28458. .28732 /rpt_family="(TTTA)n"
repeat_region 28923. .29159 /rpt_family="Alu"
repeat_region 29184. .29548 /rpt_family="Alu"
repeat_region 29764. .29870 /rpt_family="ERV1"
repeat_region /rpt_family="ERV1"

Query Match	2.3%;	Score 63;	DB 9;	Length 48217;
Best Local Similarity	100.0%;	Pred. No. 6.2e-25;		
Matches 63;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	2105	TCATCTGAGTTCAGAGAGTTCACAGACCAGCTGGCCACACATGTTGAACCCCATCTCTACT	2164	
Db	15214	TCATCTGAGTTCAGAGAGTTCACAGACCAGCTGGCCACACATGTTGAACCCCATCTCTACT	15155	
QY	2165	AAA	2167	
Db	15154	AAA	15152	
RESULT 65				
AF176815				
LOCUS	AF176815	51803 bp	DNA	linear PRI 23-DEC-1999
DEFINITION	Homo sapiens putative 8-hydroxyguanine DNA glycosylase gene, complete cds.			
ACCESSION	AF176815			
VERSION	AF176815.1	GI:6630864		
KEYWORDS	.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Hu,S.N., Dong,W., Zeng,Y.X., Yu,J. and Yang,H.M.			
AUTHORS	Hu,S.N., Dong,W., Zeng,Y.X., Yu,J. and Yang,H.M.			
TITLE	1 (bases 1 to 51803)			
JOURNAL	Hu,S.N., Dong,W., Zeng,Y.X., Yu,J. and Yang,H.M.			
REFERENCE	Sequencing and Analyzing of BAC DNA on 3p26			
AUTHORS	2 (bases 1 to 51803)			
TITLE	Hu,S.N., Dong,W., Zeng,Y.X., Yu,J. and Yang,H.M.			
JOURNAL	Direct Submission			
FEATURES	Submitted (10-AUG-1999) Human Genomic Center, Institute of Genetics, Chinese Academy of Sciences, Datun Road, Beijing 100101, P.R.China			
source	Location/Qualifiers			
	1. .51803			
	/organism="Homo sapiens"			
	/mol_type="genomic DNA"			
	/db_xref="taxon:9606"			
	/chromosome="3"			
	/map="3p26"			
mRNA	join(<26286. .26884,31142. .32101,32922. .33084,33451. .33582,34167. .34295,35086. .35395,35720. .36043,36366. .36650,37150. .37297,37715. .37851,37954. .38072,38442. .38596,39308. .>39491)			
	/product="putative 8-hydroxyguanine DNA glycosylase"			
	join(26286. .26884,31142. .32101,32922. .33084,33451. .33582,34167. .34295,35086. .35395,35720. .36043,36366. .36650,37150. .37297,37715. .37851,37954. .38072,38442. .38596,39308. .39491)			
CDS	39308. .39491)			
	/codon_start=1			
	/evidence=not experimental			
	/product="putative 8-hydroxyguanine DNA glycosylase"			
	/protein_id="AAF19605.1"			
	/db_xref="GI:6630865"			
	/translation="MGVDFDVKTFCHNLRA TKPYPECPVETCRKVYKSYSGIEYHL YHVDHNP PPQOTPLRKHKKGRQSRPANKQSPSPSEVSQSPGREVMSYAQAQRNVEVDLHGRVHRISIFDNLDVSEDEAPAEAPENGSKNKTENTPAATPKSGKHKKKKRSDNHHHHNVASATTPKLPFVVYRELEQDTPDAPRPRTSYRYIEKSAEELDEVEYDMEEDYIWLDMNERKTEGVSPIQEIPFYLMDRLKESYFESHNGDPNALVDEAVC CINCDEGCNSNVILFCDMCNLAHVQECYGPYIPEGWLCRCLQSPSRAVDCALCP NKGAFAKOTDDGRMAHVCAALMIPVCFANTVFLBPIDSIEHIPARWKLTCYCKOR GSGACIQCHKANCYTAFAHTCAOQAGLYMKMEPVRETGANGTSFSVRKTAYCDIHPP GSARRLPALSHSEGEDEDEDEEGKGSWSEKVKAKAKSRIKMKARKILAEKRAA PVSVPICIPPHRLSKITNRLTIQRKSQFMQRLHSYWTLLKQSRNGVPLRLRLQTHQS QRNCDQVGRDSEDKNWALKEQKSWQLRHLDERARLVELIRKREKLKRETIYQOI AMEMQUTPFLILLRKTLLEQLQEDGTGNIFSEVPPLSEVPDYLDHIKKPMDFTMKONL EAYRYLNFDDFEEDFNLIIVSNCLKYNAKDTI FYRAAVRLREOGGAVLROARROAKMG IDPETGMHIIPHSLAGDEATHRTDAABEBRLVLLNQKHL PVEQKLILBRLEVNVA SKQSVGRSRAKMIKKEMTALRKRLAHQRETGRDGPERRGPPSSRGLT PHPACCDKG QTDSAAEBSSSQETSGLGPNMNSTPAHEVGRRRTSVLFSKKNPKTAGPPKRPGRPKN			

Query Match	2.3%;	Score 63;	DB 9;	Length 51803;
Best Local Similarity	100.0%;	Pred. No. 6.2e-25;		
Matches 63;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	2105	TCATCTGAGTTCAGAGTTCACAGACCAGCTGGCCACACATGTTGAACCCCATCTCTACT	2164	
Db	44971	TCATCTGAGTTCAGAGTTCACAGACCAGCTGGCCACACATGTTGAACCCCATCTCTACT	45030	
QY	2165	AAA	2167	
Db	45031	AAA	45033	
RESULT 66				
AC002506/c				
LOCUS	AC002506	54659 bp	DNA	linear HTG 13-JUN-2002
DEFINITION	Homo sapiens clone 440E5, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces.			
ACCESSION	AC002506			
VERSION	AC002506.2	GI:21408066		
KEYWORDS	HTG; HTGS PHASE1.			
SOURCE	Homo sapiens			
ORGANISM	Homo sapiens (human)			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
AUTHORS	1 (bases 1 to 54659)			
	Loftus,B.J., Kim,U.J., Sneddon,V.P., Kalush,F., Brandon,R., Fuhrmann,J., Mason,T., Crosby,M.L., Barnstead,M., Cronin,L., Deslattes Mays,A., Cao,Y., Xu,R.X., Kang,H.L., Mitchell,S., Eichler,E.E., Harris,P.C., Venter,J.C. and Adams,M.D.			
	Genome duplications and other features in 12 Mb of DNA sequence from human chromosome 16p and 16q			
	Genomics 60 (3), 295-308 (1999)			
JOURNAL	99425270			
MEDLINE	10493829			
PUBMED	2 (bases 1 to 54659)			
REFERENCE	Adams,M.D., Loftus,B.J., Zhou,L., Phillips,C., Brandon,R.C., Fuhrmann,J., Kim,U.J., Kerlavage,A.R. and Venter,J.C.			
AUTHORS	Human chromosome 16p13 BAC clone LANT cosmid-440E5			
TITLE	Unpublished			
JOURNAL	3 (bases 1 to 54659)			
REFERENCE	Adams,M.D.			
AUTHORS	Direct Submission			
TITLE	Submitted (26-AUG-1997) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA			
JOURNAL	On Jun 13, 2002 this sequence version replaced gi:2623293.			
COMMENT	* NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.			
	1 2418: contig of 2418 bp in length			
	* 2419 19809: gap of unknown length			
	* 19810 54659: contig of 34850 bp in length.			
FEATURES	Location/Qualifiers			
source	1. .54659			
	/organism="Homo sapiens"			
	/mol_type="genomic DNA"			
	/db_xref="taxon:9606"			
	/clone="440E5"			
ORIGIN	RESQMTPSHGSPVGPPLPIMSLRQRKGRSPRPSSSSSDSDSDKSTEDPMDLPAN GFGGNQPVKKSFLVYRNDCSLPRSSSDSESSSSSSAASDRSTTPSGRGKPSF SRGTFPEDSSEDTSGTENEAYSVGTGRGVSHMVRKSLGRGAGWLSEDESDPLDALD VMACRGYPSPALIIDPKMPREGMFHGVIPVPLEVLKLGEOQMOGEAREHLYLVL FPDNKRITWQWLPRTKLVPVLGVNQDLDEKMLEGRKSNIRKSVQIAYHRLQHRKSVQG EQSSETSDSD"			

Query Match 2.3%; Score 63; DB 2; Length 54659;
Best Local Similarity 100.0%; Pred. No. 6.2e-25;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2105 TCATCTGAGTCAAGAGTTCAGACCGCTGCGCCACATGCTGAACCCCATCTCTACT 2164
|||||
Db 46338 TCATCTGAGTCAAGAGTTCAGACCGCTGCGCCACATGCTGAACCCCATCTCTACT 46279

QY 2165 AAA 2167
|||

Db 46278 AAA 46276

RESULT 67
HS342B11 56458 bp DNA linear PRI 04-MAR-2003
LOCUS Human DNA sequence from clone CTA-342B11 on chromosome
DEFINITION 22q12.1-12.3, complete sequence.
ACCESSION AL008719
VERSION AL008719.1 GI:3550041
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 56458)
AUTHORS Clark, G.
TITLE Direct Submission
JOURNAL Submitted (04-MAR-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk
On Sep 8, 1998 this sequence version replaced gi:3242181.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep
CTA-342B11 is
from the human BAC library described in U-J. Kim et al. (1996)
Genomics 34, 213-218.
VECTOR: pBAC108L

----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk

This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest, except on the rare
occasion of the clone being a YAC.
This sequence was generated from part of bacterial clone contigs of
human chromosome 22, constructed by the Sanger Centre Chromosome 22
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr22.

FEATURES
Source
1..56458
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="22"
/map="q12.1-12.3"
/clone="CTA-342B11"
/clone_lib="CIT978SK-A1"

ORIGIN
Query Match 2.3%; Score 63; DB 9; Length 56458;
Best Local Similarity 100.0%; Pred. No. 6.2e-25;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2105 TCATCTGAGTCAAGAGTTCAGACCGCTGCGCCACATGCTGAACCCCATCTCTACT 2164
|||||
Db 25894 TCATCTGAGTCAAGAGTTCAGACCGCTGCGCCACATGCTGAACCCCATCTCTACT 25953

QY 2165 AAA 2167
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Db 25954 AAA 25956

RESULT 68
AC044883 57851 bp DNA linear HTG 28-AUG-2002
LOCUS AC044883/c
DEFINITION Homo sapiens chromosome 12 clone RP11-714A22 map 12, LOW-PASS
SEQUENCE SAMPLING.
ACCESSION AC044883
VERSION AC044883.1 GI:7543850
KEYWORDS HTG; HTGS PHASEO.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 57851)
AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.
TITLE Homo sapiens chromosome 12, clone RP11-714A22
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 57851)
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,
Boguslavsky, L., Boukhgalter, B., Brown, A., Burkett, G.,
Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S.,
Collamore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S.,
Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D.,
Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczy, J.,
Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
Meldrim, J., Menus, L., Mihova, T., Miranda, C., Mienga, V., Morrow, J.,
Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
O'Neil, D., Oliver, T.M., Oliver, J., Peterson, K., Pierre, N.,
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Testaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
Young, G., Zainoun, J., Zimmer, A. and Zody, M.

----- Direct Submission
Submitted (12-APR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 57851)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,
Boguslavsky, L., Boukhgalter, B., Brown, A., Burkett, G.,
Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S.,
Collamore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S.,
Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D.,
Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczy, J.,
Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
Meldrim, J., Menus, L., Mihova, T., Miranda, C., Mienga, V., Morrow, J.,
Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
O'Neil, D., Oliver, T.M., Oliver, J., Peterson, K., Pierre, N.,
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,

TITLE
JOURNAL
COMMENT

Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
Strange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (28-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L9583
Center clone name: 714_A_22

* NOTE: This record contains 70 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

1 721: contig of 721 bp in length
* 722 821: gap of 100 bp
* 822 1551: contig of 730 bp in length
* 1552 1651: gap of 100 bp
* 1652 2376: contig of 725 bp in length
* 2377 2476: gap of 100 bp
* 2477 3227: contig of 751 bp in length
* 3228 3327: gap of 100 bp
* 3328 4057: contig of 730 bp in length
* 4058 4157: gap of 100 bp
* 4158 4868: contig of 711 bp in length
* 4869 4968: gap of 100 bp
* 4969 5687: contig of 719 bp in length
* 5688 5787: gap of 100 bp
* 5788 6477: contig of 690 bp in length
* 6478 6577: gap of 100 bp
* 6578 7287: contig of 710 bp in length
* 7288 7387: gap of 100 bp
* 7388 8147: contig of 760 bp in length
* 8148 8247: gap of 100 bp
* 8248 9036: contig of 789 bp in length
* 9037 9136: gap of 100 bp
* 9137 9941: contig of 805 bp in length
* 9942 10041: gap of 100 bp
* 10042 10724: contig of 683 bp in length
* 10725 10824: gap of 100 bp
* 10825 11549: contig of 725 bp in length
* 11550 11649: gap of 100 bp
* 11650 12387: contig of 738 bp in length
* 12388 12487: gap of 100 bp
* 12488 13148: contig of 661 bp in length
* 13149 13248: gap of 100 bp
* 13249 13958: contig of 710 bp in length
* 13959 14058: gap of 100 bp
* 14059 14789: contig of 731 bp in length
* 14790 14889: gap of 100 bp
* 14890 15604: contig of 715 bp in length
* 15605 15704: gap of 100 bp
* 15705 16401: contig of 697 bp in length
* 16402 16501: gap of 100 bp
* 16502 17235: contig of 734 bp in length
* 17236 17335: gap of 100 bp

* 17336 18090: contig of 755 bp in length
* 18091 18190: gap of 100 bp
* 18191 18926: contig of 736 bp in length
* 18927 19026: gap of 100 bp
* 19027 19775: contig of 749 bp in length
* 19776 19875: gap of 100 bp
* 19876 20586: contig of 711 bp in length
* 20587 20686: gap of 100 bp
* 20687 21431: contig of 745 bp in length
* 21432 21531: gap of 100 bp
* 21532 22245: contig of 714 bp in length
* 22246 22345: gap of 100 bp
* 22346 23055: contig of 710 bp in length
* 23056 23155: gap of 100 bp
* 23156 23891: contig of 736 bp in length
* 23892 23991: gap of 100 bp
* 23992 24746: contig of 755 bp in length
* 24747 24846: gap of 100 bp
* 24847 25633: contig of 787 bp in length
* 25634 25733: gap of 100 bp
* 25734 26526: contig of 793 bp in length
* 26527 26626: gap of 100 bp
* 26627 27357: contig of 731 bp in length
* 27358 27457: gap of 100 bp
* 27458 28173: contig of 716 bp in length
* 28174 28273: gap of 100 bp
* 28274 28988: contig of 715 bp in length
* 28989 29088: gap of 100 bp
* 29089 29793: contig of 705 bp in length
* 29794 29894: gap of 100 bp
* 29894 30675: contig of 782 bp in length
* 30676 30775: gap of 100 bp
* 30776 31534: contig of 759 bp in length
* 31535 31634: gap of 100 bp
* 31635 32410: contig of 776 bp in length
* 32411 32510: gap of 100 bp
* 32511 33182: contig of 672 bp in length
* 33183 33282: gap of 100 bp
* 33283 33959: contig of 677 bp in length
* 33960 34059: gap of 100 bp
* 34060 34798: contig of 739 bp in length
* 34799 34898: gap of 100 bp
* 34899 35656: contig of 758 bp in length
* 35657 35756: gap of 100 bp
* 35757 36448: contig of 692 bp in length
* 36449 36548: gap of 100 bp
* 36549 37313: contig of 765 bp in length
* 37314 37413: gap of 100 bp
* 37414 38197: contig of 784 bp in length
* 38198 38297: gap of 100 bp
* 38298 39019: contig of 722 bp in length
* 39020 39119: gap of 100 bp
* 39120 39836: contig of 717 bp in length
* 39837 39936: gap of 100 bp
* 39937 40639: contig of 703 bp in length
* 40639 40739: gap of 100 bp
* 40740 41377: contig of 638 bp in length
* 41378 41477: gap of 100 bp
* 41478 42165: contig of 688 bp in length
* 42166 42265: gap of 100 bp
* 42266 42970: contig of 705 bp in length
* 42971 43070: gap of 100 bp
* 43071 43844: contig of 774 bp in length
* 43845 43944: gap of 100 bp
* 43945 44663: contig of 719 bp in length
* 44664 44763: gap of 100 bp
* 44764 45453: contig of 690 bp in length
* 45454 45553: gap of 100 bp
* 45554 46359: contig of 806 bp in length
* 46360 46459: gap of 100 bp
* 46460 47193: contig of 734 bp in length

Query Match

2.3%; Score 63; DB 2; Length 57851;

Best Local Similarity 100.0%; Pred. No. 6.2e-25; Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2105 TCATCTGAGGTCAGAGGTTCAAGACCAGCCTGGCCACATGTGTGAACCCCATCTCTACT 2164
|||||
Db 8430 TCATCTGAGGTCAGAGGTTCAAGACCAGCCTGGCCACATGTGTGAACCCCATCTCTACT 8371

QY 2165 AAA 2167
|||
Db 8370 AAA 8368

RESULT 69
BX511044_6
WPCOMMENT

Sequence split into 7 fragments LOCUS BX511044 Accession BX511044

Fragment Name Begin End
BX511044_0 1 110000
BX511044_1 100001 210000
BX511044_2 200001 310000
BX511044_3 300001 410000
BX511044_4 400001 510000
BX511044_5 500001 610000
BX511044_6 600001 663813
Continuation (7 of 7) of BX511044 from base 600001 (BX511044 Homo sapiens chromosome 1 c

Query Match 2.3%; Score 63; DB 2; Length 63813;
Best Local Similarity 100.0%; Pred. No. 6.2e-25;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2105 TCATCTGAGGTCAGAGGTTCAAGACCAGCCTGGCCACATGTGTGAACCCCATCTCTACT 2164
|||||
Db 4249 TCATCTGAGGTCAGAGGTTCAAGACCAGCCTGGCCACATGTGTGAACCCCATCTCTACT 4308

QY 2165 AAA 2167
|||
Db 4309 AAA 4311

RESULT 70
HSJ168B21/c
LOCUS HSJ168B21 67973 bp DNA linear PRI 04-MAR-2003
DEFINITION Human DNA sequence from clone RP1-168B21 on chromosome 6q26-27,
complete sequence.

ACCESSION AL118518 GI:6911654

VERSION AL118518.13

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 67973)
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

COMMENT

Direct Submission
Submitted (04-MAR-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone request: clonerequest@sanger.ac.uk
On Feb 7, 2000 this sequence version replaced gi:6822187.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Project8/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr6

----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk

This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest, except on the rare
occasion of the clone being a YAC.

RP1-168B21 is from the library RPCI-1 constructed by the group of
Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pcypac2.

FEATURES

Location/Qualifiers
1..67973
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="6"
/map="q26-27"
/clone="RP1-168B21"
/clone_1ib="RPCI-1"

ORIGIN

Query Match 2.3%; Score 63; DB 9; Length 67973;
Best Local Similarity 100.0%; Pred. No. 6.2e-25;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2105 TCATCTGAGGTCAGAGGTTCAAGACCAGCCTGGCCACATGTGTGAACCCCATCTCTACT 2164
|||||
Db 54564 TCATCTGAGGTCAGAGGTTCAAGACCAGCCTGGCCACATGTGTGAACCCCATCTCTACT 54505

QY 2165 AAA 2167
|||
Db 54504 AAA 54502

RESULT 71
AC011113/c
LOCUS AC011113 68118 bp DNA linear HTG 28-NOV-2001
DEFINITION Homo sapiens clone RP11-11405, LOW-PASS SEQUENCE SAMPLING.

ACCESSION AC011113 GI:17048143

VERSION AC011113.3

KEYWORDS HTG; HTGS PHASE0.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 68118)
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

COMMENT

Direct Submission
Submitted (28-NOV-2001)
Unpublished
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Barna,N., Beckerly,R., Boguslavsky,L., Boukhgalter,B.,
Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
Cooke,P., Dearellano,K., Dewar,K., Domingo,M., Donelan,L., Doyle,M.,
Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,
Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Lehoczky,J., Liu,C., Locke,K., Macdonald,P., Margulis,N.,
McEwan,P., McGurk,A., McKernan,K., McDonald,P., Marquis,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Testaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
Direct Submission

JOURNAL

COMMENT

Submitted (01-OCT-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Nov 22, 2001 this sequence version replaced gi:9581939.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L1960

Center clone name: 114_O_5

* NOTE: This record contains 84 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

* 1 675: contig of 675 bp in length

* 676 775: gap of 100 bp

* 776 1499: contig of 724 bp in length

* 1500 1599: gap of 100 bp

* 1600 2319: contig of 720 bp in length

* 2320 2419: gap of 100 bp

* 2420 3141: contig of 722 bp in length

* 3142 3241: gap of 100 bp

* 3242 3948: contig of 707 bp in length

* 3949 4048: gap of 100 bp

* 4049 4770: contig of 722 bp in length

* 4771 4870: gap of 100 bp

* 4871 5598: contig of 728 bp in length

* 5599 5698: gap of 100 bp

* 5699 6413: contig of 715 bp in length

* 6414 6513: gap of 100 bp

* 6514 7230: contig of 717 bp in length

* 7231 7330: gap of 100 bp

* 7331 8041: contig of 711 bp in length

* 8042 8141: gap of 100 bp

* 8142 8783: contig of 642 bp in length

* 8784 8883: gap of 100 bp

* 8884 9601: contig of 718 bp in length

* 9602 9701: gap of 100 bp

* 9702 10399: contig of 698 bp in length

* 10400 10499: gap of 100 bp

* 11233: contig of 734 bp in length

* 11234 11333: gap of 100 bp

* 11334 12047: contig of 714 bp in length

* 12048 12147: gap of 100 bp

* 12148 12868: contig of 721 bp in length

* 12869 12968: gap of 100 bp

* 12969 13679: contig of 711 bp in length

* 13680 13779: gap of 100 bp

* 13780 14488: contig of 709 bp in length

* 14489 14588: gap of 100 bp

* 14589 15294: contig of 706 bp in length

* 15295 15394: gap of 100 bp

* 15395 16111: contig of 717 bp in length

* 16112 16211: gap of 100 bp

* 16212 16928: contig of 717 bp in length

* 16929 17028: gap of 100 bp

* 17029 17754: contig of 726 bp in length

* 17755 17854: gap of 100 bp

* 17855 18516: contig of 662 bp in length

* 18517 18616: gap of 100 bp

* 18617 19345: contig of 729 bp in length

* 19346 19445: gap of 100 bp

* 19446 20174: contig of 729 bp in length

* 20175 20274: gap of 100 bp

* 20275 20984: contig of 710 bp in length

* 20985 21084: gap of 100 bp

* 21085 21793: contig of 709 bp in length

* 21794 21893: gap of 100 bp

* 21894 22608: contig of 715 bp in length

* 22609 22708: gap of 100 bp

* 22709 23411: contig of 703 bp in length

* 23412 23511: gap of 100 bp

* 23512 24224: contig of 713 bp in length

* 24225 24324: gap of 100 bp

* 24325 25014: contig of 690 bp in length

* 25015 25114: gap of 100 bp

* 25115 25833: contig of 719 bp in length

* 25834 25933: gap of 100 bp

* 25934 26662: contig of 729 bp in length

* 26663 26762: gap of 100 bp

* 26763 27443: contig of 681 bp in length

* 27444 27543: gap of 100 bp

* 27544 28269: contig of 726 bp in length

* 28270 28369: gap of 100 bp

* 28370 29079: contig of 710 bp in length

* 29080 29179: gap of 100 bp

* 29180 29899: contig of 720 bp in length

* 29900 29999: gap of 100 bp

* 30000 30720: contig of 721 bp in length

* 30721 30820: gap of 100 bp

* 30821 31533: contig of 713 bp in length

* 31534 31633: gap of 100 bp

* 31634 32335: contig of 702 bp in length

* 32336 32435: gap of 100 bp

* 32436 33126: contig of 691 bp in length

* 33127 33226: gap of 100 bp

* 33227 33944: contig of 718 bp in length

* 33945 34044: gap of 100 bp

* 34045 34752: contig of 708 bp in length

* 34753 34852: gap of 100 bp

* 34853 35568: contig of 716 bp in length

* 35569 35668: gap of 100 bp

* 35669 36396: contig of 728 bp in length

* 36397 36496: gap of 100 bp

* 36497 37205: contig of 709 bp in length

* 37206 37305: gap of 100 bp

* 37306 37999: contig of 694 bp in length

* 38000 38099: gap of 100 bp

* 38100 38830: contig of 731 bp in length

* 38831 38930: gap of 100 bp

* 38931 39642: contig of 712 bp in length

* 39643 39742: gap of 100 bp

* 39743 40464: contig of 722 bp in length

* 40465 40564: gap of 100 bp

* 40565 41280: contig of 716 bp in length

* 41281 41380: gap of 100 bp

* 41381 42090: contig of 710 bp in length

* 42091 42190: gap of 100 bp

* 42191 42872: contig of 682 bp in length

* 42873 42972: gap of 100 bp

* 42973 43704: contig of 732 bp in length

* 43705 43804: gap of 100 bp

* 43805 44509: contig of 705 bp in length

* 44510 44609: gap of 100 bp

* 44610 45322: contig of 713 bp in length

* 45323 45422: gap of 100 bp

* 45423 46128: contig of 706 bp in length

* 46129 46228: gap of 100 bp

* 46229 47001: contig of 773 bp in length

* 47002 47101: gap of 100 bp

* 47102 47815: contig of 714 bp in length

* 47816 47915: gap of 100 bp

* 47916 48642: contig of 727 bp in length

* 48643 48742: gap of 100 bp

* 48743 49461: contig of 719 bp in length
* 49462 49561: gap of 100 bp
* 49562 50284: contig of 723 bp in length
* 50285 50384: gap of 100 bp
* 50385 51109: contig of 725 bp in length
* 51110 51209: gap of 100 bp
* 51210 51872: contig of 663 bp in length
* 51873 51972: gap of 100 bp
* 51973 52686: contig of 714 bp in length
* 52687 52786: gap of 100 bp
* 52787 53493: contig of 707 bp in length
* 53494 53594: gap of 100 bp
* 53594 54289: contig of 696 bp in length
* 54290 54389: gap of 100 bp
* 54390 55106: contig of 717 bp in length
* 55107 55206: gap of 100 bp
* 55207 55938: contig of 732 bp in length
* 55939 56038: gap of 100 bp
* 56039 56748: contig of 710 bp in length
* 56749 56848: gap of 100 bp
* 56849 57558: contig of 710 bp in length
* 57559 57658: gap of 100 bp
* 57659 58378: contig of 720 bp in length
* 58379 58478: gap of 100 bp
* 58479 59195: contig of 717 bp in length

Query Match 2.3%; Score 63; DB 2; Length 68118;
Best Local Similarity 100.0%; Pred. No. 6.2e-25;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2105 TCATCTGAGTCAAGAGTTCACAGCCAGCTGGCCACATGTGTGAACCCCATCTCTACT 2164
Db 51636 TCATCTGAGTCAAGAGTTCACAGCCAGCTGGCCACATGTGTGAACCCCATCTCTACT 51577

OY 2165 AAA 2167
Db 51576 AAA 51574

RESULT 72
AL359834 70248 bp DNA linear PRI 03-DEC-2001
LOCUS Human DNA sequence from clone RP11-121P12 on chromosome 1, complete
DEFINITION sequence.
ACCESSION AL359834 GI:17384081
VERSION AL359834.18
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 70248)
REFERENCE Direct Submission
AUTHORS Submitted (02-DEC-2001) Wellcome Trust Sanger Institute, Hinxton,
JOURNAL Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Dec 5, 2001 this sequence version replaced gi:17154282.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em; EMBL; Sw; S;

SWISSPROT; Tr; TREMBL; Wp; WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
Group. Further information can be found at
<http://www.sanger.ac.uk/HGP/Chr1>
RP11-121P12 is from the library RPCI-11.1 constructed by the group
of Pieter de Jong. For further details see
<http://www.chori.org/bacpac/home.htm>
VECTOR: pBACe3.6
IMPORTANT: This sequence is not the entire insert of clone
RP11-121P12 it may be shorter because we sequence overlapping
sections only once, except for a short overlap.
The true left end of clone RP11-92G12 is at 68249 in this sequence.
The true right end of clone RP11-469A15 is at 2000 in this
sequence.

FEATURES
Source Location/Qualifiers
1..70248

/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="1"
/clone="RP11-121P12"
/clone_lib="RPCI-11.1"

ORIGIN

Query Match 2.3%; Score 63; DB 9; Length 70248;
Best Local Similarity 100.0%; Pred. No. 6.2e-25;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2105 TCATCTGAGTCAAGAGTTCACAGCCAGCTGGCCACATGTGTGAACCCCATCTCTACT 2164
Db 24944 TCATCTGAGTCAAGAGTTCACAGCCAGCTGGCCACATGTGTGAACCCCATCTCTACT 25003

OY 2165 AAA 2167
Db 25004 AAA 25006

RESULT 73
AC139768 78491 bp DNA linear PRI 26-MAR-2003
LOCUS Homo sapiens 12 BAC RP11-454E5 (Roswell Park Cancer Institute Human
DEFINITION BAC Library) complete sequence.
ACCESSION AC139768
VERSION AC139768.14 GI:29244593
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 78491)
REFERENCE Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
AUTHORS Alsbrooks,S.L., Amaratunga,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkelt,C., Burrell,K.L., Byrd,N.C.,
Carron,T.F., Carter,M., Cavaros,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chiu,D., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Davila,M.L., Davis,C., Davy-Carroll,L., Dedertch,D.A.,
Delaney,K.R., Delgado,O., Dem,A.L., Ding,Y., Dinh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Emerling,S.,
Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P.,
Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Hale,S.,
Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S.,
Hamilton,K., Han,J., Harris,C., Harris,K., Hart,M., Havlak,P.,
Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hognes,M.,
Holloway,C., Hollins,B., Homel,F., Howard,S., Huber,J., Hulyk,S.,
Hume,J., Ioshikhes,I., Jackson,L.E., Jacobson,B., Jia,Y.,
Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U.,

King,L., Kovrah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N.,
Leal,B., Lee,E., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O.,
Lieu,C., Liu,J., Liu,W., Louisedge,H., Lozado,R.J., Lu,X.,
Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapua,P.,
Marondel,I., Martin,R., Martindale,A., Martinez,B., Massey,E.,
Mawhiney,E., Mcleod,M.P., Meador,M., Mei,G., Merscher,S.,
Metzker,M., Miller,A., Miner,G., Miner,Z., Mitchell,T.,
Mohabbat,K., Montgomery,K.T., Morgan,M., Morris,S., Moser,M.,
Neal,D., Nelson,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokenko,S., Oguh,M., Okwuonu,G.,
Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shim,C., Shooshbari,N., Sisson,I.,
Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N., Thomas,S.,
Usmani,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R., Wang,Q.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Kucherlapati,R.,
Weinstock,G. and Gibbs,R.

TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 78491)
AUTHORS Worley,K.C.
JOURNAL Direct Submission
TITLE Submitted (13-FEB-2003) Human Genome Sequencing Center, Department
JOURNAL of Molecular and Human Genetics, Baylor College of Medicine, One
3 (bases 1 to 78491)
REFERENCE 3 (bases 1 to 78491)
AUTHORS Worley,K.C.
JOURNAL Direct Submission
TITLE Submitted (22-MAR-2003) Human Genome Sequencing Center, Department
JOURNAL of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 78491)
REFERENCE 4 (bases 1 to 78491)
AUTHORS Worley,K.C.
JOURNAL Direct Submission
TITLE Submitted (26-MAR-2003) Human Genome Sequencing Center, Department
JOURNAL of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
COMMENT On Mar 26, 2003 this sequence version replaced gi:29150318.
INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email
gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the
entire insert of this clone. Overlapping regions of clones are only
sequenced and submitted once, so the sequence for the remainder of
the insert may be found in the record for the adjacent clones.
Overlapping clones are noted at the beginning and end of the
Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches
of a local database that includes entries from dbSTS, GDB, and
local mapping efforts.
Repeats are identified using RepeatMasker (A. Smit and P. Green,
unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST
(Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the
EST and cDNA sequences. Genes demonstrate at least two exons
flanked by consensus splice sites that maintained sequence
continuity across the splice junctions. Sequences that are not
identical matches are annotated as similar.

SEQUENCING READ COVERAGE:Sequencing is completed to a minimum
standard of double strand coverage with a minimum of 2 clones and 2
reads with no ambiguities or 2 chemistries with a minimum of 2
clones and 3 reads with no ambiguities. If the sequence quality for
a region does not meet this standard, it will be indicated in the
annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality
standards - estimated error rate less than 1 per 10,000 bases.
Reports of lowest quality individual bases and measures of base
quality are listed below. Description of the metrics can be found
at URL:
[http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.ht](http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html)
ml.

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	1136..1253
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	2240..2456
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	6459..6489
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repeat_region 12421.12683
/rpt_family="AluSx"
repeat_region 12794.12893
/rpt_family="AluJb"
repeat_region 12912.13384
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complement(13726.14026)
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repeat_region 14036.14347
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Best Local Similarity 100.0%; Pred. No. 6.2e-25;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2105 TCATCTGAGGTCAAGAGTTCAGACCAAGCCCTGGCCCAACATGTGTGAACCCCATCTCTACT 2164
Db 65216 TCATCTGAGGTCAAGAGTTCAGACCAAGCCCTGGCCCAACATGTGTGAACCCCATCTCTACT 65157

OY 2165 AAA 2167
Db 65156 AAA 65154

RESULT 74
AX957048/c 86131 bp DNA linear PAT 08-JAN-2004
LOCUS AX957048
DEFINITION Sequence 1 from Patent WO03093826.
ACCESSION AX957048
VERSION AX957048.1 GI:40785349

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 Benjamin, S., Clusel, C., Daur, A. and Essioux, L.

AUTHORS Assays for identifying cholesterol - lowering molecules
JOURNAL Patent: WO 03093826-A 1 13-NOV-2003;

FEATURES Clinigenetics (FR)

source Location/Qualifiers

1.86131
/organism="Homo sapiens"
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5852.5871
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 6.2e-25;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2105 TCATCTGAGGTCAAGAGTTCAGACCAAGCCCTGGCCCAACATGTGTGAACCCCATCTCTACT 2164
Db 13366 TCATCTGAGGTCAAGAGTTCAGACCAAGCCCTGGCCCAACATGTGTGAACCCCATCTCTACT 13307

OY 2165 AAA 2167
Db 65156 AAA 65154

Db 13306 AAA 13304

RESULT 75

AP000664/c

LOCUS AP000664 94779 bp DNA linear PRI 15-MAR-2003
DEFINITION Homo sapiens genomic DNA, chromosome 11q clone: CMB9-40G4, complete
sequences.

ACCESSION AP000664

VERSION AP000664.4 GI:14189744

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P.,
Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.

TITLE Homo sapiens genomic DNA

JOURNAL Published Only in Database (1999)

AUTHORS 2 (bases 1 to 94779)

Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P.,
Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.

TITLE Direct Submission

JOURNAL Submitted (04-NOV-1999) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suenriro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail: hattori@gsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)

COMMENT On May 22, 2001 this sequence version replaced gi:9798609.

FEATURES

source

1.94779
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/db_xref="taxon:9606"
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/clone="CMB9-40G4"

ORIGIN

Query Match 2.3%; Score 63; DB 9; Length 94779;
Best Local Similarity 100.0%; Pred. No. 6.2e-25;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2105 TCATCTGAGGTCAAGAGTTCAGACCAAGCCCTGGCCCAACATGTGTGAACCCCATCTCTACT 2164

Db 69172 TCATCTGAGGTCAAGAGTTCAGACCAAGCCCTGGCCCAACATGTGTGAACCCCATCTCTACT 69113

OY 2165 AAA 2167

Db 69112 AAA 69110

Search completed: October 28, 2004, 17:01:05
Job time : 11370 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 28, 2004, 13:07:25 ; Search time 8250 Seconds
(without alignments)
11943.398 Million cell updates/sec

Title: US-09-745-605-1
Perfect score: 2704
Sequence: 1 ggaagtgcgtcattcagt.....aaaaaaaaaaaaaa 2704

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 32822875 seqs, 18219865908 residues

Word size : 0

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_hlc: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_gss1: *
9: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match	Length	DB ID	Description
No.					
1	742	27.4	784	6	CD364928 UI-H-FT2-
2	715	26.4	749	6	CD366342 UI-H-FT1-
3	697	25.8	767	6	CB529471 UI-H-FT2-
4	696	25.7	704	6	CB529490 UI-H-FT2-
5	674	24.9	731	4	CB986561 AGENCOURT
6	652	24.1	1035	4	BMS49959 AGENCOURT
7	647	23.9	714	4	BG743853 602722605
8	646	23.9	738	6	CD364943 UI-H-FT2-
9	643	23.8	1043	5	BQ053807 AGENCOURT
10	632	23.4	904	2	BQ712547 AGENCOURT
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12	573	21.2	702	7	CN480770 UI-H-FT2-
13	572	21.2	648	6	CD687842 EST4363 h
14	567	21.0	602	1	AI638519 tt08f02.x
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16	545	20.2	760	6	CB956896 AGENCOURT
17	532	19.7	672	1	AM003948 wq84h01.x
18	527	19.5	739	6	CD366944 UI-H-FT2-
19	519	19.2	842	6	CD520950 AGENCOURT
20	515	19.0	1050	4	BM800975 AGENCOURT
21	512	18.9	785	6	CD366908 UI-H-FT2-
22	498	18.4	634	2	AM963563 EST375636
23	492	18.2	594	1	AI422743 tf29g12.x
24	479	17.7	980	2	BF026131 601669819

C 25	467	17.3	534	2	AW293413	AW293413 UI-H-BI2-
C 26	442	16.3	444	1	AA921765	AA921765 om43g11.b
C 27	433	16.0	484	4	BG413358	BG413358 7037c12.x
C 28	430	15.9	630	2	BE044439	BE044439 ho45e03.x
C 29	421	15.6	846	4	BG743877	BG743877 602722632
C 30	416	15.4	876	5	BU166292	BU166292 AGENCOURT
C 31	414	15.3	527	1	AI968397	AI968397 wu02f07.x
C 32	406	15.0	457	2	BE467670	BE467670 hz67f07.x
C 33	399	14.8	657	2	AW026300	AW026300 wv11d02.x
C 34	398	14.7	968	5	BQ898498	BQ898498 AGENCOURT
C 35	397	14.7	663	5	BU617383	BU617383 UI-H-DFO-
C 36	380	14.1	705	5	BQ000581	BQ000581 UI-H-DPO-
C 37	380	14.1	712	6	CD366710	CD366710 UI-H-FT2-
C 38	379	14.0	487	4	BG058624	BG058624 nafo8b08.
C 39	373	13.8	614	1	AV733301	AV733301 AV733301
C 40	367	13.6	421	7	W72366	W72366 zd62f01.s1
C 41	367	13.6	761	6	CD630759	CD630759 56071680J
C 42	360	13.3	793	6	CD630761	CD630761 56071688J
C 43	358	13.2	442	2	BE246373	BE246373 TCBAPIE29
C 44	354	13.1	354	2	AM197989	AM197989 xo29a01.x
C 45	354	13.1	405	1	AA908670	AA908670 o104d01.b
C 46	340	12.6	396	1	AA908670	AA908670 o104d01.b
C 47	340	12.6	426	2	AM630293	AM630293 hb81a11.y
C 48	321	11.9	372	1	AI948861	AI948861 wq37d09.x
C 49	316	11.7	451	7	H74227	H74227 yu03f06.s1
C 50	314	11.6	935	2	BF027036	BF027036 601671280
C 51	311	11.5	369	2	AM512079	AM512079 xx70a08.x
C 52	309	11.4	670	4	BG744563	BG744563 602722632
C 53	307	11.4	506	6	CD107362	CD107362 AGENCOURT
C 54	278	10.3	280	6	CD630758	CD630758 56071680H
C 55	275	10.2	282	2	AM403028	AM403028 UI-HF-BK0
C 56	273	10.1	431	1	AI651934	AI651934 wb51c08.x
C 57	272	10.1	332	1	AA604443	AA604443 np57g04.x
C 58	267	9.9	557	2	AM138797	AM138797 UI-H-BI1-
C 59	261	9.7	855	5	BQ440846	BQ440846 AGENCOURT
C 60	258	9.5	436	7	H73135	H73135 yu03f06.r1
C 61	255	9.4	774	5	BU183701	BU183701 AGENCOURT
C 62	252	9.3	631	6	CB046322	CB046322 NISC_gf03
C 63	250	9.2	354	1	AI289790	AI289790 qw12b12.x
C 64	249	9.2	321	1	AI521522	AI521522 to64b07.x
C 65	247	9.1	315	2	AM080386	AM080386 xe41e10.x
C 66	245	9.1	493	2	AM379005	AM379005 RC3-HT023
C 67	240	8.9	411	1	AA554342	AA554342 nl03e08.b
C 68	233	8.6	243	1	AI366936	AI366936 qw18b04.x
C 69	223	8.2	245	6	CA432799	CA432799 UI-H-CO0-
C 70	214	7.9	789	1	AV713600	AV713600 AV713600
C 71	204	7.5	466	5	BX279875	BX279875 BX279875
C 72	202	7.5	1026	4	BMS51726	BMS51726 AGENCOURT
C 73	200	7.4	321	1	AA381714	AA381714 EST94847
C 74	199	7.4	201	1	AM515147	AM515147 xu92b03.x
C 75	194	7.2	294	1	AI917364	AI917364 ts83f07.x
C 76	193	7.1	449	7	W74027	W74027 zd62f01.r1
C 77	190	7.0	411	2	BE698598	BE698598 RCI-UT003
C 78	186	6.9	532	2	AM615053	AM615053 hb81a11.x
C 79	179	6.6	563	5	BX486863	BX486863 DKF2P686M
C 80	166	6.1	271	1	AI540770	AI540770 tn90f03.x
C 81	164	6.1	368	6	CD630760	CD630760 56071688H
C 82	160	5.9	274	4	AI970450	AI970450 wr10h09.x
C 83	153	5.7	221	1	BI045155	BI045155 RC6-FN020
C 84	152	5.6	565	2	BF917980	BF917980 IL3-UT011
C 85	147	5.4	148	2	AM572670	AM572670 xx92c11.x
C 86	135	5.0	1802	4	BM917678	BM917678 AGENCOURT
C 87	132	4.9	431	7	H79453	H79453 yu28e08.r1
C 88	131	4.8	396	7	H79338	H79338 yu28e08.s1
C 89	130	4.8	294	2	BE698718	BE698718 RCI-UT003
C 90	127	4.7	689	4	BG744542	BG744542 602722605
C 91	106	3.9	107	7	CO647397	CO647397 ILLUMIGEN
C 92	105	3.9	107	1	AA916304	AA916304 on22d04.8
C 93	105	3.9	424	2	BE939977	BE939977 RCI-UT003
C 94	104	3.8	514	2	BE671926	BE671926 7a46d07.x
C 95	99	3.7	450	6	CA306719	CA306719 UI-H-FT1-
C 96	97	3.6	615	6	CB957321	CB957321 AGENCOURT
C 97	94	3.5	864	4	BI838780	BI838780 603082388

c	98	87	3.2	233	4	BG314915	BG314915	OP2.0.213
	99	85	3.1	85	2	AM059854	AM059854	HuTH.bset
	100	85	3.1	569	5	BU198430	BU198430	DCBCHF05

ALIGNMENTS

RESULT 1
CD364928/c 784 bp mRNA linear EST 05-AUG-2004
LOCUS UI-H-FT2-bjn-g-19-0-UI.s1 NCI CGAP_FT2 Homo sapiens cDNA clone
DEFINITION UI-H-FT2-bjn-g-19-0-UI 3', mRNA sequence.

ACCESSION CD364928
VERSION CD364928.1 GI:31149018
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 784)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.iowa.edu/distribution/cgap.html
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source location/Qualifiers
1. .784
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT2-bjn-g-19-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP FT2"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: Ecor I; Site 2: Not I; NCI-CGAP_FT2 is a subtracted cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

ORIGIN
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT2
TAG_SEQ=GGCCATGCCG"

Query Match 27.4%; Score 742; DB 6; Length 784;
Best Local Similarity 100.0%; Pred. No. 2.7e-312;
Matches 742; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	750	TACTATGTGGGATATACAGCTCATCTCCAGCAGCCCTCCACCCAGAGTACGTGCTG	691
QY	408	CATGTCTACGAGCACCCTGTCAAAGCCTTAAAGTCACCACTGGGCTTCGACAGCAATAAGAAAT	467
DB	690	CATGTCTACGAGCACCCTGTCAAAGCCTTAAAGTCACCACTGGGCTTCGACAGCAATAAGAAAT	631
QY	468	GGCACCCTGTGTGACCAATCTGACATGCTGCATGGAACATGGGGAAGAGATGTGATTAT	527
DB	630	GGCACCCTGTGTGACCAATCTGACATGCTGCATGGAACATGGGGAAGAGATGTGATTAT	571
QY	528	ACCTGGAAGGCCCTGGGGCAAGCAGCCCAATGATGCCATTAATGGTCCATCCTCCCATC	587
DB	570	ACCTGGAAGGCCCTGGGGCAAGCAGCCCAATGATGCCATTAATGGTCCATCCTCCCATC	511
QY	588	TCCTGGAGATGGGGAGAAAGTATATGACCTTCATCTGGCTGGCCAGGAACCTGTGAC	647
DB	510	TCCTGGAGATGGGGAGAAAGTATATGACCTTCATCTGGCTGGCCAGGAACCTGTGAC	451
QY	648	AGAACTTCTCAAGCCCCCATCTTGCAGGAAGCTCTGTGAAGGTGCTGTGATGACCA	707
DB	450	AGAACTTCTCAAGCCCCCATCTTGCAGGAAGCTCTGTGAAGGTGCTGTGATGACCA	391
QY	708	GATTCCTCATGTGCTCTGTGTCTCTGTTGGTGCCCTCTGCTCAGTCTCTTTGTA	767
DB	390	GATTCCTCATGTGCTCTGTGTCTCTGTTGGTGCCCTCTGCTCAGTCTCTTTGTA	331
QY	768	CTGGGGCTATTCTTTGGTTTCTGAAGAGAGAGACAAGAGTACATTGAAGAGAAG	827
DB	330	CTGGGGCTATTCTTTGGTTTCTGAAGAGAGAGACAAGAGTACATTGAAGAGAAG	271
QY	828	AAGAGGTGACATTTGTGGGAAACTCCTTAACATATGCCCCATTCTGAGAGAACACA	887
DB	270	AAGAGGTGACATTTGTGGGAAACTCCTTAACATATGCCCCATTCTGAGAGAACACA	211
QY	888	GAGTACGACACAAATCCCTCACAATAATAGAACAAATCTTAAAGAAAGATCCAGCAATACG	947
DB	210	GAGTACGACACAAATCCCTCACAATAATAGAACAAATCTTAAAGAAAGATCCAGCAATACG	151
QY	948	GTTTACTCCACTGTGGAATAACGAAAAAGATGGAATATCCCACTACTGCTCAGCATG	1007
DB	150	GTTTACTCCACTGTGGAATAACGAAAAAGATGGAATATCCCACTACTGCTCAGCATG	91
QY	1008	CCAGACACACCAAGGCTATTGTGCTATGAGAAATGTTATCTAGACAGCAGTCACTCCCT	1067
DB	90	CCAGACACACCAAGGCTATTGTGCTATGAGAAATGTTATCTAGACAGCAGTCACTCCCT	31
QY	1068	AAGTCTGTGCTCAAAAAAAA 1089	
DB	30	AAGTCTGTGCTCAAAAAAAA 9	

RESULT 2
CD366342/c 749 bp mRNA linear EST 05-AUG-2004
LOCUS UI-H-FT1-bjt-g-24-0-UI.s1 NCI CGAP_FT1 Homo sapiens cDNA clone
DEFINITION UI-H-FT1-bjt-g-24-0-UI 3', mRNA sequence.

ACCESSION CD366342
VERSION CD366342.1 GI:31150432
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 749)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

JOURNAL
COMMENT

Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Humminghake, U of I
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/cgap.html>
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES

Source

Location/Qualifiers

1. 749
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-bjt-g-24-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_FTI"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI_CGAP_FTI is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Humminghake of the University of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match 26.4%; Score 715; DB 6; Length 749;
Best Local Similarity 100.0%; Pred. No. 1.6e-300;
Matches 715; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1324 GAAGTATTCCTATAGAAATGTAATGCAAGGTCACACATATTATGACAGAGCCCTGTGTAT 1383
|||||
DB 732 GAAGTATTCCTATAGAAATGTAATGCAAGGTCACACATATTATGACAGAGCCCTGTGTAT 673
|||||

QY 1384 TAATGATGGCTCCAGGTCAGTGTCTGAGTTTCATTCATCCAGGGCTTGATGTCAGG 1443
|||||
DB 672 TAATGATGGCTCCAGGTCAGTGTCTGAGTTTCATTCATCCAGGGCTTGATGTCAGG 613
|||||

QY 1444 ATTATACCAAGAGTCTTGCTAACAGAGGGCAAGAGCAAAAACAGACAGACAGTCCA 1503
|||||
DB 612 ATTATACCAAGAGTCTTGCTAACAGAGGGCAAGAGCAAAAACAGACAGACAGTCCA 553
|||||

QY 1504 GCAGAGCAGATGCACCTGACAAAATGATGTATTATTGGCTCTATAAATACTATGTGCC 1563
|||||
DB 552 GCAGAGCAGATGCACCTGACAAAATGATGTATTATTGGCTCTATAAATACTATGTGCC 493
|||||

QY 1564 CAGCACTATGCTGAGCTTACACTAATTGGTCAGACGCTGCTCTGCCCTCATGAATTGG 1623
|||||
DB 492 CAGCACTATGCTGAGCTTACACTAATTGGTCAGACGCTGCTCTGCCCTCATGAATTGG 433
|||||

QY 1624 CTCCAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT 1683
|||||
DB 432 CTCCAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT 373
|||||

QY 1684 AGGCCAGGTGTGATCCACAGACTTGAAGTCAAAAGTTCAAAAGATGAAGATCAGG 1743
|||||
DB 372 AGGCCAGGTGTGATCCACAGACTTGAAGTCAAAAGTTCAAAAGATGAAGATCAGG 313
|||||

QY 1744 GTAGCTGACCATGTTTGGCAGATCTATTAATGAGACACAGAAAGTGCATGGCCCAAGG 1803
|||||
DB 312 GTAGCTGACCATGTTTGGCAGATCTATTAATGAGACACAGAAAGTGCATGGCCCAAGG 253
|||||

QY 1804 ACAAGGACCTCCAGCCAGGCTTCATTTATGCACTTGTGCTGCAAAAAGTCTAGGTT 1863
|||||
DB 252 ACAAGGACCTCCAGCCAGGCTTCATTTATGCACTTGTGCTGCAAAAAGTCTAGGTT 193
|||||

QY 1864 TTAAGGCTGTGCCAGAACCCATCCCAATAAAGAGACCGAGTCTGAAGTCACATTGTAAT 1923
|||||
DB 192 TTAAGGCTGTGCCAGAACCCATCCCAATAAAGAGACCGAGTCTGAAGTCACATTGTAAT 133
|||||

QY 1924 CTAGTGTAGAGACTTGGAGTCAGGCACTGAGTGGGCGACGGGGCGAGTGGGTA 1983
|||||
DB 132 CTAGTGTAGAGACTTGGAGTCAGGCACTGAGTGGGCGACGGGGCGAGTGGGTA 73
|||||

QY 1984 CTTGTAACCTTTAAAGATGTTAATTCATTCATATGATATTATTAAAGACCTA 2038
|||||
DB 72 CTTGTAACCTTTAAAGATGTTAATTCATTCATATGATATTATTAAAGACCTA 18
|||||

RESULT 3

CB529471/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgabs-r@mail.nih.gov

Tissue Procurement: Dr. Gary W. Humminghake, U of I

CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

<http://genome.uiowa.edu/distribution/cgap.html>

Seq primer: M13 FORWARD

POLYA=Yes.

FEATURES

Source

Location/Qualifiers

1. 767
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT2-bjh-m-17-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"

/lab host="DH10B (Life Technologies)"
/clone lib="NCI_CGAP_FT2"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: Ecor I; Site_2: Not I; NCI_CGAP_FT2 is a subtraced cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV egfp), moi 500, 3 hours; Adenoviral vector (Ad5 CMV egfp), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was subtraced according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT2
TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match 25.8%; Score 697; DB 6; Length 767;
Best Local Similarity 100.0%; Pred. No. 1.1e-292;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 393 CAGAGTACGCTGCTGATGTCTACGAGCAGCTGTCAAAGCCTAAAGTCACCATGGGTCG 452
|||||
Db 705 CAGAGTACGCTGCTGATGTCTACGAGCAGCTGTCAAAGCCTAAAGTCACCATGGGTCG 646
QY 453 CAGAGCAATAAGATGGACCTGTGTGACCAATCTGACATGCTGCATGGAACATGGGAA 512
|||||
Db 645 CAGAGCAATAAGATGGACCTGTGTGACCAATCTGACATGCTGCATGGAACATGGGAA 586
QY 513 GAGGATGTGATTTATACCTGGAAGGCCCTGGGGCAAGCAGCCCAATGATCCCATATGGG 572
|||||
Db 585 GAGGATGTGATTTATACCTGGAAGGCCCTGGGGCAAGCAGCCCAATGATCCCATATGGG 526
QY 573 TCCATCCTCCCATCTCTCTGGAGATGGGAGAAAGTATATGACCTTCACTGCGTTGCC 632
|||||
Db 525 TCCATCCTCCCATCTCTCTGGAGATGGGAGAAAGTATATGACCTTCACTGCGTTGCC 466
QY 633 AGGAACCTGTGAGCAGAAACTTCTCAAGCCCCATCCTTGCCAGAGAGCTCTGTGAAGGT 692
|||||
Db 465 AGGAACCTGTGAGCAGAAACTTCTCAAGCCCCATCCTTGCCAGAGAGCTCTGTGAAGGT 406
QY 693 GCTGCTGATGACCCAGATTCTCCATGGTCTCTCTGTCTCTCTGTTGGTGGCCCTCTG 752
|||||
Db 405 GCTGCTGATGACCCAGATTCTCCATGGTCTCTCTGTCTCTCTGTTGGTGGCCCTCTG 346
QY 753 CTCAGTCTTTTGTACTGGGGCTATTCTTTGGTTTCTGAAGAGAGAGACAAGAAGAG 812
|||||
Db 345 CTCAGTCTTTTGTACTGGGGCTATTCTTTGGTTTCTGAAGAGAGAGACAAGAAGAG 286
QY 813 TACATTGAAGAAGAAGAAGAGAGAGATTTGTGGGAAACTCCTTAACATATGCCCCCAT 872
|||||
Db 285 TACATTGAAGAAGAAGAAGAGAGAGATTTGTGGGAAACTCCTTAACATATGCCCCCAT 226
QY 873 TCTGAGAGAACACAGAGTAGACACAATCCCTCACACTAATAGACAATCCTAAAGAA 932
|||||
Db 225 TCTGAGAGAACACAGAGTAGACACAATCCCTCACACTAATAGACAATCCTAAAGAA 166
QY 933 GATCCAGCAATAACGGTTTACTCCACTGTGGAATAACCGAAAAAGATGGAATCCCCAC 992
|||||

Db 165 GATCCAGCAATAACGGTTTACTCCACTGTGGAATATCCGAAAAAGATGGAATCCCCAC 106
QY 993 TCACTGCTCAGATGCGCAGACACACCAGGCTATTGCTTATGAGATGTATCTAGACA 1052
|||||
Db 105 TCACTGCTCAGATGCGCAGACACACCAGGCTATTGCTTATGAGATGTATCTAGACA 46
QY 1053 GCAGTGCACTCCCTTAAGTCTGTGCTCAAAAAAAAAA 1089
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Db 45 GCAGTGCACTCCCTTAAGTCTGTGCTCAAAAAAAAAA 9

RESULT 4

CB529490/c 704 bp mRNA linear EST 05-AUG-2004
LOCUS
DEFINITION UI-H-FT2-bjh-a-16-0-UI.s1 NCI_CGAP_FT2 Homo sapiens cDNA clone
UI-H-FT2-bjh-a-16-0-UI 3', mRNA sequence.

ACCESSION CB529490
VERSION CB529490.1 GI:29390229
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 704)
NCI_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/cgap.html
Seq primer: M13 FORWARD
POLVA=Yes.

FEATURES
source

Location/Qualifiers
1..704
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT2-bjh-a-16-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_FT2"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: Ecor I; Site_2: Not I; NCI_CGAP_FT2 is a subtraced cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV egfp), moi 500, 3 hours; Adenoviral vector (Ad5 CMV egfp), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was subtraced according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage

ORIGIN TAG_LIB=UI-H-FT2
TAG_SEQ=GGCCATGCCG"

Query Match 25.7%; Score 696; DB 6; Length 704;
Best Local Similarity 100.0%; Pred. No. 3.1e-292;
Matches 696; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 394 AGAGTACGTGCTGATGCTACGAGCACTGTCAAAGCCTAAAGTCACCATGGGTCTGC 453
|||||
DB 704 AGAGTACGTGCTGATGCTACGAGCACTGTCAAAGCCTAAAGTCACCATGGGTCTGC 645
OY 454 AGAGCAATAAGATGGCACCTGTGTGACCAATCTGACATGCTGCATGGAAACATGGGGAAG 513
|||||
DB 644 AGAGCAATAAGATGGCACCTGTGTGACCAATCTGACATGCTGCATGGAAACATGGGGAAG 585
OY 514 AGGATGTGATTATACCTGGGAAGGCCCTGGGGCAAGCAAGCAATGAGTCCCATTAATGGGT 573
|||||
DB 584 AGGATGTGATTATACCTGGGAAGGCCCTGGGGCAAGCAAGCAATGAGTCCCATTAATGGGT 525
OY 574 CCATCCTCCCATCTCTGAGAGATGGGGAAGATGATGACCTTCATCTGCGTTGCCA 633
|||||
DB 524 CCATCCTCCCATCTCTGAGAGATGGGGAAGATGATGACCTTCATCTGCGTTGCCA 465
OY 634 GGAACCCCTGTACAGCAAACTTCTCAAGCCCCATCTTGCCAGGAAGCTGTGGAAGGTG 693
|||||
DB 464 GGAACCCCTGTACAGCAAACTTCTCAAGCCCCATCTTGCCAGGAAGCTGTGGAAGGTG 405
OY 694 CTGCTGATGACCCAGATTCTCCATGCTCTCTGTCTCTCTGTTGGTGGTCCCTCTCTGC 753
|||||
DB 404 CTGCTGATGACCCAGATTCTCCATGCTCTCTGTCTCTCTGTTGGTGGTCCCTCTCTGC 345
OY 754 TCAGTCTCTTGTACTGGGGCTATTCTTGGTTCTGAAGAGAGAGAGACAAGAGAGT 813
|||||
DB 344 TCAGTCTCTTGTACTGGGGCTATTCTTGGTTCTGAAGAGAGAGAGACAAGAGAGT 285
OY 814 ACATTGAAGAGAAGAGAGAGTGGACATTGTGCGGAACTCCTAACATATGCCCATTT 873
|||||
DB 284 ACATTGAAGAGAAGAGAGTGGACATTGTGCGGAACTCCTAACATATGCCCATTT 225
OY 874 CTGAGAGAACACAGATGACACAATCCCTCAGACTAATAGAACAAATCCTAAAGGAAG 933
|||||
DB 224 CTGAGAGAACACAGATGACACAATCCCTCAGACTAATAGAACAAATCCTAAAGGAAG 165
OY 934 ATCCAGCAATAACGGTTTACTCCACTGTGGAATACCGAAAAAGATGGAATCCCACT 993
|||||
DB 164 ATCCAGCAATAACGGTTTACTCCACTGTGGAATACCGAAAAAGATGGAATCCCACT 105
OY 994 CACTGCTCAGATGCCAGACACACCAAGGCTATTGCTATGAGAAATGTTATCTAGACAG 1053
|||||
DB 104 CACTGCTCAGATGCCAGACACACCAAGGCTATTGCTATGAGAAATGTTATCTAGACAG 45
OY 1054 CAGTGCACTCCCTTAAGTCTCTGCTCAAAAAAAAAA 1089
|||||
DB 44 CAGTGCACTCCCTTAAGTCTCTGCTCAAAAAAAAAA 9

RESULT 5
CB986561 731 bp mRNA linear EST 01-MAY-2003
LOCUS AGENCOURT_13646958 NIH_MGC_184 Homo sapiens cDNA clone
DEFINITION IMAGE:30327727 5', mRNA sequence.

ACCESSION CB986561
VERSION CB986561.1 GI:30281081
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 731)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
plate: NDCM137 row: d column: 08
High quality sequence stop: 599.

FEATURES

Source

1. 731
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30327727"
/lab_host="DH10B (T1 phage-resistant)"
/clone_1b="NIH MGC 184"
/note="Organ: Pooled-glandular; Vector: pDNR-LIB; Site_1:
SfiI (ggccatctggcc); Site_2: SfiI (ggcgccctggcc);
Library is oligo-dT primed and directionally cloned. cDNA
was prepared from a glandular pool of tissues from thyroid,
parathyroid, adrenal, cortex and pineal gland. 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCCGAGGCGGCGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.38
kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 24.9%; Score 674; DB 6; Length 731;
Best Local Similarity 100.0%; Pred. No. 1.2e-282;
Matches 674; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 TTTCAGTGGCTGACTTCCAGAGAGCAATATGCTGTTCCCAACATGCTCACCTCAT 73
|||||
DB 6 TTTCAGTGGCTGACTTCCAGAGAGCAATATGCTGTTCCCAACATGCTCACCTCAT 65
OY 74 CTATATCCTTTGGCAGCTCACAGGCTCAGACCTCTGAGCCCGTGAAGAGCTGTGG 133
|||||
DB 66 CTATATCCTTTGGCAGCTCACAGGCTCAGACCTCTGAGCCCGTGAAGAGCTGTGG 125
OY 134 TTCCGTTGGTGGGCGGTGACTTTCCCTGAAAGTCCAAAGTAAGCAAGTTGACTTAT 193
|||||
DB 126 TTCCGTTGGTGGGCGGTGACTTTCCCTGAAAGTCCAAAGTAAGCAAGTTGACTTAT 185
OY 194 TGTCTGACCTTCAACACAAACCCCTTGTCAACATACAGCCAGAAAGGGCACTATCAT 253
|||||
DB 186 TGTCTGACCTTCAACACAAACCCCTTGTCAACATACAGCCAGAAAGGGCACTATCAT 245
OY 254 AGTGACCAAAATCGTAATAGGAGAGATGACTTCCAGATGAGGCTACTCCCTGAA 313
|||||
DB 246 AGTGACCAAAATCGTAATAGGAGAGATGACTTCCAGATGAGGCTACTCCCTGAA 305
OY 314 GCTCAGCAACTGAAGAAGATGACTCAGGATCTACTATGTGGGATATACAGCTCATC 373
|||||
DB 306 GCTCAGCAACTGAAGAAGATGACTCAGGATCTACTATGTGGGATATACAGCTCATC 365
OY 374 ACTCAGCAGCCCTCCACCCAGAGATGCTGCTCATGTCTACGAGACCTGTCAAAGCC 433
|||||
DB 366 ACTCAGCAGCCCTCCACCCAGAGATGCTGCTCATGTCTACGAGACCTGTCAAAGCC 425
OY 434 TAAAGTACCATGGGTCTGACAGCAATAAGATGGACCTGTGTGACCAATCTGACATG 493
|||||
DB 426 TAAAGTACCATGGGTCTGACAGCAATAAGATGGACCTGTGTGACCAATCTGACATG 485
OY 494 CTGCATGAACATGGGGAAGAGATGATTATACCTGGAAGCCCTGGGGAAGCAGC 553
|||||
DB 486 CTGCATGAACATGGGGAAGAGATGATTATACCTGGAAGCCCTGGGGAAGCAGC 545


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Oy 554 CAATGATGCCATAATGGTCCATCTCCCATCTCTGTGAGATGGGAGAAAGTGATAT 613
Db 546 CAATGATGCCATAATGGTCCATCTCTCCCATCTCTGTGAGATGGGAGAAAGTGATAT 605
Oy 614 GACCTTCATCTGCGTTGCCAGAACCTGTGACGAGAACTTTCAGCCCCCATCTTGC 673
Db 606 GACCTTCATCTGCGTTGCCAGAACCTGTGACGAGAACTTTCAGCCCCCATCTTGC 665
Oy 674 CAGGAAGCTCTGTG 687
Db 666 CAGGAAGCTCTGTG 679

RESULT 6
LOCUS BM549959 1035 bp mRNA linear EST 20-FEB-2002
DEFINITION AGENCOURT 6544167 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5745910
5', mRNA Sequence.
ACCESSION BM549959
VERSION BM549959.1 GI:18785781
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1035)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM12769 row: j column: 23
High quality sequence start: 12
High quality sequence stop: 663.
location/Qualifiers
source 1..1035
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/db_xref="taxon:9606"
/clone="IMAGE:5745910"
/tissue_type="leukocyte"
/lab_host="DH10B"
/clone_lib="NIH_MGC_118"
/note="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV
(destroyed); RNA source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
and directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
1.2-3.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrogen). Research Genetics tracking code 027. Note:
this is a NIH_MGC Library."

ORIGIN

Query Match 24.1%; Score 652; DB 4; Length 1035;
Best Local Similarity 100.0%; Pred.No. 4.7e-273;
Matches 652; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 174 GTAAGCAAGTTGACTCTATTGTTGTGGACCTTCAACAACCCCTCTGTACCAATACAG 233
Db 158 GTAAGCAAGTTGACTCTATTGTTGTGGACCTTCAACAACCCCTCTGTACCAATACAG 217
Oy 234 CCAGAGGGGGCACTATGATAGTGAACCCAAATCGTAATAGGAGAGATAGACTTCCCA 293
Db 218 CCAGAGGGGGCACTATGATAGTGAACCCAAATCGTAATAGGAGAGATAGACTTCCCA 277
Oy 294 GATGAGGCTACTCCCTGAAGCTCAGCAAACTGAAGAATGACTCAGGGATCTACTAT 353
Db 278 GATGAGGCTACTCCCTGAAGCTCAGCAAACTGAAGAATGACTCAGGGATCTACTAT 337
Oy 354 GTGGGATATACAGCTCATCACTCCAGCAGCCCTCCAGGAGTAGCTGCTGATGTC 413
Db 338 GTGGGATATACAGCTCATCACTCCAGCAGCCCTCCAGGAGTAGCTGCTGATGTC 397
Oy 414 TACGAGCACCTGTCAAAGCCTAAAGTCACCATGGGTGTCAGAGCAATAGAATGCGACC 473
Db 398 TACGAGCACCTGTCAAAGCCTAAAGTCACCATGGGTGTCAGAGCAATAGAATGCGACC 457
Oy 474 TGTGTGACCAATCTGACATGCTGCATGGAACATGGGAGAGATGTGATTATACCTGG 533
Db 458 TGTGTGACCAATCTGACATGCTGCATGGAACATGGGAGAGATGTGATTATACCTGG 517
Oy 534 AAGGCCCTGGGGCAAGCAGCCCAATGAGTCCCATATATGGTCCATCCTCCCATCTCTGG 593
Db 518 AAGGCCCTGGGGCAAGCAGCCCAATGAGTCCCATATATGGTCCATCCTCCCATCTCTGG 577
Oy 594 AGATGGGAGAAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCTGTGACGAGAAAC 653
Db 578 AGATGGGAGAAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCTGTGACGAGAAAC 637
Oy 654 TTCTCAAGCCCATCTTGGCAGGAAGCTGTGTGAAGTGCTGCTGATGACC 705
Db 638 TTCTCAAGCCCATCTTGGCAGGAAGCTGTGTGAAGTGCTGCTGATGACC 689

RESULT 7
LOCUS BG743853 714 bp mRNA linear EST 15-MAY-2001
DEFINITION 602722605F1 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:4849224 5',
mRNA sequence.
ACCESSION BG743853
VERSION BG743853.1 GI:14054506
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 714)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM1688 row: i column: 01
High quality sequence stop: 706.
location/Qualifiers
source 1..714
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/mol_type="mRNA"
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/clone="IMAGE:4849224"
/tissue_type="natural killer cells, cell line"
/lab_host="DH10B (phage-resistant)"
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QY	633	AGGAACCCGTGTACGACGAAACTTCTCAAGCCCCATCCTTGGCCAGGAAGCTCTGTGAAGT	692
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QY	693	GCTGCTGATGACCCAGATTCTCCATGTTCTCTCTGTTCTCTGTTGGTCCCTCTG	752
Db	405	GCTGCTGATGACCCAGATTCTCCATGTTCTCTCTCTGTTCTCTGTTGGTCCCTCTG	346
QY	753	CTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTCTGAAGAGAGAGACAAGAAG	812
Db	345	CTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTCTGAAGAGAGAGACAAGAAG	286
QY	813	TACATTGAAGAAGAAGAGAGTGGACATTTGTGGGAACTCTTACATATGCCCCAT	872
Db	285	TACATTGAAGAAGAAGAGAGTGGACATTTGTGGGAACTCTTACATATGCCCCAT	226
QY	873	TCTGAGAGAACAACAAGTACGACAATCCCTCACACTAATAGAACAATCTTAAAGAA	932
Db	225	TCTGAGAGAACAACAAGTACGACAATCCCTCACACTAATAGAACAATCTTAAAGAA	166
QY	933	GATCCAGCAATACGGTTTACTCCACTGTGGAATACCGAAAAAGATGGAATCCCCAC	992
Db	165	GATCCAGCAATACGGTTTACTCCACTGTGGAATACCGAAAAAGATGGAATCCCCAC	106
QY	993	TCACTGCTCACGATGCCAGACACACCAAGGCTATTTGGCTATGAGAATGTTATCTAGACA	1052
Db	105	TCACTGCTCACGATGCCAGACACACCAAGGCTATTTGGCTATGAGAATGTTATCTAGACA	46
QY	1053	GCAGTGCACTCCCTAAGTCTCTGCTCAAAAAAAAA 1089	
Db	45	GCAGTGCACTCCCTAAGTCTCTGCTCAAAAAAAAA 9	

RESULT 9	
BQ053807	
LOCUS	
DEFINITION	BQ053807 1043 bp mRNA linear EST 29-MAR-2002
	AGENCOURT_7027738 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5935701
	5', mRNA sequence.
ACCESSION	BQ053807
VERSION	BQ053807.1 GI:19813147
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1043) NIH-MGC http://mgc.nci.nih.gov/ . National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
AUTHORS	Contact: Robert Strausberg, Ph.D.
TITLE	Email: cgapbs-r@mail.nih.gov
JOURNAL	Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
COMMENT	CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov Plate: L1CM2123 row: n column: 22 High quality sequence stop: 610.
FEATURES	Location/Qualifiers
source	1..1043

laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

Query Match	23.8%	Score 643	DB 5	Length 1043
Best Local Similarity	100.0%	Pred. No. 3.9e-269		
Matches 643	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	368	CTCATCACTCCAGCAGCCCTCCACCCAGGAGTACGTCGTGCATGTCTACGAGCACTGTC		427
Db	1	CTCATCACTCCAGCAGCCCTCCACCCAGGAGTACGTCGTGCATGTCTACGAGCACTGTC		60
QY	428	AAAGCCTAAAGTCAACCATGGGTCTGCAGAGCAATAAGAAATGGCACTGTGTGACCAATCT		487
Db	61	AAAGCCTAAAGTCAACCATGGGTCTGCAGAGCAATAAGAAATGGCACTGTGTGACCAATCT		120
QY	488	GACATGCTGCATGGAACATGGGGAAAGAGATGTGATTTATACCTGGAAGGCCCTGGGGCA		547
Db	121	GACATGCTGCATGGAACATGGGGAAAGAGATGTGATTTATACCTGGAAGGCCCTGGGGCA		180
QY	548	AGCAGCCAATGAGTCCCATATGGGTCCATCCTCCCATCTCTGAGATGGGAGAAAG		607
Db	181	AGCAGCCAATGAGTCCCATATGGGTCCATCCTCCCATCTCTGAGATGGGAGAAAG		240
QY	608	TGATATGACCTTCATCTGCGTTGCCAGGAACCTGTGACAGAAACTTCTCAAGCCCAT		667
Db	241	TGATATGACCTTCATCTGCGTTGCCAGGAACCTGTGACAGAAACTTCTCAAGCCCAT		300
QY	668	CCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGATGCCAGATTCCTCCATGTCCTCT		727
Db	301	CCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGATGCCAGATTCCTCCATGTCCTCT		360
QY	728	GTGTCTCCTGTTGGTGCCCTCTCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTT		787
Db	361	GTGTCTCCTGTTGGTGCCCTCTCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTT		420
QY	788	TCTGAAGAGAGAGAGACAAGAAGATACATTGAAGAGAAGAAGAGATGACATTGTGCG		847
Db	421	TCTGAAGAGAGAGAGACAAGAAGATACATTGAAGAGAAGAAGAGATGACATTGTGCG		480
QY	848	GGAACCTCTTAACATATGCCCCATTCTGAGAGAAACAAGAGTACGACACAATCCCTCA		907
Db	481	GGAACCTCTTAACATATGCCCCATTCTGAGAGAAACAAGAGTACGACACAATCCCTCA		540
QY	908	CACATAATAGAACCAATCCTAAAGGAAGATCCAGCAATAACGTTTACTCCACTGTGGAAT		967
Db	541	CACATAATAGAACCAATCCTAAAGGAAGATCCAGCAATAACGTTTACTCCACTGTGGAAT		600
QY	968	ACCGAAAAAGATGGAATAATCCCCACTCACTGCTCAGCATGCCA 1010		
Db	601	ACCGAAAAAGATGGAATAATCCCCACTCACTGCTCAGCATGCCA 643		

FEATURES	source
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov	
Plate: LLCM2123 row: n column: 22	
High quality sequence stop: 610.	
Location/Qualifiers	
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/organism="Homo sapiens"	
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/clone="IMAGE:5935701"	
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/clone_1ib="NIH_MGC_106"	
/note="Organ: blood; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGGAG(G). Library constructed by Ling Hong in the	
GGCAAGGAG(G). Library constructed by Ling Hong in the	

Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
plate: LNCM2521 row: m column: 15
High quality sequence stop: 637.
Location/Qualifiers

FEATURES

Source

1. 904
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/clone="IMAGE:6303158"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_113"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN

Query Match 23.4%; Score 632; DB 5; Length 904;
Best Local Similarity 100.0%; Pred. No. 2.5e-264;
Matches 632; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 62 CCTCACCCCTCATATATCTTTGGCAGCTCACAGGTCAGCAGCCTCTGACCGTGAA 121
DB 1 CCTCACCCCTCATATATCTTTGGCAGCTCACAGGTCAGCAGCCTCTGACCGTGAA 60
OY 122 AGAGCTGTGCGTCCGTTGGTGGGGCGGTGACTTCCCTCTGAAGTCCAAAGTAAAGCA 181
DB 61 AGAGCTGTGCGTCCGTTGGTGGGGCGGTGACTTCCCTCTGAAGTCCAAAGTAAAGCA 120
OY 182 AGTGAATCTATGTGTGGAAGCTTCAACACAAACCCCTCTGTCTACCATACAGCCAGAAAG 241
DB 121 AGTGAATCTATGTGTGGAAGCTTCAACACAAACCCCTCTGTCTACCATACAGCCAGAAAG 180
OY 242 GGGCACTATCATAGTGAAGCAAAATCGTAATAGGAGAGAGTAGACTTCCAGATGAGG 301
DB 181 GGGCACTATCATAGTGAAGCAAAATCGTAATAGGAGAGAGTAGACTTCCAGATGAGG 240
OY 302 CTACTCCCTGAAGCTCAGCAAACTGAAGAAGATGACTCAGGATCTACTATGTGGGAT 361
DB 241 CTACTCCCTGAAGCTCAGCAAACTGAAGAAGATGACTCAGGATCTACTATGTGGGAT 300
OY 362 ATACAGCTCATCTCCAGCAGCCCTCCACCCAGAGTACGTGCTGATGTCTACGAGCA 421
DB 301 ATACAGCTCATCTCCAGCAGCCCTCCACCCAGAGTACGTGCTGATGTCTACGAGCA 360
OY 422 CCTGTCAAAGCCTAAAGTCAACCATGGGTCTGCAGAGCAATAGATGGCACTGTGTGAC 481
DB 361 CCTGTCAAAGCCTAAAGTCAACCATGGGTCTGCAGAGCAATAGATGGCACTGTGTGAC 420
OY 482 CAATCTGACATGCTGATGGAACATGGGGAAGAGATGTATTATACCTGGAAGCCCT 541
DB 421 CAATCTGACATGCTGATGGAACATGGGGAAGAGATGTATTATACCTGGAAGCCCT 480
OY 542 GGGCAAGCAGCAATGAGTCCCATATAGGTGCTCCATCTCCCATCTCTGAGATGGGG 601
DB 481 GGGCAAGCAGCAATGAGTCCCATATAGGTGCTCCATCTCCCATCTCTGAGATGGGG 540
OY 602 AGAAGTATATGACCTTCACTGCGTGGCCAGAGAACCTGTACAGAGAACTTCTCAAG 661
DB 541 AGAAGTATATGACCTTCACTGCGTGGCCAGAGAACCTGTACAGAGAACTTCTCAAG 600
OY 662 CCCCATCTTGCCAGGAAGCTCTGTGAAGGTG 693
|||||

Db 601 CCCCATCTTGCCAGGAAGCTCTGTGAAGGTG 632

RESULT 11
BE326659/c
LOCUS
DEFINITION
BE326659 593 bp mRNA linear EST 14-JUL-2000
hr62h10.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:3133123 3'
similar to TR:O15430 O15430 LEUKOCYTE ANTIGEN CD84. ;, mRNA
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
AUTHORS
TITLE
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL
COMMENT
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 449.
Location/Qualifiers

FEATURES

Source

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/note="Organ: kidney; Vector: pTT3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Plasmid DNA from the normalized library NCI CGAP Kid3 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 1322376-1323911, 1456007-1456775, and
150552-1502855). Subtraction by Bento Soares and M.
Fatima Bonaldo."

ORIGIN

Query Match 21.8%; Score 589; DB 2; Length 593;
Best Local Similarity 100.0%; Pred. No. 1.5e-245;
Matches 589; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 490 CATGCTGATGAAATGGGGAGAGGATGATTATACCTGGAAGGCCCTGGGCAAG 549
DB 589 CATGCTGATGAAATGGGGAGAGGATGATTATACCTGGAAGGCCCTGGGCAAG 530
OY 550 CAGCCAATGATGCCATATAGGTGCTCCATCTCCCATCTCTGAGATGGGAGAAAGTG 609
DB 529 CAGCCAATGATGCCATATAGGTGCTCCATCTCCCATCTCTGAGATGGGAGAAAGTG 470
OY 610 ATATGACCTTCACTGCGTTGCCAGGAACCTGTACAGAGAACTTCAAGCCCATCC 669
DB 469 ATATGACCTTCACTGCGTTGCCAGGAACCTGTACAGAGAACTTCAAGCCCATCC 410
OY 670 TTGCCAGGAAGCTCTGTGAAGGTGCTGTATGACCCAGATTCTCTCATGTCTCTCTGT 729
DB 409 TTGCCAGGAAGCTCTGTGAAGGTGCTGTATGACCCAGATTCTCTCATGTCTCTCTGT 350
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RESULT 13
LOCUS CD687842 648 bp mRNA linear EST 25-JUN-2003
DEFINITION EST4363 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION CD687842
VERSION CD687842.1 GI:32206062
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 648)
AUTHORS Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and Zeng,Y.-X.
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gzsums.edu.cn.
Location/Qualifiers
1..648
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/mol_type="mRNA"
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/issue_type="normal nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

ORIGIN
Query Match 21.2%; Score 572; DB 6; Length 648;
Best Local Similarity 100.0%; Pred. No. 3.9e-238;
Matches 572; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 33 GAGAGCAATATGGCTGTTCCCAACATGCTCAGCCTCATCTATATCCTTGGCAGCTC 92
DB 77 GAGAGCAATATGGCTGTTCCCAACATGCTCAGCCTCATCTATATCCTTGGCAGCTC 136
QY 93 ACAGGGTCAGCAGCCTCTGAGCCCGTGAAGAGCTGTCGTTCCGTTGGTGGGCGCTG 152
DB 137 ACAGGGTCAGCAGCCTCTGAGCCCGTGAAGAGCTGTCGTTCCGTTGGTGGGCGCTG 196
QY 153 ACTTTCCCTGAAGTCCAAAGTAAAGCAAGTTGACTTATTTGCTGAGCCTTCAACACA 212
DB 197 ACTTCCCTGAAGTCCAAAGTAAAGCAAGTTGACTTATTTGCTGAGCCTTCAACACA 256
QY 213 ACCCTCTTGTCAACATACAGCCAGAGGGGGCACTATCATAGTGACCCAAATCGTAAT 272
DB 257 ACCCTCTTGTCAACATACAGCCAGAGGGGGCACTATCATAGTGACCCAAATCGTAAT 316
QY 273 AGGAGAGAGTAGACTTCCAGATGAGGCTACTTCCCTGAAGCTCAGCAAACTGAAGAAG 332
DB 317 AGGAGAGAGTAGACTTCCAGATGAGGCTACTTCCCTGAAGCTCAGCAAACTGAAGAAG 376
QY 333 AATGACTCAGGATCTACTATGTGGGATATACAGCTCATCTCAGCAGCCCTCCACC 392
DB 377 AATGACTCAGGATCTACTATGTGGGATATACAGCTCATCTCAGCAGCCCTCCACC 436
QY 393 CAGAGTAGTGTGCTGATGTCTACGAGCAGCTGTCAAAGCTTAAAGTACCAATGGGTCTG 452
DB 437 CAGAGTAGTGTGCTGATGTCTACGAGCAGCTGTCAAAGCTTAAAGTACCAATGGGTCTG 496
QY 453 CAGAGCAATAAGATGGCACTGTGTGACCAATCTGACATGCTGATGGAATGGGAA 512
DB 497 CAGAGCAATAAGATGGCACTGTGTGACCAATCTGACATGCTGATGGAATGGGAA 556
QY 513 GAGATGTGATTTATCTGGAAGGCCCTGGGGCAAGCCAATGAGTCCCAATATGGG 572

DB 557 GAGATGTGATTTATACCTGGAAAGCCCTGGGGCAAGCAGCCAATGATCCCAATATGGG 616
QY 573 TCCATCCTCCCACTCTCCTGGAGATGGGAGA 604
DB 617 TCCATCCTCCCACTCTCCTGGAGATGGGAGA 648
RESULT 14
LOCUS AI638519/c 602 bp mRNA linear EST 14-DEC-1999
DEFINITION tt08f02.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2240187 3', mRNA sequence.
ACCESSION AI638519
VERSION AI638519.1 GI:4690753
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 602)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
www-bio.lnl.gov/bbrp/image/image.html
Insert Length: 840 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 462.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2240187"
/issue_type="pooled germ cell tumors"
/lab_host="DH10B"
/clone_lib="NCI CGAP GC6"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonoids 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN
Query Match 21.0%; Score 567; DB 1; Length 602;
Best Local Similarity 100.0%; Pred. No. 6e-236;
Matches 567; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1444 ATTATACCAAGAGTCTTGCTACAGAGGGCAAGAACCAAAACAGACAGCAAGTCCA 1503
DB 594 ATTATACCAAGAGTCTTGCTACAGAGGGCAAGAACCAAAACAGACAGCAAGTCCA 535
QY 1504 GCAGAGCAGATGCACTGACAAATGAGATGATTAATTGGCTGTATAAATATGTGCC 1563
DB 534 GCAGAGCAGATGCACTGACAAATGAGATGATTAATTGGCTGTATAAATATGTGCC 475
QY 1564 CAGCACTATGCTGAGCTTACACTAATTGCTCAGACGTCGTGCTCCTCATGAATTGG 1623
DB 474 CAGCACTATGCTGAGCTTACACTAATTGCTCAGACGTCGTGCTCCTCATGAATTGG 415

Oy	1624	CTCCAAATGAATGAAC	TACTTTCATGAGCAG	TGTGTAGCAGG	CCCTGACCA	CAGATTCC	CAG	1683
Db	414	CTCCAAATGAATGAAC	TACTTTCATGAGCAG	TGTGTAGCAGG	CCCTGACCA	CAGATTCC	CAG	355
Oy	1684	AGGGCCAGGTGTGAT	CCACAGAGCTTGAAG	GTCAAAAGTTCA	CAAGATGAAG	AATCAG	1743	
Db	354	AGGGCCAGGTGTGAT	CCACAGAGCTTGAAG	GTCAAAAGTTCA	CAAGATGAAG	AATCAG	295	
Oy	1744	GTAGCTGACCATGTT	TGGCAGATATCTAAT	TGAGACACAGA	AGTGTGCATG	GGCCCAAG	1803	
Db	294	GTAGCTGACCATGTT	TGGCAGATATCTAAT	TGAGACACAGA	AGTGTGCATG	GGCCCAAG	235	
Oy	1804	ACAAGACCTCCAGC	AGGCTTCATTATGCA	CTTGCTGCAAA	AGAAAGTCTAG	GT	1863	
Db	234	ACAAGACCTCCAGC	AGGCTTCATTATGCA	CTTGCTGCAAA	AGAAAGTCTAG	GT	175	
Oy	1864	TTAAGGCTGTGCCA	GAACCCATCCCAATA	AAGAGACCGAGT	CTGAAGTCA	CATTGTAAT	1923	
Db	174	TTAAGGCTGTGCCA	GAACCCATCCCAATA	AAGAGACCGAGT	CTGAAGTCA	CATTGTAAT	115	
Oy	1924	CTAGTGTAGAGACT	TGTGAGTCAAGCA	GTGAGACTGTG	GGGCGACGGG	GGCAGTGGGT	1983	
Db	114	CTAGTGTAGAGACT	TGTGAGTCAAGCA	GTGAGACTGTG	GGGCGACGGG	GGCAGTGGGT	55	
Oy	1984	CTGTAAACCTTTAA	AGATGTTAAT	2010				
Db	54	CTGTAAACCTTTAA	AGATGTTAAT	28				

RESULT 15
BI767020 920 bp mRNA linear EST 25-SEP-2001
LOCUS 603054228F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5203638 5',
DEFINITION mRNA sequence.
ACCESSION BI767020
VERSION BI767020.1 GI:15758598
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 920)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: L1AM1510 row: h column: 07
High quality sequence stop: 743.
location/Qualifiers
1. 920

FEATURES
source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5203638"
/lab_host="DH10B"
/clone_lib="NIH_MGC_122"
/note="Organ: pooled lung and spleen; Vector: PCMV-SPORT6;
Site_1: NotI; Site_2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
primed, and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber

(Invitrogen). Research Genetics tracking code 026. Note:
this is a NIH_MGC Library."
ORIGIN
Query Match 20.3%; Score 550; DB 4; Length 920;
Best Local Similarity 99.7%; Pred. No. 1.5e-228;
Matches 720; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Oy	31	CAGAGGCAATATGG	CTGTTCCCAACATG	CCCTCACCCTCAT	TATATCTTGG	CAGC	90	
Db	1	CAGAGGCAATATGG	CTGTTCCCAACATG	CCCTCACCCTCAT	TATATCTTGG	CAGC	60	
Oy	91	TCACAGGTCAGCAG	CCCTGTGACCCG	TGAAGAGCTG	TGCGTTCC	GTGGCCG	150	
Db	61	TCACAGGTCAGCAG	CCCTGTGACCCG	TGAAGAGCTG	TGCGTTCC	GTGGCCG	120	
Oy	151	TGACTTTCCCCCT	GAAATGCAAGTGA	AGCAAGTTGACT	TATTTGCTGA	ACCTCAACA	210	
Db	121	TGACTTTCCCCCT	GAAATGCAAGTGA	AGCAAGTTGACT	TATTTGCTGA	ACCTCAACA	180	
Oy	211	CAACCCCTTGTG	TACCAATACAGC	CAAGAGGGGCA	CTATCATAGT	GAACCAAAATCG	270	
Db	181	CAACCCCTTGTG	TACCAATACAGC	CAAGAGGGGCA	CTATCATAGT	GAACCAAAATCG	240	
Oy	271	ATAGGAGAGAGTA	GAATCTTCCAGAT	GTGAGGCTACT	CTCCTGAAGCT	CAGCAAACTGA	330	
Db	241	ATAGGAGAGAGTA	GAATCTTCCAGAT	GTGAGGCTACT	CTCCTGAAGCT	CAGCAAACTGA	300	
Oy	331	AGATGACTCAGGA	TGATTAATATAT	TGTTGGGATATA	CACTCATCACT	CCAGCAGCCCTCA	390	
Db	301	AGATGACTCAGGA	TGATTAATATAT	TGTTGGGATATA	CACTCATCACT	CCAGCAGCCCTCA	360	
Oy	391	CCCAGAGTACGTG	TCATGCTACGAG	CACCTGTCAAA	AGCCTAAAGTCA	CACCATGGGTC	450	
Db	361	CCCAGAGTACGTG	TCATGCTACGAG	CACCTGTCAAA	AGCCTAAAGTCA	CACCATGGGTC	420	
Oy	451	TGCAGAGCAATA	GAATGGCACTGT	TGACCAATGCA	TGCTGCATGGA	CAATGGGG	510	
Db	421	TGCAGAGCAATA	GAATGGCACTGT	TGACCAATGCA	TGCTGCATGGA	CAATGGGG	480	
Oy	511	AAGAGGATGTG	ATTATTAACCTG	GGAAGGCCCTG	GGGCAAGCA	CCCAATGAGT	570	
Db	481	AAGAGGATGTG	ATTATTAACCTG	GGAAGGCCCTG	GGGCAAGCA	CCCAATGAGT	540	
Oy	571	GGTCCATCTCC	CCATCTCTGGA	GTGGGA-GAA	GTATATGAC	CTTCATGCGGT	629	
Db	541	GGTCCATCTCC	CCATCTCTGGA	GTGGGA-GAA	GTATATGAC	CTTCATGCGGT	600	
Oy	630	GCCAGGAACCT	GTACAGAACTT	CTCAAGCCCA	CTCTGCGAG	GAAGCTGTGAA	689	
Db	601	GCCAGGAACCT	GTACAGAACTT	CTCAAGCCCA	CTCTGCGAG	GAAGCTGTGAA	660	
Oy	690	GGTGTGCTGAT	GACCCAGATT	CTCCATGTC	CTCTGTGTCT	CCTGTTGGCCCTC	749	
Db	661	GGTGTGCTGAT	GACCCAGATT	CTCCATGTC	CTCTGTGTCT	CCTGTTGGCCCTC	720	
Oy	750	CT 751						
Db	721	CT 722						

RESULT 16
CB956896 760 bp mRNA linear EST 29-APR-2003
LOCUS CB956896
DEFINITION AGENCOURT_13778830 NIH_MGC_184 Homo sapiens cDNA clone
IMAGE:30351632 5', mRNA sequence.
ACCESSION CB956896
VERSION CB956896.1 GI:30213013
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 760)
AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: NDCM149 row: h column: 09
High quality sequence stop: 493.

FEATURES

source

1. .760
/organism="Homo sapiens"
/db_xref="taxon:9606"
/mol_type="mRNA"
/clone="IMAGE:30351632"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_184"
/note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1:
SfiI (ggccattatggc); Site_2: SfiI (ggccgctccggc);
Library is oligo-dT primed and directionally cloned. cDNA
was prepared from a glandular pool of tissues from thyroid,
parathyroid, adrenal, cortex and pineal gland. 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.38
kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 545; DB 6; Length 760;
Matches 545; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1454 GAGTCTTGCTACCAAGAGGGCAAGAGACCAAAACAGACAGACAGTCCAGCAAGACAG 1513
DB 3 GAGTCTTGCTACCAAGAGGGCAAGAGACCAAAACAGACAGACAGTCCAGCAAGACAG 62
QY 1514 ATGCACCTGACAAAATGGATGTATTATTGGCTCTATAAATCTATGTGCCAGCACTATG 1573
DB 63 ATGCACCTGACAAAATGGATGTATTATTGGCTCTATAAATCTATGTGCCAGCACTATG 122
QY 1574 CTGAGCTTACATAATGTGTGACAGCGTGTCTGCTCCCTCATGAATTTGGCTCCAAATGA 1633
DB 123 CTGAGCTTACATAATGTGTGACAGCGTGTCTGCTCCCTCATGAATTTGGCTCCAAATGA 182
QY 1634 ATGAATACTTTCATGAGCAGTTGTAGCAGGCGCTGACCACAGATTTCCAGAGGCGCAGGT 1693
DB 183 ATGAATACTTTCATGAGCAGTTGTAGCAGGCGCTGACCACAGATTTCCAGAGGCGCAGGT 242
QY 1694 GTGATCCACAGACTTGAAGTCAAAAGTTCAAAAGATGAAGAATCAGGGTAGCTGACC 1753
DB 243 GTGATCCACAGACTTGAAGTCAAAAGTTCAAAAGATGAAGAATCAGGGTAGCTGACC 302
QY 1754 ATGTTGGCAGATACTATAATGAGACACAGAAAGTGTGCATGGCCCAAGACAGGACCT 1813
DB 303 ATGTTGGCAGATACTATAATGAGACACAGAAAGTGTGCATGGCCCAAGACAGGACCT 362
QY 1814 CCAGCCAGGCTTCATTATGCACTTGTGCTGCAAAAGAAAGTCTAGGTTTAAAGGCTGT 1873
DB 363 CCAGCCAGGCTTCATTATGCACTTGTGCTGCAAAAGAAAGTCTAGGTTTAAAGGCTGT 422
QY 1874 GCCAGAACCCATCCCAATAAAGAGACCGAGTGTGAAGTCAATTTGAATCTAGTGTAGG 1933
DB 423 GCCAGAACCCATCCCAATAAAGAGACCGAGTGTGAAGTCAATTTGAATCTAGTGTAGG 482

QY 1934 AGACTTGAGTACAGCAGTGAAGACTGTGTGGGCAACGGGGGACAGTGGTACTTGTAAACC 1993
DB 483 AGACTTGAGTACAGCAGTGAAGACTGTGTGGGCAACGGGGGACAGTGGTACTTGTAAACC 542
QY 1994 TTTAA 1998
DB 543 TTTAA 547

RESULT 17
AM003948/c
LOCUS
DEFINITION
wq84h01.x1 NCI CGAP GC6 Homo sapiens CDNA clone IMAGE:2478769 3'
similar to TR:O15430 O15430 LEUKOCYTE ANTIGEN CD84. ; mRNA
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AM003948
AM003948
AM003948.1 GI:5850864
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
1 (bases 1 to 672)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 467.

FEATURES

source

1. .672
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2478769"
/issue_type="pooled germ cell tumors"
/lab_host="DH10B"
/clone_lib="NCI_CGAP GC6"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA
from the normalized library NCI CGAP GC4 was prepared, and
ss circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (clonoids
1257096-1258631, 1469064-1470983, and 1475592-1476743).
Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match

Best Local Similarity 99.8%; Score 532; DB 1; Length 672;
Matches 582; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 746 CCTCTGCTCAGTCTCTTTGTACTGGGCTATTCTTTGGTTTCTGAAGAGAGAGACA 805
DB 583 CCTCTGCTCAGTCTCTTTGTACTGGGCTATTCTTTGGTTTCTGAAGAGAGAGACA 524
QY 806 AGAAGATACATTGAAGAGAGAGAGAGATGACATTGTCCGGAACCTCTAACATATG 865
DB 523 AGAAGATACATTGAAGAGAGAGAGAGATGACATTGTGTCCGGAACCTCTAACATATG 464

Qy	866	CCCCATTCTGGAGAGACACAGATGACACACAATCCCTCAGCTAATAGAACAACTCT	925
Db	463	CCCCATTCTGGAGAGACACAGATGACACACAATCCCTCAGCTAATAGAACAACTCT	404
Qy	926	AAAGGAAGATCCAGCAATAACGGTTTACTCCACTGTGGAATACCGAAAAAGATGAAAA	985
Db	403	AAAGGAAGATCCAGCAATAACGGTTTACTCCACTGTGGAATACCGAAAAAGATGAAAA	344
Qy	986	TCCCCACTCACTGCTCAGATGCGACACACCAAGGCTATTGCTATGAGATGTTAT	1045
Db	343	TCCCCACTCACTGCTCAGATGCGACACACCAAGGCTATTGCTATGAGATGTTAT	284
Qy	1046	CTAGACAGAGTGACACTCCCTAAGTCTGTCTCAAAAAAACAATTTCTCGCCCAA	1105
Db	283	CTAGACAGAGTGACACTCCCTAAGTCTGTCTCAAAAAAACAATTTCTCGCCCAA	224
Qy	1106	GAAAAACAATCAGAAAGATTCATCTGATTGACTAGAAACATCAAGGAGAAATGAAACCGT	1165
Db	223	GAAAAACAATCAGAAAGATTCATCTGATTGACTAGAAACATCAAGGAGAAATGAAACCGT	164
Qy	1166	TGACTTTTTCAGAGATAAATTATCTGATGCTTCTTATGATTAAAGTTCGTAATTC	1225
Db	163	TGACTTTTTCAGAGATAAATTATCTGATGCTTCTTATGATTAAAGTTCGTAATTC	104
Qy	1226	CATCCACTGCTGAGAAATCTCCTCAAAACCAGAGGTTTAATCACTTCATCCCAAAAATG	1285
Db	103	CATCCACTGCTGAGAAATCTCCTCAAAACCAGAGGTTTAATCACTTCATCCCAAAAATG	44
Qy	1286	GGATTGTGAATGTCAGCAAAACCATAAAAAAGTGTAGAGT	1328
Db	43	GGATTGTGAATGTCAGCAAAACCATAAAAAAGTGTAGAGT	1

RESULT 18
CD366944/c 739 bp mRNA linear EST 05-AUG-2004
LOCUS UI-H-FT2-bjp-i-06-0-UI.s1 NCI CGAP_FT2 Homo sapiens cDNA clone
DEFINITION UI-H-FT2-bjp-i-06-0-UI 3', mRNA sequence.
ACCESSION CD366944
VERSION CD366944.1 GI:31151034
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 739)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
Source
1. 739
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT2-bjp-i-06-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP_FT2"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI CGAP_FT2 is a subtracted cDNA library constructed from

a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT2
TAG_SEQ=GGCCATGCCG"

Qy	414	TACAGCACCTGTCAAGCCTTAAGTCAACCATGGGTCTGACAGACAATAAGATGGACC	473
Db	684	TACAGCACCTGTCAAGCCTTAAGTCAACCATGGGTCTGACAGACAATAAGATGGACC	625
Qy	474	TGTGTGACCAATCTGACATGCTGCATGGAACATGGGGAAGAGATGTATTATACCTGG	533
Db	624	TGTGTGACCAATCTGACATGCTGCATGGAACATGGGGAAGAGATGTATTATACCTGG	565
Qy	534	AAGGCCCTGGGGCAAGCAGCCCAATGAGTCCCATATATGGGTTCATCTCCCATCTCTGG	593
Db	564	AAGGCCCTGGGGCAAGCAGCCCAATGAGTCCCATATATGGGTTCATCTCCCATCTCTGG	505
Qy	594	AGATGGGAGAAAGTGATATGACCTTCATCTGCGTTGCCAGAAACCTGTGACAGAAAC	653
Db	504	AGATGGGAGAAAGTGATATGACCTTCATCTGCGTTGCCAGAAACCTGTGACAGAAAC	445
Qy	654	TTCTCAAGCCCCCATCTTGCCAGAAAGCTGTGAAAGTGTCTGTGATGACCCAGATTCC	713
Db	444	TTCTCAAGCCCCCATCTTGCCAGAAAGCTGTGAAAGTGTCTGTGATGACCCAGATTCC	385
Qy	714	TCCATGGTCTCTCTGTCTCTCTGTGGTGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCT	773
Db	384	TCCATGGTCTCTCTGTCTCTCTGTGGTGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCT	325
Qy	774	CTATTCTTTGGTTTCTGAAGAGAGAGACCAAGAGATGATGAAAGAGAGAGAGA	833
Db	324	CTATTCTTTGGTTTCTGAAGAGAGAGACCAAGAGATGATGAAAGAGAGAGAGA	265
Qy	834	GTGACATTTGTGCGAAACTCTTAACATATGCCCCCATTTCTGAGAGAAACACAGAGTAC	893
Db	264	GTGACATTTGTGCGAAACTCTTAACATATGCCCCCATTTCTGAGAGAAACACAGAGTAC	205
Qy	894	GACACAATCCCTCACACTTAATAGAACATCTTAAGAGAGATCCAGCAATACGGTTTAC	953
Db	204	GACACAATCCCTCACACTTAATAGAACATCTTAAGAGAGATCCAGCAATACGGTTTAC	145
Qy	954	TCCACTGTGGAATACCGAAAAAGATGAAAAATCCCACTCACTGCTCAGATGCCAGAC	1013
Db	144	TCCACTGTGGAATACCGAAAAAGATGAAAAATCCCACTCACTGCTCAGATGCCAGAC	85
Qy	1014	ACACCAAGGCTATTGGCTATGAGAAATGT	1042
Db	84	ACACCAAGGCTATTGGCTATGAGAAATGT	56


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RESULT 19
CD520950
LOCUS
DEFINITION
CD520950      842 bp      mRNA      linear      EST 06-JUN-2003
AGENCOURT_14356154 NIH_MGC_191 Homo sapiens cDNA clone
IMAGE:304I3029 5', mRNA sequence.
CD520950
VERSION
CD520950.1   GI:31452668
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 842)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: NDCM207 row: f column: 14
High quality sequence stop: 464.
Location/Qualifiers
1..842

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30413029"
/tissue_type="pooled"
/lab_host="DH10B (T1 phage-resistant)"
/clone_id="NIH_MGC_191"
/note="vector: pDNR-LIB; Site_1: SfiI (ggccattatggcc);
Site_2: SfiI (ggcgccctggcc); Library is oligo-dT primed
and directionally cloned. PBMC - Peripheral Blood
Mononuclear Cells. RNA was pooled from 3/6hour stimulation
with PMA adn Ionomycin. 5' and 3' adaptors were used in
cloning as follows: 5' adaptor sequence:
5'-CACGGCCATATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCCGAGCGCGCCGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.69
kb (range 0.70-5.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH MGC Library."

```

Query Match	19.2%;	Score 519;	DB 6;	length 842;
Best Local Similarity	99.8%;	Pred. No. 5e-215;		
Matches 569;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	25	GACTTCAGAGAGCAATATGCTGCTTCCCCAACATGCTCACCCTCATCTATATCCTTT	84	
Db	5	GACTTCAGAGAGCAATATGCTGCTTCCCCAACATGCTCACCCTCATCTATATCCTTT	64	
QY	85	GGCAGCTCACAGGGTCAAGCCTCTGAGCCCGTGAAAGAGCTGTCGGTTCGGTTGGTG	144	
Db	65	GGCAGCTCACAGGGTCAAGCCTCTGAGCCCGTGAAAGAGCTGTCGGTTCGGTTGGTG	124	
QY	145	GGGCCGTGACTTTCGCCCTGTAAGTCCAAAGTAAAGCAAGTTGACTCTATTGTCTGGACTT	204	
Db	125	GGGCCGTGACTTTCGCCCTGTAAGTCCAAAGTAAAGCAAGTTGACTCTATTGTCTGGACTT	184	
QY	205	TCAACACAAACCCCTCTTGTGCACCATACAGCCAGAGGGGGCACTATCATAGTGACCACAA	264	

Db	185	TCACACAACCCCTCTGTGCACCATACAGCCAGAAAGGGGCACTATCATAGTGCACCCAAA	244
Qy	265	ATCGTAATAGGGAGAGAGTAGACTTCCAGATGGAGGCTACTCCCTGAAGCTCAGCAAAAC	324
Db	245	ATCGTAATAGGGAGAGAGTAGACTTCCAGATGGAGGCTACTCCCTGAAGCTCAGCAAAAC	304
Qy	325	TGAGAAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCTCAGCAGAC	384
Db	305	TGAGAAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCTCAGCAGAC	364
Qy	385	CTTCCACCCAGGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAGCCTAAAGTCAACA	444
Db	365	CTTCCACCCAGGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAGCCTAAGTCAACA	424
Qy	445	TGGGCTGCAGAGCAATAAGATGGCACTGTGTGACCAATCTGACATGCTGCATGGAAC	504
Db	425	TGGGCTGCAGAGCAATAAGATGGCACTGTGTGACCAATCTGACATGCTGCATGGAAC	484
Qy	505	ATGGGGAAGAAGATGTGATTTTATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTCCC	564
Db	485	ATGGGGAAGAAGATGTGATTTTATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTCCC	544
Qy	565	ATAATGGGTCCATCTCCTCCCATCTCCTGGA	594
Db	545	ATAATGGGTCCATCTCCTCCCATCTCCTGGA	574

RESULT	20
BM800975	
LOCUS	
DEFINITION	BM800975 1050 bp mRNA linear EST 05-MAR-2002 AGENCOURT_6420769 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5541322 5', mRNA sequence.
ACCESSION	BM800975
VERSION	BM800975.1 GI:19117798
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 1050) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
AUTHORS	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
TITLE	Tissue Procurement: ATCC/DCTD/DTF
JOURNAL	cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
COMMENT	Plate: L1AM12238 row: n column: 11 High quality sequence stop: 584.

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FEATURES
  source
    Location/Qualifiers
      1..1050
        /organism="Homo sapiens"
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        /db_xref="taxon:9606"
        /clone="IMAGE:5541322"
        /tissue_type="melanotic melanoma"
        /lab_host="DH10B (phage-resistant)"
        /clone_1ib="NIH_MGC_72"
        /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
        Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
        Average insert size 2 kb. Library constructed by Life
        Technologies."
ORIGIN
Query Match      19.0%; Score 515; DB 4; Length 1050;
Best Local Similarity 99.8%; Pred. No. 2.7e-213;
Matches 565; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY	417	GAGCACTGTCAAAGCCTAAAGTCACCATGGGCTCTGCAGAGCAATTAAGATGGCACTGT	476
Db	51	GAGCACTGTCAAAGCCTAAAGTCACCATGGGCTCTGCAGAGCAATTAAGATGGCACTGT	110
QY	477	GTGACCAATCTGACATGCTGCATGGAACATGGGGAAGAGATGTGATTTAACCTGGAAG	536
Db	111	GTGACCAATCTGACATGCTGCATGGAACATGGGGAAGAGATGTGATTTAACCTGGAAG	170
QY	537	GCCCTGGGGCAAGCAGCAATGATGCCATAATGGGTCCATCCTCCCACTCTCCTGAGA	596
Db	171	GCCCTGGGGCAAGCAGCAATGATGCCATAATGGGTCCATCCTCCCACTCTCCTGAGA	230
QY	597	TGGGGAAGAAAGTGATATGACCTTCACTGCGTTGCCAGGAACCTGTCAAGAAACTTC	656
Db	231	TGGGGAAGAAAGTGATATGACCTTCACTGCGTTGCCAGGAACCTGTCAAGAAACTTC	290
QY	657	TCAAGCCCCCATCTCTGGCCAGGAAGCTGTGAAAGTGCTGTGATGACCCAGATTCTCC	716
Db	291	TCAAGCCCCCATCTCTGGCCAGGAAGCTGTGAAAGTGCTGTGATGACCCAGATTCTCC	350
QY	717	ATGTCCTCCTGTGTCTCCTGTGGTGCCCCCTCCTGCTCAGTCTTTGTACTGGGGCTA	776
Db	351	ATGTCCTCCTGTGTCTCCTGTGGTGCCCCCTCCTGCTCAGTCTTTGTACTGGGGCTA	410
QY	777	TTTCTTTGGTTTCTGAAGAGAGAGACAAGAAGTACATTGAAGAGAGAAGAAGAGTG	836
Db	411	TTTCTTTGGTTTCTGAAGAGAGAGACAAGAAGTACATTGAAGAGAGAAGAAGAGTG	470
QY	837	GACATTGTGGGAAACTCCTAACATATGCCCCCATTTCTGAGAGAAACAGAGTACGAC	896
Db	471	GACATTGTGGGAAACTCCTAACATATGCCCCCATTTCTGCGAGAAACAGAGTACGAC	530
QY	897	ACAATCCCTCACACTAATAGAACATCTTAAAGGAAGATCCAGCAAAATACGGTTTACTCC	956
Db	531	ACAATCCCTCACACTAATAGAACATCTTAAAGGAAGATCCAGCAAAATACGGTTTACTCC	590
QY	957	ACTGTGGAATATCCGAAAAAGATGGA	982
Db	591	ACTGTGGAATATCCGAAAAAGATGGA	616

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RESULT 21
CD366908/c
LOCUS
DEFINITION
CD366908 785 bp mRNA linear EST 05-AUG-2004
UI-H-FT2-bjp-a-22-0-UI.s1 NCI CGAP_FT2 Homo sapiens cDNA clone
UI-H-FT2-bjp-a-22-0-UI 3', mRNA sequence.
ACCESSION
CD366908
VERSION
CD366908.1 GI:31150998
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 785)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html
Seq primer: M13 FORWARD
POLY=A=Yes.
FEATURES
location/Qualifiers
1..785
/organism="Homo sapiens"
/mol_type="mRNA"

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/db_xref="taxon:9606"
/clone="UI-H-FT2-bjp-a-22-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_1b="NCI_CGAP_F12"
/notes="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI_CGAP_F12 is a subtracted cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT2
TAG_SEQ=GGCCATGCCG"

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ORIGIN

Query Match	18.9%;	Score 512;	DB 6;	Length 785;
Best Local Similarity	99.8%;	Pred. NO. 5.7e-212;		
Matches 562;	Conservative	0;	Mismatches 1;	Indels 0;
			Gaps	0;

QY	527	TACCTGAAGGCCCTTGGGGCAAGCAGCCCAATGAGTCCCATTAATGGGTCCATCTCCCAT	586
Db	571	TACCTGAAGGCCCTGGGGCAAGCAGCCCAATGAGTCCCATTAATGGGTCCATCTCCCAT	512
QY	587	CTCCTGAGATGGGGAGAAAAGTATATGACTTCATCTGCGTTGCCAGAACCTGTCTAG	646
Db	511	CTCCTGAGATGGGGAGAAAAGTATATGACTTCATCTGCGTTGCCAGAACCTGTCTAG	452
QY	647	CAGAACTTCTCAAGCCCCCATCCTTGCCAGAGACTCTGTGAAGTGTCTGATGACCC	706
Db	451	CAGAACTTCTCAAGCCCCCATCCTTGCCAGAGACTCTGTGAAGTGTCTGATGACCC	392
QY	707	AGATTCTCCATGGTCCCTCTGTGTCTCCTGTGGTGCCCCCTCCTGCTCAGTCTTTGT	766
Db	391	AGATTCTCCATGGTCCCTCTGTGTCTCCTGTGGTGCCCCCTCCTGCTCAGTCTTTGT	332
QY	767	ACTGGGGCTATTCTTTGGTTTCTGAAGAGAGAGACAAGAGATACATTGAAGAGAA	826
Db	331	ACTGGGGCTATTCTTTGGTTTCTGAAGAGAGAGACAAGAGATACATTGAAGAGAA	272
QY	827	GAAGAGATGGACATTTGTGCGGAACTCCTAACATATGCCCCCATTTGAGAGAAACAC	886
Db	271	GAAGAGATGGACATTTGTGCGGAACTCCTAACATATGCCCCCATTTGAGAGAAACAC	212
QY	887	AGAGTACGACACATCCCTCACACTAATAGAACATCCTAAAGAAAGATCCAGCAAAATAC	946
Db	211	AGAGTACGACACATCCCTCACACTAATAGAACATCCTAAAGAAAGATCCAGCAAAATAC	152
QY	947	GGTTACTCCACTGTGGAAATACCGAAAAAGATGGAAAAATCCCCACTACTGTCAAGAT	1006
Db	151	GGTTACTCCACTGTGGAAATACCGAAAAAGATGGAAAAATCCCCACTACTGTCAAGAT	92
QY	1007	GCCAGACACCAAGGCTATTGTGCTATGAGATGTTATCTAGACAGCAGTGCCTCCCC	1066

RESULT 22	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES	ORIGIN
AW963563	634 bp	mRNA	linear	EST 01-JUN-2000										
AW963563	EST375636	MAGE resequences, MAGH Homo sapiens cDNA, mRNA sequence.												
AW963563	GI:8153399													
EST.														
Homo sapiens (human)														
Homo sapiens														
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;														
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.														
1 (bases 1 to 634)														
Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C.,														
Holt, I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and														
Quackenbush, J.														
Assessment of gene expression patterns in a model of colon tumor														
metastasis using a 19,200 element cDNA microarray														
Unpublished (2000)														
Contact: John Quackenbush														
The Institute for Genomic Research														
9712 Medical Center Dr., Rockville, MD 20850, USA														
Tel: 301 838 3528														
Fax: 301 838 0208														
Email: johnq@tigr.org														
Plate: 189														
Seq primer: Reverse.														
Location/Qualifiers														
1..634														
/organism="Homo sapiens"														
/mol_type="mRNA"														
/db_xref="taxon:9606"														
/clone_id="MAGE resequences, MAGH"														
/note="Vector: pBluescriptsK"														
Query Match	18.4%	Score 498;	DB 2;	Length 634;										
Best Local Similarity	100.0%;	Pred. No. 7.4e-206;												
Matches 498;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;										
2 GAAAGTGGCTTCATTTTCAGTGGCTGACTTCCAGAGAGCAATATGGCTGTTCCCAACATG	61													
1 GAAAGTGGCTTCATTTTCAGTGGCTGACTTCCAGAGAGCAATATGGCTGTTCCCAACATG	60													
62 CCTCACCCTCATCTATATTCCTTTGGCAGCTCACAGGCTCAGAGCCTCTGGACCCGTGAA	121													
61 CCTCACCCTCATCTATATTCCTTTGGCAGCTCACAGGCTCAGAGCCTCTGGACCCGTGAA	120													
122 AGAGCTGGTGGTTCCTGGTGGTGGGCGGTGACTTTCCCTGAAAGTCCAAAGTAAGCA	181													
121 AGAGCTGGTGGTTCCTGGTGGTGGGCGGTGACTTTCCCTGAAAGTCCAAAGTAAGCA	180													
182 AGTTGACTTATTTGTCGAGCCTTCAACACAAACCCCTTGTCAACATACAGCCAGAGG	241													

Oy		422	CCTGTCMAAGCCTAAAGTCAACCATGGGTCTGCAGAGCAATAGAATGGCACCTGTGTGAC	481
Db		421	CCTGTCAAAGCCTAAAGTCAACCATGGGTCTGCAGAGCAATAAAGATGGCACCTGTGTGAC	480
Oy		482	CAATCTGACATGCTGCAT	499
Db		481	CAATCTGACATGCTGCAT	498
RESULT 23				
AI422743/c				
LOCUS				
DEFINITION	AI422743	594 bp	mRNA	linear EST 30-MAR-1999
	tcf29g12.x1	NCI CGAP Brn23	Homo sapiens	CDNA clone IMAGE:2097670 3'
	similar to TR:O15430	O15430	LEUKOCYTE ANTIGEN CD84.	; mRNA
	sequence.			
ACCESSION	AI422743			
VERSION	AI422743			
KEYWORDS	AI422743.1	GI:4268674		
SOURCE	EST.			
ORGANISM	Homo sapiens (human)			
	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	1 (bases 1 to 594)			
AUTHORS	NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.			
TITLE	National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGP), Tumor Gene Index			
JOURNAL	Unpublished (1998)			
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Insert Length: 1108 Std Error: 0.00 Seq primer: -40UP from G1bco High quality sequence stop: 445. Location/Qualifiers 1. 594 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:2097670" /tissue_type="glioblastoma (pooled)" /lab_host="DH10B" /clone_1lb="NCI_CGAP_Brn23" /note="Organ: brain; Vector: pTTT3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCATTCTGAAGTGGAGCCGCCCATATCTTTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTTT3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."			
FEATURES				
source				
ORIGIN				
Query Match	18.2%;	Score 492;	DB 1;	Length 594;
Best Local Similarity	99.7%;	Pred. No. 3.1e-203;		
Matches 592;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
Oy		486	CTGACATGCTGCATGGAACATGGGAGAGGATGTGATTATACCTGGAAGCCCTGGGG	545
Db		594	CTGACATGCTGCATGGAACATGGGAGAGGATGTGATTATACCTGGAAGCCCTGGGG	535
Oy		546	CAAGCAGCCAATGATCCCATATGGGTTCATCTCCCCTCTCTGAGATGGGGAGA	605

Db 534 CAAGCAGCCATGAGTCCCATATGGGTCCATCTCCNCATCTCTGGAGATGGGAGAA 475

Qy 606 AGTGATATGACCTTCATCTGCGTTGCCAGAACCTGTGACGACGAAAACTTCTCAAGCCCC 665

Db 474 AGTGATATGACCTTCATCTGCGTTGCCAGAACCTGTGACGACGAAAACTTCTCAAGCCCC 415

Qy 666 ATCCCTGGCAGGAAGCTCTGTGAAGGTGCTGTGATGACCCAGATTCTCCATGGTCTC 725

Db 414 ATCCCTGGCAGGAAGCTCTGTGAAGGTGCTGTGATGACCCAGATTCTCCATGGTCTC 355

Qy 726 CTGTGTCCTCTGTGGTGCCCTCTGCTCAGTCTCTTTGTACTGGGCTATTCTTTGG 785

Db 354 CTGTGTCCTCTGTGGTGCCCTCTGCTCAGTCTCTTTGTACTGGGCTATTCTTTGG 295

Qy 786 TTTCTGAAGAGAGAGACAGAAAGATACATTGAAGAGAAGAGAGATGGACATTTGT 845

Db 294 TCTCTGAAGAGAGAGACAGAAAGATACATTGAAGAGAAGAGAGATGGACATTTGT 235

Qy 846 CGGAAACTCTTAACATATGCCCCCATTTCTGAGAGAAACACAGATACGACAAATCCCT 905

Db 234 CGGAAACTCTTAACATATGCCCCCATTTCTGAGAGAAACACAGATACGACAAATCCCT 175

Qy 906 CACACTAATAGAACAACTCTTAAGGAAGATCCAGCAAAATACGGTTTACTCCACTGTGAA 965

Db 174 CACACTAATAGAACAACTCTTAAGGAAGATCCAGCAAAATACGGTTTACTCCACTGTGAA 115

Qy 966 ATACCGAAAAAGATGAAAAATCCCACTCACTGCTCAGATGCCAGACACCAAGGCTA 1025

Db 114 ATACCGAAAAAGATGAAAAATCCCACTCACTGCTCAGATGCCAGACACCAAGGCTA 55

Qy 1026 TTTGCCCTATGAAATGTTATCTAGACAGAGTCACTCCCTAAGTCTCTGCTC 1079

Db 54 TTTGCCCTATGAAATGTTATCTAGACAGAGTCACTCCCTAAGTCTCTGCTC 1

RESULT 24

BF026131 980 bp mRNA linear EST 10-OCT-2000

LOCUS 601669819P1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3952876 5',

DEFINITION mRNA sequence.

ACCESSION BF026131

VERSION BF026131.1 GI:10733843

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 980)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC/DCTD/DTP

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: image.lnl.nih.gov

Plate: L1CM823 row: e column: 05

High quality sequence stop: 690.

FEATURES

source

1..980

location/Qualifiers

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:3952876"

/tissue_type="melanotic melanoma"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH MGC 20"

/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 17.7%; Score 479; DB 2; length 980;

Best Local Similarity 99.8%; Pred. No. 1.4e-197;

Matches 599; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 424 TGTCAAGCCTAAAGTCACCATGGGTCTGCAGAGCAATAGAATGGCACCCTGTGTACCA 483

Db 1 TGTCAAGCCTAAAGTCACCATGGGTCTGCAGAGCAATAGAATGGCACCCTGTGTACCA 60

Qy 484 ATCTGACATGCTGCATGGAACATGGGGAAGAGATGATTATACCTGGAAGGCCCTGG 543

Db 61 ATCTGACATGCTGCATGGAACATGGGGAAGAGATGATTATACCTGGAAGGCCCTGG 120

Qy 544 GGCAAGCAGCCATGAGTCCCATATATGGGTCCATCTCCCATCTCTGAGATGGGAG 603

Db 121 GGCAAGCAGCCATGAGTCCCATATATGGGTCCATCTCCCATCTCTGAGATGGGAG 180

Qy 604 AAGTGATATGACCTTCATCTGCGTTGCCAGGAACCTGTCCAGACGAACCTTCTCAAGCC 663

Db 181 AAGTGATATGACCTTCATCTGCGTTGCCAGGAACCTGTCCAGACGAACCTTCTCAAGCC 240

Qy 664 CCATCTCTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCATGGTCC 723

Db 241 CCATCTCTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCATGGTCC 300

Qy 724 TCTGTGTCTCTGTGTGGTGGCCCTCTGCTCAGTCTCTTTGTACTGGGCTATTCTTT 783

Db 301 TCTGTGTCTCTGTGTGGTGGCCCTCTGCTCAGTCTCTTTGTACTGGGCTATTCTTT 360

Qy 784 GGTTCCTGAAGAGAGAGACAAGAAGTACATTGAAGAGAAGAGAGTGGACATT 843

Db 361 GGTTCCTGAAGAGAGAGACAAGAAGTACATTGAAGAGAAGAGAGTGGACATT 420

Qy 844 GTGGGAAACTCCTAACATA-TGCCCCCATTTCTGAGAGAACACAGAGTACGACAAATC 902

Db 421 GTGGGAAACTCCTAACATA-TGCCCCCATTTCTGAGAGAACACAGAGTACGACAAATC 480

Qy 903 CCTCACACTAATAGAACAACTCTAAAGAGATCCAGCAATACGGTTTACTCCACTGTG 962

Db 481 CCTCACACTAATAGAACAACTCTAAAGAGATCCAGCAATACGGTTTACTCCACTGTG 540

Qy 963 GAAATACCGAAAAAGATGAAAAATCCCACTCACTGCTCAAGATGCCAGACACCAAGG 1022

Db 541 GAAATACCGAAAAAGATGAAAAATCCCACTCACTGCTCAAGATGCCAGACACCAAGG 600

RESULT 25

AW293413/c 534 bp mRNA linear EST 16-JAN-2000

LOCUS UI-H-B12-ah1-h-12-0-UI-s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone

DEFINITION IMAGE:2727407 3', mRNA sequence.

ACCESSION AW293413

VERSION AW293413.1 GI:6700049

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 534)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first

strand cDNA and therefore this may represent a bonafide poly A
tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:
NCI-CGAP clone distribution information can be found through the
I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward
POLYA=Yes.

FEATURES
Source

1. 534
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2727407"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_Sub4"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not 1; Site 2: Eco RI; The
NCI_CGAP_Sub4 library is a subtracted library derived from
the NCI_CGAP_Sub2 library which is a subtracted library
derived from the NCI_CGAP_Sub1 library, which is a
subtracted library derived from BI. BI constitutes a
mixture of 21 normalized or subtracted NCI_CGAP
libraries: NCI_CGAP_Co4, NCI_CGAP_Pr22, NCI_CGAP_Pr28,
NCI_CGAP_Co10, NCI_CGAP_Co16, NCI_CGAP_Kid5,
NCI_CGAP_Kid12, NCI_CGAP_Kid3, NCI_CGAP_Kid11,
NCI_CGAP_Lym2, NCI_CGAP_Br2, NCI_CGAP_Co8, NCI_CGAP_CLL1,
NCI_CGAP_Le12, NCI_CGAP_Br23, NCI_CGAP_Lu5,
NCI_CGAP_Lu24, NCI_CGAP_Lu19, NCI_CGAP_GC4, NCI_CGAP_GC6,
NCI_CGAP_Brn25. These 21 libraries were pooled and a
single-stranded DNA preparation of the resulting mixture
was used as a tracer in a subtractive hybridization with
a driver whose composition is detailed below:
NCI_CGAP_Kid3 pool 1 : LLAM 3334-3337, 3682-3683,
3798-3803 (IMAGE cloneids 1322376-1323911,
1456008-1456775, 1500552-1502855) NCI_CGAP_Kid5 pool 1 :
LLAM 3338-3342, 3722-3725, 3776-3778 (IMAGE cloneids
1323912-1325831, 1471368-1472903, 1492104-1493255)
NCI_CGAP_Lu5 pool 1 : LLAM 3575-3582, 3851-3854 (IMAGE
cloneids 1414920-1417991, 1520904-1522439) NCI_CGAP_GC4
pool 1 : LLAM 3164-3167, 3716-3720, 3733-3735 (IMAGE
cloneids 1257096-1258631, 1469064-1470983,
1475592-1476743) NCI_CGAP_Pr22 pool 1 : LLAM 2457-2459,
2758-2759, 3062-3068 (IMAGE cloneids 985608-986759,
1101192-1101959, 1217928-1220615) NCI_CGAP_Co10 pool 1 :
LLAM 2644-2653, 2871-2872 (IMAGE cloneids 1057416-1061255,
114584-1145351) Subtraction was performed as previously
described [Bonaldo, Lennon & Soares (1996) : Normalization
and Subtraction: Two Approaches To Facilitate Gene
Discovery. Genome Research 6, 791-806.]
TAG_TISSUE=germ cell
TAG_LIB=NCI_CGAP_GC4
TAG_SEQ=AAATC"

ORIGIN

Query Match 17 3%; Score 467; DB 2; Length 534;
Best Local Similarity 99.8%; Pred. No. 2.5e-192;
Matches 517; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1521 TGACAAAATGATGTAATTAATGGCTCTATAAATATGTGCCAGACATATGCTGAGCT 1580
DB 534 TGACAAAATGATGTAATTAATGGCTCTATAAATATGTGCCAGACATATGCTGAGCT 475
OY 1581 TACACTAATGTCAGACGTGCTGTCTGCCCTCATGAATTTGGCTCCAATGAATGAAT 1640
DB 474 TACATTAAATGTCAGACGTGCTGTCTGCCCTCATGAATTTGGCTCCAATGAATGAAT 415
OY 1641 ACTTCATGAGCAGTTGTAGCAGGCTGACACACAGATTCACAGAGGGCCAGGTGTGATC 1700
DB 414 ACTTCATGAGCAGTTGTAGCAGGCTGACACACAGATTCACAGAGGGCCAGGTGTGATC 355
OY 1701 CACAGGACTGAGGTCAGAGTTCAAGATGAAGATCAAGGCTAGCTGACCATGTTTG 1760
DB 354 CACAGGACTGAGGTCAGAGTTCAAGATGAAGATCAAGGCTAGCTGACCATGTTTG 295

OY 1761 GCAGATACTATAATGAGACACAGAGTGTGCATGGCCCAAGACAGACACTCCAGCCA 1820
DB 294 GCAGATACTATAATGAGACACAGAGTGTGCATGGCCCAAGACAGACACTCCAGCCA 235
OY 1821 GGCTCATTTATGACACTGTGTCTGCAAAAGAAAGTCTAGGTTTAAAGCTGTGCCAGAA 1880
DB 234 GGCTCATTTATGACACTGTGTCTGCAAAAGAAAGTCTAGGTTTAAAGCTGTGCCAGAA 175
OY 1881 CCCATCCCAATTAAGAGACCGAGTCTGAAGTCACATTTGAATCTAGTGTAGAGACTTG 1940
DB 174 CCCATCCCAATTAAGAGACCGAGTCTGAAGTCACATTTGAATCTAGTGTAGAGACTTG 115
OY 1941 GAGTCAGCAGTGAAGACTGTGTGGGCAAGGGGGCAGTGGTACTTGTAAACCTTTAAG 2000
DB 114 GAGTCAGCAGTGAAGACTGTGTGGGCAAGGGGGCAGTGGTACTTGTAAACCTTTAAG 55
OY 2001 ATGTTAATTCATTCAATAGATATTATTAAACCTTA 2038
DB 54 ATGTTAATTCATTCAATAGATATTATTAAACCTTA 17

RESULT 26
AA921765/c
LOCUS
DEFINITION
om43g11.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:1543844 3', mRNA sequence.
AA921765
ACCESSION
AA921765.1 GI:3069074
VERSION
AA921765.1
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE
1 (bases 1 to 444)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)

JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1101 Std Error: 0.00
Seq primer: -40m13 fwd. RT from Amersham
High quality sequence stop: 443.

FEATURES
source

1. 444
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1543844"
/lab_host="DH10B"
/clone_lib="Soares_NFL_T_GBC_S1"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBHL19W, testis NHT, and B-cell
NCI_CGAP GCBI) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 16 3%; Score 442; DB 1; Length 444;
Best Local Similarity 100.0%; Pred. No. 2.1e-181;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 740 GGTGCCCTCTGCTCAGTCTCTTTGTAAGTGGGCTATTCTTTGTTCTGAAGAGAGA 799

|||||
Db 443 GGTGCCCCCTCTGCTCAGTCTTGTGTAAGGGCTATTCTTGTGTTCTGAAGAGAGA 384
Qy 800 GAGACAAGAGAGTACATTGAAGAGAGAGAGAGTGCACATTTGCGGAAACTCCTAA 859
Db 383 GAGACAAGAGAGTACATTGAAGAGAGAGAGAGTGCACATTTGCGGAAACTCCTAA 324
Qy 860 CATATGCCCCCATTTCTGGAGAGAACAGAGTACGACACAATCCCTCACTAATAGAAC 919
Db 323 CATATGCCCCCATTTCTGGAGAGAACAGAGTACGACACAATCCCTCACTAATAGAAC 264
Qy 920 AATCCTAAAGAGAGATCCAGCAATACGGTTTACTCCACTGTGGAATAACCGAAAAAGAT 979
Db 263 AATCCTAAAGAGAGATCCAGCAATACGGTTTACTCCACTGTGGAATAACCGAAAAAGAT 204
Qy 980 GAAAAATCCCCACTCACTGCTCAGGATGCCAGACACACCAAGGCTATTGCTTATGAGAA 1039
Db 203 GAAAAATCCCCACTCACTGCTCAGGATGCCAGACACACCAAGGCTATTGCTTATGAGAA 144
Qy 1040 TGTATCTAGACAGAGTGCACCTCCCTAAGTCTCTGCTCAAAAAAACAATTCTCGG 1099
Db 143 TGTATCTAGACAGAGTGCACCTCCCTAAGTCTCTGCTCAAAAAAACAATTCTCGG 84
Qy 1100 CCCAAGAAACAATCAGAGAATTGACTGATTGACTAGAAACAATCAGAGAAGATGAA 1159
Db 83 CCCAAGAAACAATCAGAGAATTGACTGATTGACTAGAAACAATCAGAGAAGATGAA 24
Qy 1160 GAACGTGACTTTTTCACAGA 1181
Db 23 GAACGTGACTTTTTCACAGA 2

RESULT 27
BG413358/c 484 bp mRNA linear EST 13-MAR-2001
LOCUS 7037c12.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3576214 3'
DEFINITION similar to TR:Q9Z178 Q9Z178 CD84 LEUKOCYTE ANTIGEN. ;, mRNA
sequence.
ACCESSION BG413358
VERSION BG413358.1 GI:13318911
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 484)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL, send email to:
info@image.lnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 479.
location/Qualifiers
1. 484
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3576214"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Kid11"
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
Plasmid DNA from the normalized library NCI_CGAP_Kid3 was

prepared, and as circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 1322376-1323911, 1456007-1456775, and
1500552-1502855). Subtraction by Bento Soares and M.
Fatima Bonaldo. "

ORIGIN
Query Match 16.0%; Score 433; DB 4; Length 484;
Best Local Similarity 99.8%; Pred. No. 1.7e-177;
Matches 483; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 596 ATGGGAGAAAGTATATGACCTTCATCTGCGTTGCCAGAAACCTGTACAGCAAACTT 655
Db 484 ATGGGAGAAAGTATATGACCTTCATCTGCGTTGCCAGAAACCTGTACAGCAAACTT 425
Qy 656 CTCAGCCCCCATCTTGCCAGAAAGCTCTGTGAAGGTGCTGTATGACCCAGATTCTC 715
Db 424 CTCAGCCCCCATCTTGCCAGAAAGCTCTGTGAAGGTGCTGTATGACCCAGATTCTC 365
Qy 716 CATGCTCCTCCTGTGCTCTGTGTGTCGCCCTCCTGCTCACTCTTTGTACTGGGCT 775
Db 364 CATGCTCCTCCTGTGCTCTGTGTGTCGCCCTCCTGCTCACTCTTTGTACTGGGCT 305
Qy 776 ATTTCTTGGTTTCTGAAGAGAGAGACAAGAAGTACATTGAAGAGAGAGAGT 835
Db 304 ATTTCTTGGTTTCTGAAGAGAGAGACAAGAAGTACATTGAAGAGAGAGAGT 245
Qy 836 GGACATTTGTGGGAAACTCTTAACATATATGCCCCCATTTCTGAGAGAACACAGAGTACGA 895
Db 244 GGACATTTGTGGGAAACTCTTAACATATATGCCCCCATTTCTGAGAGAACACAGAGTACGA 185
Qy 896 CACAATCCCTCACACTAATAGAACAAATCCTAAAGAGAGATCCAGCAATAACGGTTTACTC 955
Db 184 CACAATCCCTCACACTAATAGAACAAATCCTAAAGAGAGATCCAGCAATAACGGTTTACTC 125
Qy 956 CACTGTGAAATACCGAAAAAGATGAAAAATCCCACTCACTGCTCAGGATGCCAGAC 1015
Db 124 CACTGTGAAATACCGAAAAAGATGAAAAATCCCACTCACTGCTCAGGATGCCAGAC 65
Qy 1016 ACCAAGCTATTGCTTAAGAGATGTTATCTAGACAGAGTCACTCCCTAAGTCTCT 1075
Db 64 ACCAAGCTATTGCTTAAGAGATGTTATCTAGACAGAGTCACTCCCTAAGTCTCT 5
Qy 1076 GCTC 1079
Db 4 GCTC 1

RESULT 28
BE044439/c 630 bp mRNA linear EST 08-JUN-2000
LOCUS BE044439/c
DEFINITION ho45e03.x1 Soares NFL T_GBC_S1 Homo sapiens cDNA clone
IMAGE:3040348 3' similar to TR:O15430 O15430 LEUKOCYTE ANTIGEN
CD84. ;, mRNA sequence.
ACCESSION BE044439
VERSION BE044439.1 GI:8361492
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 630)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Seq primer: -40UP from Gibco

FEATURES High quality sequence stop: 433.
Location/Qualifiers
1. 630
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3040348"
/lab_host="DH10B"
/clone_lib="Soares_NFL T GBC S1"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI CGAP GCB1) were mixed, and as circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 15.9%; Score 430; DB 2; Length 630;
Best Local Similarity 99.8%; Pred. No. 3.4e-176;
Matches 480; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 857 TAACATATGCCCCCACTTCTGGAGAGACAGAGTACGACACATCCCTCAGACTAATAG 916
|||||
DB 505 TAACATATGCCCCCACTTCTGGAGAGACAGAGTACGACACATCCCTCAGACTAATAG 446

QY 917 AACATCCTAAAGAGATCCAGCAATACGGTTTACTCCACTGTGGAATAACCGAAAA 976
|||||
DB 445 AACATCCTAAAGAGATCCAGCAATACGGTTTACTCCACTGTGGAATAACCGAAAA 386

QY 977 GATGAAATCCCACTCACTGCTCAGATGCCAGACACACCAAGGCTATTGGCTATGA 1036
|||||
DB 385 GATGAAATCCCACTCACTGCTCAGATGCCAGACACACCAAGGCTATTGGCTATGA 326

QY 1037 GAATGTTATCTAGACAGCAGTGCACTCCCTAAGTCTCTGCTCAAAAAAAACAATTCT 1096
|||||
DB 325 GAATGTTATCTAGACAGCAGTGCACTCCCTAAGTCTCTGCTCAAAAAAAACAATTCT 266

QY 1097 CGGCCCAAGAAACAATCAGAGAATTCACTGATTGACTAGAAACATCAAGAAAT 1156
|||||
DB 265 CGGCCCAAGAAACAATCAGAGAATTCACTGATTGACTAGAAACATCAAGAAAT 206

QY 1157 GAAGACGTGACTTTTTCAGAGATAATTACTCTGATGCTTCTTTAGATTAAAGAT 1216
|||||
DB 205 GAAGACGTGACTTTTTCAGAGATAATTACTCTGATGCTTCTTTAGATTAAAGAT 146

QY 1217 TCGTAATTCATCCACTGCTGAGAAATCTCCTCAAAACCCAGAAAGTTTAATCACTTCATC 1276
|||||
DB 145 TCATTAATTCATCCACTGCTGAGAAATCTCCTCAAAACCCAGAAAGTTTAATCACTTCATC 86

QY 1277 CCAAAATGGATGTGTAATGTCAGCAAAACCATTAATAAAAGTCTTAGAATTCCTAT 1336
|||||
DB 85 CCAAAATGGATGTGTAATGTCAGCAAAACCATTAATAAAAGTCTTAGAATTCCTAT 26

QY 1337 A 1337
|
DB 25 A 25

RESULT 29
BG743877 846 bp mRNA linear EST 15-MAY-2001
LOCUS BG743877
DEFINITION 602722632F1 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:4849374 5',
mRNA sequence.
ACCESSION BG743877
VERSION BG743877.1 GI:14054530
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 846)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM1688 row: 0 column: 07
High quality sequence stop: 782.
Location/Qualifiers
1. 846

FEATURES
source
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4849374"
/tissue_type="natural killer cells, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 106"
/note="Organ: blood; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 15.6%; Score 421; DB 4; Length 846;
Best Local Similarity 99.4%; Pred. No. 2.8e-172;
Matches 621; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 921 ATCTAAAGAGATCCAGCAAAATCGTTTACTCCACTGTGGAATAACGAAAAAGATG 980
|||||
DB 15 ATCTAAAGAGATCCAGCAAAATCGTTTACTCCACTGTGGAATAACGAAAAAGATG 74

QY 981 GAAATCCCACTCACTGCTCAGATGCCAGACACACCAAGGCTATTGGCTATGAGAT 1040
|||||
DB 75 GAAATCCCACTCACTGCTCAGATGCCAGACACACCAAGGCTATTGGCTATGAGAT 134

QY 1041 GTTATCTAGACAGCAGTGCACTCCCTAAGTCTCTGCTCAAAAAAAACAATTCTCGGC 1100
|||||
DB 135 GTTATCTAGACAGCAGTGCACTCCCTAAGTCTCTGCTCAAAAAAAACAATTCTCGGC 194

QY 1101 CCAAGAAAAACAATCAGAGAATTCACTGATTGACTAGAAACATCAAGGAAGATGAAG 1160
|||||
DB 195 CCAAGAAAAACAATCAGAGAATTCACTGATTGACTAGAAACATCAAGGAAGATGAAG 254

QY 1161 AACGTTGACTTTTTCAGAGATAATTACTCTGATGCTTCTTTAGATTAAAGATTGCT 1220
|||||
DB 255 AACGTTGACTTTTTCAGAGATAATTACTCTGATGCTTCTTTAGATTAAAGATTGCT 314

QY 1221 AATTCATCACTGCTGAGAAATCTCTCAAAACCCAGAAAGTTTAATCACTTATCCCAA 1280
|||||
DB 315 AATTCATCACTGCTGAGAAATCTCTCAAAACCCAGAAAGTTTAATCACTTATCCCAA 374

QY 1281 AATGGGATTTGTAATGTCAGCAAAACCATTAATAAAAGTGTAGAAATTCCTATAGAA 1340
|||||
DB 375 AATGGGATTTGTAATGTCAGCAAAACCATTAATAAAAGTGTAGAAATTCCTATAGAA 434

QY 1341 ATGTAATGCAAGGTCACACATATTAAATGACAGCCTGTTGTAATTAATGATGGCTCCAGGT 1400
|||||
DB 435 ATGTAATGCAAGGTCACACATATTAAATGACAGCCTGTTGTAATTAATGATGGCTCCAGGT 494

QY 1401 CAGTGTCTGAGATTTCATTCATCCAGGGCTTGATGTCAGGATTATACCAAGAGTCTT 1460
|
Db 495 CAGTGTCTGAGATTTCATTCATCCAGGGCTTGATGTCAGGATTATACCAAGAGTCTG 554
QY 1461 GCTACGAGAGGGCAAGAACCAAAAAGACAGACAGCAAGTCCAGCAGAAGCAGATGCACC 1520
|
Db 555 GCTACGAGAGGGCAAGAACCAAAAAGACAGACAGCAAGTCCAGCAGAAGCAGATGCACC 614
QY 1521 TGACAAAAATGGATGTATTAAATTGG 1545
|
Db 615 TGACAAAAATGGATGTATTAAATTGG 639
RESULT 30
BU166292 876 bp mRNA linear EST 04-SEP-2002
LOCUS AGENCOURT_7944604 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6148660
DEFINITION 5', mRNA sequence.
ACCESSION BU166292
VERSION BU166292.1 GI:22680244
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13480 row: h column: 05
High quality sequence stop: 724.
location/Qualifiers
FEATURES
source 1..876
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6148660"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_72"
/note="Organ: skin; Vector: pCMV-Sport6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2 kb. Library constructed by Life
Technologies."
ORIGIN
Query Match 15.4%; Score 416; DB 5; Length 876;
Best Local Similarity 99.3%; Pred. No. 4.2e-170;
Matches 736; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
QY 947 GGTTACTCCACTGTGGAATATCCGAAAAAGATGGAATAATCCCACTCACTGCTCAGCAT 1006
|
Db 1 GGTTACTCCACTGTGGAATATCCGAAAAAGATGGAATAATCCCACTCACTGCTCAGCAT 60
QY 1007 GCCAGACACCAAGGCTATTGGCTTATGAGAATGTATCTAGACAGAGTGCACTCCCC 1066
|
Db 61 GCCAGACACCAAGGCTATTGGCTTATGAGAATGTATCTAGACAGAGTGCACTCCCC 120
QY 1067 TAAGTCTCTGCTCAAAAAAACAATCTCGGCCCAAGAAAAACAATCAGAAGAATTCA 1126
|
Db 121 TAAGTCTCTGCTC-AAAAAACAATCTCGGCCCAAGAAAAACAATCAGAAGAATTCA 179
QY 1127 CTGATTTGACTAGAAACATCAAGAGAGATGAAGACGTTGACTTTTTCAGAGATAAAT 1186
|

Db 180 CTGATTTGACTAGAAACATCAAGAGAAATGAAGAACGTTGACTTTTTCAGAGATAAAT 239
QY 1187 TATCTCTGATGCTCTTGTAGATTTAAGAGTTCGTAATTCATCCACTGCTGAGAAATCTC 1246
|
Db 240 TATCTCTGATGCTCTTGTAGATTTAAGAGTTCATTAATTCATCCACTGCTGAGAAATCTC 299
QY 1247 CTCAAACCCAGAAAGTTTAATCACTTCATCCCAAAAAATGGGATTGTGAATGTACAGAAAC 1306
|
Db 300 CTCAAACCCAGAAAGTTTAATCACTTCATCCCAAAAAATGGGATTGTGAATGTACAGAAAC 359
QY 1307 CATPAAAAAAAGTGCTTAGAAGTATTCCTATAGAAATGTAAATGCAAGGTCACACATATTA 1366
|
Db 360 CATPAAAAAAAGTGCTTAGAAGTATTCCTATAGAAATGTAAATGCAAGGTCACACATATTA 419
QY 1367 ATGACAGCCTGTTGTATTAAATGATGGCTCCAGGTCAGTGTCTGAGTTTCATTCCATCCC 1426
|
Db 420 ATGACAGCCTGTTGTATTAAATGATGGCTCCAGGTCAGTGTCTGAGTTTCATTCCATCCC 479
QY 1427 AGGCTTGGATGTCAGGATTATACCAAGAGCTTGTGCTACAGAGGGCAAGAACCAAA 1486
|
Db 480 AGGCTTGGATGTCAGGATTATACCAAGAGCTTGTGCTACAGAGGGCAAGAACCAAA 539
QY 1487 ACAGACAGACCAAGTCCAGCAGAAGCAGATGCACCTGACAAAAATGATGTATTAAATTGGC 1546
|
Db 540 ACAGACAGACCAAGTCCAGCAGAAGCAGATGCACCTGACAAAAATGATGTATTAAATTGGC 599
QY 1547 TCTATAAAGTATGTGCCCAGCACTATGCTGAGCTTACATAATTGGTCAGACGTCGTC 1606
|
Db 600 TCTATAAAGTATGTGCCCAGCACTATGCTGAGCTTACATAATTGGTCAGACATGTCGTC 659
QY 1607 TGCCCTCATGAATTTGGCTCCAAATGAATGAATGAATGACTTTCATGAGCAGTTGTAGAGGCC 1666
|
Db 660 TGCCCTCATGAATTTGGCTCCAAATGAATGAATGAATGACTTTCATGAGCAGTTGTAGAGGCC 719
QY 1667 TGACCAACAGATTCCACAGGG 1687
|
Db 720 TGACCAACAGATTCCACAGGG 740
RESULT 31
AI968397/c AI968397 527 bp mRNA linear EST 09-MAR-2000
LOCUS wu02f07.x1 NCI_CGAP_G66 Homo sapiens cDNA clone IMAGE:2515813 3',
DEFINITION mRNA sequence.
ACCESSION AI968397
VERSION AI968397.1 GI:5765215
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert length: 1050 Std Error: 0.00
Seg primer: -40UP from Gibco
High quality sequence stop: 449.
location/Qualifiers
FEATURES
source 1..527
/organism="Homo sapiens"

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2515813"
/issue_type="pooled germ cell tumors"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_GC6"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA
from the normalized library NCI_CGAP_GC4 was prepared, and
88 circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneids
1257096-1258631, 1469064-1470983, and 1475592-1476743).
Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 15.3%; Score 414; DB 1; Length 527;
Best Local Similarity 99.6%; Pred. No. 3.3e-169;
Matches 514; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 802 GACAGAAGAGTACATTGAAAGAGAAGAGAGTGCATTTGTCGGGAACTCCTAACA 861
DB 527 GACAGAAGAGTACATTGAAAGAGAAGAGAGTGCATTTGTCGGGAACTCCTAACA 468
OY 862 TATGCCCATTTCTGGAGAGAACACAGAGTACGACAAATCCCTCACACTTAATGAACAA 921
DB 467 TATGCCCATTTCTGGAGAGAACACAGAGTACGACAAATCCCTCACACTTAATGAACAA 408
OY 922 TCCTAAAGGAAGATCCAGCAATACGTTTACTCCACTGTGGAATACCGAATAAGATGG 981
DB 407 TCCTAAAGGAAGATCCAGCAATACGTTTACTCCACTGTGGAATACCGAATAAGATGG 348
OY 982 AAAATCCCACCTCACTGCTCAGATGCCAGACACCAAGGCTATTGCTATGAGAATG 1041
DB 347 AAAATCCCACCTCACTGCTCAGATGCCAGACACCAAGGCTATTGCTATGAGAATG 288
OY 1042 TTATCTAGACAGCAGTGCACCTCCCTAAGTCTCTGCTCAAAAAAACAATTCTCGGCC 1101
DB 287 TTATCTAGACAGCAGTGCACCTCCCTAAGTCTCTGCTCAAAAAAACAATTCTCGGCC 228
OY 1102 CAAGAAAAACAATCAGAAAGATTCACTGATTGTGATGAAACATCAAGAGAATGAAGA 1161
DB 227 CAAGAAAAACAATCAGAAAGATTCACTGATTGTGATGAAACATCAAGAGAATGAAGA 168
OY 1162 ACGTTGACTTTTTCAGAGTAATATCTCTGATGCTTCTTTAGATTTAAGATTGCTGA 1221
DB 167 ACGTTGACTTTTTCAGAGTAATATCTCTGATGCTTCTTTAGATTTAAGATTGCTGA 108
OY 1222 ATTCATCCACTGCTGAGAAATCTCTCAAAACCGAGAAGTTTAATCACTTCAATCCCAA 1281
DB 107 ATTCATCCACTGCTGAGAAATCTCTCAAAACCGAGAAGTTTAATCACTTCAATCCCAA 48
OY 1282 AATGGATTGTGAATGTCAAGCAAAACCATAAAAAAG 1317
DB 47 AATGGATTGTGAATGTCAAGCAAAACCATAAAAAAG 12

RESULT 32
BE467670/c 457 bp mRNA linear EST 27-JUL-2000
LOCUS BE467670
DEFINITION h267f07.x1 NCI_CGAP_lu24 Homo sapiens cDNA clone IMAGE:3213061 3',
mRNA sequence.
ACCESSION BE467670
VERSION BE467670.1 GI:9513445
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 457)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

JOURNAL Tumor Gene Index
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco.

FEATURES

Source

1..457
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3213061"
/issue_type="carcinoid"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_lu24"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; Plasmid DNA from the normalized
library NCI_CGAP_lu5 was prepared, and 88 circles were
made in vitro. Following HAP purification, this DNA was
used as tracer in a subtractive hybridization reaction.
The driver was PCR-amplified cDNAs from a pool of 5,000
clones made from the same library (cloneids
1414920-1417991 and 1520904-1522439). Subtraction by Bento
Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 15.0%; Score 406; DB 2; Length 457;
Best Local Similarity 99.8%; Pred. No. 1e-165;
Matches 456; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 854 TCCTAACATATGCCCCCATTTCTGAGAGAGACACAGAGTACGACACAATCCCTCACACTAA 913
DB 457 TCCTAACATATGCCCCCATTTCTGAGAGAGACACAGAGTACGACACAATCCCTCACACTAA 398
OY 914 TAGAACAATCCTTAAAGAGATCCAGCAATACGTTTACTCCACTGTGGAATACCGAA 973
DB 397 TAGAACAATCCTTAAAGAGATCCAGCAATACGTTTACTCCACTGTGGAATACCGAA 338
OY 974 AAAGATGAATAATCCCACTCACTGCTCAAGATGCCAGACACCAAGGCTATTGCTTA 1033
DB 337 AAAGATGAATAATCCCACTCACTGCTCAAGATGCCAGACACCAAGGCTATTGCTTA 278
OY 1034 TGAGATGTATCTAGACAGAGTGCACCTCCCTAAGTCTCTGCTCAAAAAAACAAT 1093
DB 277 TGAGATGTATCTAGACAGAGTGCACCTCCCTAAGTCTCTGCTCAAAAAAACAAT 218
OY 1094 TCTGGGCCCAAGAAACAATCAGAAAGATTCACTGATTGTGACTAGAAACATCAAGGAAG 1153
DB 217 TCTGGGCCCAAGAAACAATCAGAAAGATTCACTGATTGTGACTAGAAACATCAAGGAAG 158
OY 1154 AATGAAGACGTGACTTTTTCAGAGTAATATCTCTGATGCTTCTTTAGATTTAAG 1213
DB 157 AATGAAGACGTGACTTTTTCAGAGTAATATCTCTGATGCTTCTTTAGATTTAAG 98
OY 1214 AGTTGTAATTCATCCACTGCTGAGAAATCTCCTCAAAACCGAGAAGTTTAATCACTTC 1273
DB 97 AGTTGTAATTCATCCACTGCTGAGAAATCTCCTCAAAACCGAGAAGTTTAATCACTTC 38
OY 1274 ATCCCAAAATGGGATTGTGAATGTCAACCAACATA 1310
DB 37 ATCCCAAAATGGGATTGTGAATGTCAACCAACATA 1

RESULT 33
AW026300/c 657 bp mRNA linear EST 09-MAR-2000
LOCUS AW026300

DEFINITION	wv11d02.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2529219 3'
ACCESSION	similar to TR:O15430 O15430 LEUKOCYTE ANTIGEN CD84. ;, mRNA sequence.
VERSION	AW026300
KEYWORDS	AW026300.1 GI:5879830
SOURCE	EST.
ORGANISM	Homo sapiens (human)
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE	NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGA), Tumor Gene Index
JOURNAL COMMENT	Unpublished (1998) Contact: Robert Strausberg, Ph.D. Email: cgapbs-rt@mail.nih.gov Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: www-bio.lnl.gov/bdrp/image/image.html Insert length: 1097 Std Error: 0.00 Seq primer: -40UP from Gibco High quality sequence stop: 438.
FEATURES	location/Qualifiers
Source	1..657 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:2529219" /tissue_type="glioblastoma (pooled)" /lab_host="DH10B" /clone_lib="NCI_CGAP_Brn23" /note="Organ: brain; Vector: pRT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAGTCGTGAAGTGAGCGGCCGCATCTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT73 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."
ORIGIN	
Query Match	14.8%; Score 399; DB 2; Length 657;
Best Local Similarity	99.8%; Pred. No. 1.le-162;
Matches 449; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
OY	630 GCCAGGAACCCCTGTCAAGAAACTTCTCAAGCCCCCATCTTGCCAGGAAGCTCTGTGA 689
Db	450 GCCAGGAACCCCTGTCAAGAAACTTCTCAAGCCCCCATCTTGCCAGGAAGCTCTGTGA 391
OY	690 GGTCGTCTGATGACCCAGATTCTCCTCATGGTCTCTCTCTCTCTCTCTCTCTCTCTCT 749
Db	390 GGTCGTCTGATGACCCAGATTCTCCTCATGGTCTCTCTCTCTCTCTCTCTCTCTCTCT 331
OY	750 CTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTCTGAAGAGAGAGACAAGA 809
Db	330 CTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTCTGAAGAGAGAGACAAGA 271
OY	810 GAGTACATTGAAGAAGAAGAAGTGACATTGTTCGGAAACTCCTAACATATGCCCC 869
Db	270 GAGTACATTGAAGAAGAAGAAGTGACATTGTTCGGAAACTCCTAACATATGCCCC 211
OY	870 CATTTGAGAGAACACACAGTAACACAAATCCCTCACATAATAGAACAACTCTAAG 929
Db	210 CATTTGAGAGAACACAGTAACACAAATCCCTCACATAATAGAACAACTCTAAG 151

QY	930	GAAGATCCAGCAAAATACGGTTTACTCTCCACTGTGAAATAACCGAAAAAGATGAAAAATCCC	989
Db	150	GAAGATCCAGCAAAATACGGTTTACTCTCCACTGTGAAATAACCGAAAAAGATGAAAAATCCC	91
QY	990	CACTCACTGCTCAGCATGCGCCAGACACACCAAGGCTATTGGCTATGAGAATGTATTCTAG	1049
Db	90	CACTCACTGCTCAGCATGCGCCAGACACACCAAGGCTATTGGCTATGAGAATGTATTCTAG	31
QY	1050	ACAGCAGTGCACTCCCTTAAGTCTGTGCTC	1079
Db	30	ACAGCAGTGCACTCCCTTAAGTCTGTGCTC	1
RESULT 34			
BQ898498		668 bp mRNA linear	EST 16-AUG-2002
LOCUS			
DEFINITION		AGENCOURT 8228971 lupski_dorsal_root_ganglion Homo sapiens CDNA	
ACCESSION		clone IMAGE:6182103 5', mRNA sequence.	
VERSION		BQ898498	
KEYWORDS		BQ898498.1 GI:22290512	
SOURCE		EST.	
ORGANISM		Homo sapiens (human)	
REFERENCE		Homo sapiens	
AUTHORS		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
TITLE		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
JOURNAL		1 (bases 1 to 968)	
COMMENT		NIH-MGC http://mgs.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgaabs-r@mail.nih.gov Tissue Procurement: Dr. James R. Lupski CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM13567 row: i column: 16 High quality sequence stop: 611. Location/Qualifiers 1. 968 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:6182103" /sex="male" /tissue_type="dorsal root ganglia" /dev_stage="adult, 36 yr" /lab_host="DH10B" /clone_lib="lupski_dorsal root ganglion" /notes="Vector: PCMV-SPORT6 (Life Technologies); Site_1: NotI; Site_2: SalI; cDNA made by oligo-dT priming. Directionally cloned using the following adaptors: 5'-TCGACCCACGCGTCCG-3' and 5'-GACTAGTCTTAGATCGGAGCGGCCCT(15)-3'. Size selected > 1 kb for average insert length 1.7 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life Technologies."	
FEATURES			
Source			
ORIGIN			
Query Match	14.7%;	Score 398;	DB 5; Length 968;
Best Local Similarity	99.6%;	Pred. No. 2.9e-162;	
Matches 568;	Conservative 0;	Mismatches 1;	Indels 1; Gaps 1;
QY	915	AGACAATCTCTAAGAGAGATCCAGCAAAATACGTTTACTCCACTGTGAAATACGAAA	974
Db	194	AGACAATCTCTAAGAGAGATCCAGCAAAATACGTTTACTCCACTGTGAAATACGAAA	253
QY	975	AAGATGAAAATCCCCCACTCACTGCTCAGCATGCCAGACACACCAAGGCTATTGGCTAT	1034

ADDITIONAL INFORMATION	TITLE	JOURNAL	COMMENT
http://imgc.mcgill.ca/mgc/	National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished (1999)	Contact: Robert Strausberg, Ph.D. Email: cgabs-r@mail.nih.gov Tissue Procurement: Dr. James R. Lupski CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov plate: L1AM13567 row: 1 column: 16 High quality sequence stop: 611.
FEATURES	Source	Location/Qualifiers	
	1. 968	/organism="Homo sapiens"	
		/mol_type="mRNA"	
		/db_xref="taxon:9606"	
		/clone="IMAGE:6182103"	
		/sex="male"	
		/tissue_type="dorsal root ganglia"	
		/dev_stage="adult, 36 yr"	
		/lab_host="DH10B"	
		/clone_lib="Lupski_dorsal root ganglion"	
		/note="Vector: PCMV-SPORT6 (Life Technologies); Site_1: NotI; Site_2: SalI; cDNA made by oligo-dT priming. Directionally cloned using the following adaptors: 5'-TCGACCCACGCGTCCG-3' and 5'-GACTAGTCTTAGATCGCAGCGCGCCCT(15)-3'. Size selected > 1 kb for average insert length 1.7 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life Technologies."	
ORIGIN	Query Match	Best Local Similarity	Matches
	14.7%; Score 398; DB 5; Length 968;	99.6%; Pred. No. 2.9e-162;	0; Mismatches 1; Indels 1; Gaps 1;
915	AGACATCTTAAGAGAGATCCAGCAATAACGTTTACTCCACTGTGAAATACGAAA		974
194	AGACATCTTAAGAGAGATCCAGCAATAACGTTTACTCCACTGTGAAATACGAAA		253
975	AAGATGAAATCCCACTCACTGCTCAGCATGCCAGACACACCAAGGCTATTGCTAT		1034

|||||
Db 254 AAGATGAAAATCCCCACTCACTGCTCAGCATGCCAGACACACCAAGGCTATTGGCCTAT 313
QY 1035 GAGAAATGTTATCTAGACAGCAGTGCACTCCCTTAAGTCTCTGCTC-AAAAAAAAACAAT 1093
Db 314 GAGAAATGTTATCTAGACAGCAGTGCACTCCCTTAAGTCTCTGCTCAAAAAAAAAACAAT 373
QY 1094 TCTCGCCCAAGAAAACAATCAGAGAATTCAGTATTGACTAGAAAACATCAAGGAAG 1153
Db 374 TCTCGCCCAAGAAAACAATCAGAGAATTCAGTATTGACTAGAAAACATCAAGGAAG 433
QY 1154 AATGAAGACGTTGACTTTTCCAGGATAATTCTCTGATGCTTCTTAGATTAAAG 1213
Db 434 AATGAAGACGTTGACTTTTCCAGGATAATTCTCTGATGCTTCTTAGATTAAAG 493
QY 1214 AGTTCGTAATCCATCACTGCTGAGAAATCTCTCAAAACCCAGAGGTTTAATCACTTC 1273
Db 494 AGTTCATTAATCCATCACTGCTGAGAAATCTCTCAAAACCCAGAGGTTTAATCACTTC 553
QY 1274 ATCCCAAAATGGGATTTGTAATGTCAAGCAAAACCAATAAAAAAGTGTAGAAATTTCC 1333
Db 554 ATCCCAAAATGGGATTTGTAATGTCAAGCAAAACCAATAAAAAAGTGTAGAAATTTCC 613
QY 1334 TATAGAAATGTAATGCAAGGTCACACATATTAAATGACAGCCTGTGTATTAAATGATGGC 1393
Db 614 TATAGAAATGTAATGCAAGGTCACACATATTAAATGACAGCCTGTGTATTAAATGATGGC 673
QY 1394 TCCAGGTCAAGTGTGAGATTTCATTCATCCCAAGGCTTGATGTCAAGATTATACCAA 1453
Db 674 TCCAGGTCAAGTGTGAGATTTCATTCATCCCAAGGCTTGATGTCAAGATTATACCAA 733
QY 1454 GAGTCTTGCTACGAGAGGCAAGAAGACC 1483
Db 734 GAGTCTTGCTACGAGAGGCAAGAAGACC 763

RESULT 35
BU617383/c 663 bp mRNA linear EST 23-SEP-2002
LOCUS UI-H-DF0-bew-1-13-0-UI.s1 NCI CGAP DF0 Homo sapiens cDNA clone
DEFINITION UI-H-DF0-bew-1-13-0-UI 3', mRNA sequence.
ACCESSION BU617383
VERSION BU617383.1 GI:23283598
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 663)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 70-115, >MER31A#LTR/MER4-group (matched complement)
374-650, >ALU (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source 1..663
location/Qualifiers
1..663
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-DF0-bew-1-13-0-UI"
/tissue_type="Subchondral Bone"

/dev stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP DF0"
/note="Organ: Bone; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP DF0 is a cDNA library containing the following
tissue(s): Subchondral Bone. The library was constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT7T3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (GT)18 tail. The
sequence tag for this library is GTTAAGCGTC.
TAG_TISSUE=subchondral bone
TAG_LIB=UI-H-DF0
TAG_SEQ=GTTAAGCGTC"

ORIGIN
Query Match 14.7%; Score 397; DB 5; Length 663;
Best Local Similarity 99.8%; Pred. No. 8.4e-162;
Matches 447; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2255 GAGGTGACGTGAGCTGAGATGGACACCTGCACTCCGCGCTAGGCAAGAGCAAAAC 2314
Db 448 GAGGTGACGTGAGCTGAGATGGACACCTGCACTCCGCGCTAGGCAAGAGCAAAAC 389
QY 2315 TCCAATACAACAACAACAACACCTGTGCTAGGTCACTGCGACGTAAAGATGACAA 2374
Db 388 TCCAATACAACAACAACAACACCTGTGCTAGGTCACTGCGACGTAAAGATGACAA 329
QY 2375 TCCCTACCAACACAGAGCTCACCATCTTTAATTAAAGTGAACAACATGGGGAAGGGA 2434
Db 328 TCCCTACCAACACAGAGCTCACCATCTTTAATTAAAGTGAACAACATGGGGAAGGGA 269
QY 2435 AAGGGGAATGCGCTTTTGATATGTTCCCTGACGCATATCTTGAATGAGACCTCCCTA 2494
Db 268 AAGGGGAATGCGCTTTTGATATGTTCCCTGACGCATATCTTGAATGAGACCTCCCTA 209
QY 2495 CCAAGTGATGAAGTGTGAAAACTTAATAACAATGCTGTGGGCAAGATGGGATT 2554
Db 208 CCAAGTGATGAAGTGTGAAAACTTAATAACAATGCTGTGGGCAAGATGGGATT 149
QY 2555 GAGATTATCTTCTCTCAGAAAGCATGTGAAGGAATTGAGCCAGATCTCTCCCTAC 2614
Db 148 GAGATTATCTTCTCTCAGAAAGCATGTGAAGGAATTGAGCCAGATCTCTCCCTAC 89
QY 2615 TGCAAAACCTATTGTAGTAAAGTCTTTACTATCTTAATAAACAAGATATTGTG 2674
Db 88 TGCAAAACCTATTGTAGTAAAGTCTTTACTATCTTAATAAACAAGATATTGTG 29
QY 2675 AGATTACATTAATAAAAAAAAAAAAAA 2702
Db 28 AGATTACATTAATAAAAAAAAAAAAAA 1

RESULT 36
BQ000581/c 705 bp mRNA linear EST 17-JUN-2002
LOCUS BQ000581
DEFINITION UI-H-DP0-avu-d-09-0-UI.s1 NCI CGAP_Fs1 Homo sapiens cDNA clone
IMAGE:5884376 3', mRNA sequence.
ACCESSION BQ000581
VERSION BQ000581.1 GI:19725481
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 705)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

JOURNAL Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mary Hendrix
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/BLN at: http://image.llnl.gov
The following repetitive elements were found in this cDNA
sequence: 70-115, >MER31A#LTR/MER4-group (matched complement)
374-663, >ALU (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source location/Qualifiers
1. 705

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5884376"
/tissue_type="Fibrosarcoma"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP Fsl"
/note="Vector: pT7T3-Pac (Pharmacia) with a modified
polylinker; Site_1: EcoR I; Site_2: Not I; NCI CGAP_Fsl is
a cDNA library containing the following tissue(s):
Fibrosarcoma Cell line HT-1088 (ATCC number CCL-121). The
library was constructed according to Bonaldo, Lennon and
Soares, Genome Research, 6:791-806, 1996. First strand
cDNA synthesis was primed with an oligo-dT primer
containing a Not I site. Double stranded cDNA was ligated
to an EcoR I adaptor, digested with Not I, and cloned
directionally into pT7T3-Pac vector. The oligonucleotide
used to prime the synthesis of first-strand cDNA contains
a library tag sequence that is located between the Not I
site and the (dT)18 tail. The sequence tag for this
library is GTTCTACGAG.
TAG_TISSUE=fibrosarcoma
TAG_LIB=UI-H-DP0
TAG_SEQ=GTTCTACGAG"

ORIGIN
Query Match 14.1%; Score 380; DB 5; Length 705;
Best Local Similarity 99.8%; Pred. No. 2.2e-154;
Matches 430; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2255 GAGGTGCACTGAGCTGAGATGGCACCCTGCACTCCGGCCTTAGGCAACGAGCAAAAC 2314
|||||
Db 448 GAGGTGCACTGAGCTGAGATGGCACCCTGCACTCCGGCCTTAGGCAACGAGCAAAAC 389
Oy 2315 TCCCAATACAAACAAACAAACACCTGTGCTAGTCACTGCGACCTAGCACTAAGATGAACA 2374
|||||
Db 388 TCCCAATACAAACAAACAAACACCTGTGCTAGTCACTGCGACCTAGCACTAAGATGAACA 329
Oy 2375 TCCCTACCAACACAGAGCTCACCACCTCTTATACCTTAAGTGAACACATGGGGAAGGGA 2434
|||||
Db 328 TCCCTACCAACACAGAGCTCACCACCTCTTATACCTTAAGTGAACACATGGGGAAGGGA 269
Oy 2435 AAGGGGAATGGCTGCTTTGATATGTTCCCTGACGCATATCTGAATGAGAGACCTCCCTA 2494
|||||
Db 268 AAGGGGAATGGCTGCTTTGATATGTTCCCTGACGCATATCTGAATGAGAGACCTCCCTA 209
Oy 2495 CCAAGTGATGAAGTGTGAAAAAATTAAATAACAATGCTTGTGGGCAAGAATGGGATT 2554
|||||
Db 208 CCAAGTGATGAAGTGTGAAAAAATTAAATAACAATGCTTGTGGGCAAGAATGGGATT 149
Oy 2555 GAGGATTAATCTCTCTCAGAAAGGCATGTGAAGGAATTGAGCCAGATCTCTCCCTAC 2614
|||||
Db 148 GAGGATTAATCTCTCTCAGAAAGGCATGTGAAGGAATTGAGCCAGATCTCTCCCTAC 89
Oy 2615 TGCAAAACCTTATTGTAGTAAAAAGTCTCTTACTATCTTAATAAAGATATGTG 2674
|||||

Db 88 TGCAAAACCTTATTGTAGTAAAAAGTCTCTTACTATCTTAATAAAGATATGTG 29
Oy 2675 AGATTACATA 2685
Db 28 AGATTACATA 18

RESULT 37
CD366710/c 712 bp mRNA linear EST 05-AUG-2004
LOCUS
DEFINITION
UI-H-FT2-bjo-n-03-0-UI.s1 NCI CGAP FT2 Homo sapiens cDNA clone
UI-H-FT2-bjo-n-03-0-UI 3', mRNA sequence.
ACCESSION
CD366710 GI:31150800
VERSION
CD366710.1 GI:31150800
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 (bases 1 to 712)
AUTHORS
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
CONTACT: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html

The following repetitive elements were found in this cDNA
sequence: 70-115, >MER31A#LTR/MER4-group (matched complement)
374-663, >ALU (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source location/Qualifiers

1. 712
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT2-bjo-n-03-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP FT2"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI CGAP FT2 is a subcloned cDNA library constructed from
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The mRNA samples
were a mixture of these conditions (times refer to
incubations following isolation by bronchoalveolar lavage)
(some normal donor macrophages were cultured in some of
the conditions). The mRNA samples were pooled for library
construction. Control 0 hours; control 3 hours; control 24
hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph
aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours;
Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours;
Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt
adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24
hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours;
wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours.
The library was subcloned according to Bonaldo, Lennon
and Soares, Genome Research, 6:791-806, 1996. The tissue
was provided by Dr. Gary W. Hunninghake of the University
of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT2

TITLE Homo sapiens cDNA cda clones
JOURNAL Unpublished (2000)
COMMENT Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
location/Qualifiers
1. 614
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="cdASB12"
/tissue_type="pheochromocytoma"
/dev_stage="Adult"
/lab_host="BM25.8"
/clone_lib="cda"
/note="Vector: pTriplEx2; Site_1: sf11A; Site_2: sf11B"

ORIGIN
Query Match 13.8%; Score 373; DB 1; Length 614;
Best Local Similarity 99.8%; Pred. No. 2.5e-151;
Matches 423; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2255 GAGGTGACGTGAGCTGAGATGGCACCACCTGCACTCCGGCCTAGGCAACGAGCAAAAC 2314
DB 127 GAGGTGACGTGAGCTGAGATGGCACCACCTGCACTCCGGCCTAGGCAACGAGCAAAAC 186
OY 2315 TCCAAATCAACAACAACAACAACACCTGTGCTAGTCACTGCGCAGCTAAGATGAACA 2374
DB 187 TCCAAATCAACAACAACAACAACACCTGTGCTAGTCACTGCGCAGCTAAGATGAACA 246
OY 2375 TCCCTACCAACACAGAGCTCACCACCTCTTACTTAAGTGAACAAACATGGGGAAGGGA 2434
DB 247 TCCCTACCAACACAGAGCTCACCACCTCTTACTTAAGTGAACAAACATGGGGAAGGGA 306
OY 2435 AAGGGAATGCGCTGCTTTTGATATGTTCCCTGACGCATATCTTGAATGAGACCTCCCTA 2494
DB 307 AAGGGAATGCGCTGCTTTTGATATGTTCCCTGACGCATATCTTGAATGAGACCTCCCTA 366
OY 2495 CCAAGTGAAGAAGTGTGAAAACTTAATAACAATGCTTGTGGCAAGATGGGATT 2554
DB 367 CCAAGTGAAGAAGTGTGAAAACTTAATAACAATGCTTGTGGCAAGATGGGATT 426
OY 2555 GAGGATATCTTCTCTCAGAAAGGCATTGTGAAGGAATTGAGCCAGATCTCTCCCTAC 2614
DB 427 GAGGATATCTTCTCTCAGAAAGGCATTGTGAAGGAATTGAGCCAGATCTCTCCCTAC 486
OY 2615 TGCAAAACCTTATTGTAGTAAAAAGTCTTCTTACTATCTTAATAAACAAGATATTGTG 2674
DB 487 TGCAAAACCTTATTGTAGTAAAAAGTCTTCTTACTATCTTAATAAACAAGATATTGTG 546
OY 2675 AGAT 2678
DB 547 AGAT 550

RESULT 40
W72366/c 421 bp mRNA linear EST 16-OCT-1996
LOCUS W72366
DEFINITION zd62f01.s1 Soares fetal_heart_NbHH19W Homo sapiens cDNA clone
IMAGE:345241 3' similar to gb:M81181 SODIUM/POTASSIUM-TRANSPORTING
ATPASE BETA-2 (HUMAN); contains Alu repetitive element;; mRNA
sequence.
ACCESSION W72366
VERSION W72366.1 GI:1382971
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 421)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevasakis,B., Waterson,R., Williamson,A., Wohlmann,P. and
Wilson,R.
The Washu-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 511 Std Error: 0.00
Seq primer: mob.REGA+RT.
location/Qualifiers
1. 421
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1270616"
/db_xref="taxon:9606"
/clone="IMAGE:345241"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_fetal_heart_NbHH19W"
/note="Organ: heart; Vector: pTriplEx2 (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCCGCACTTTTCTTTTCTTTT 3'] ,
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pTriplEx2 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by
M.Fatima Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
NbHL19W."

ORIGIN
Query Match 13.6%; Score 367; DB 7; Length 421;
Best Local Similarity 99.8%; Pred. No. 1.1e-148;
Matches 417; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2258 GTTGACGTGAGCTGAAGTGCAACCACTGCACTCCGGCCTAGGCAACGAGCAAACTCC 2317
DB 421 GTTGACGTGAGCTGAAGTGCAACCACTGCACTCCGGCCTAGGCAACGAGCAAACTCC 362
OY 2318 AATACAACAACAACAACAACAACCTGTGCTAGGTCAGTCTGGCACGTAAGATGAACATCC 2377
DB 361 AATACAACAACAACAACAACAACCTGTGCTAGGTCAGTCTGGCACGTAAGATGAACATCC 302
OY 2378 CTACCAACACAGAGCTCACCATCTTATTAAGTGAACAAACATGGGGAAGGGAAG 2437
DB 301 CTACCAACACAGAGCTCACCATCTTATTAAGTGAACAAACATGGGGAAGGGAAG 242
OY 2438 GGGATGCGCTGCTTTGATATGTTCCCTGACGCATATCTTGAATGAGAGACCTCCCTACCA 2497
DB 241 GGGATGCGCTGCTTTGATATGTTCCCTGACGCATATCTTGAATGAGAGACCTCCCTACCA 182
OY 2498 AGTGATGAAGAAGTGTGAAAACTTAATAACAATGCTGTGGCAAGAATGGATTGAG 2557
DB 181 AGTGATGAAGAAGTGTGAAAACTTAATAACAATGCTGTGGCAAGAATGGATTGAG 122
OY 2558 GATTATCTTCTCTCAGAAAGCATTTGGAAGGAATTGAGCCAGATCTCTCCCTACTGC 2617
DB 121 GATTATCTTCTCTCAGAAAGCATTTGGAAGGAATTGAGCCAGATCTCTCCCTACTGC 62
OY 2618 AAAACCTATTGTAGTAAAAAGTCTTCTTACTATCTTAATAAACAAGATATTGTGA 2675

Db 61 AAAACCTATTGTAGTAAAAAGTCTTCTTACTATCTTAATAAAGATATGTGA 4

RESULT 41
CD630759 761 bp mRNA linear EST 12-JAN-2004
LOCUS 56071680J1 FLP Homo sapiens cDNA, mRNA sequence.
DEFINITION CD630759
ACCESSION CD630759.1 GI:40279025
VERSION
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 761)
AUTHORS Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.

FEATURES
Source Location/Qualifiers
1..761
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"

ORIGIN
Query Match 13.6%; Score 367; DB 6; Length 761;
Best Local Similarity 100.0%; Pred. No. 1e-148;
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 763 TTGTACTGGGGCTATTCTTTGGTTTCTGAAGAGAGACAAGAGAGTACATTGAAG 822
DB 35 TTGTACTGGGGCTATTCTTTGGTTTCTGAAGAGAGACAAGAGAGTACATTGAAG 94
QY 823 AGAAGAAGAGAGTGCATTTGTGCGGAAACTCCTAACATATGCCCCCATCTGGAGAGA 882
DB 95 AGAAGAAGAGAGTGCATTTGTGCGGAAACTCCTAACATATGCCCCCATCTGGAGAGA 154
QY 883 ACACAGAGTACGACACAATCCCTCACACTAATAGACAATCCTAAAGGAAGATCCAGCAA 942
DB 155 ACACAGAGTACGACACAATCCCTCACACTAATAGACAATCCTAAAGGAAGATCCAGCAA 214
QY 943 ATACGGTTTACTCCTGCTGGAATATCCGAAAAAGATGAAAAATCCCACTCACTGCTCA 1002
DB 215 ATACGGTTTACTCCTGCTGGAATATCCGAAAAAGATGAAAAATCCCACTCACTGCTCA 274
QY 1003 CGATGCCAGACACCAAGGCTATTGTGCTTATGAGAAATGTTATCTAGACAGCAGTGCACT 1062
DB 275 CGATGCCAGACACCAAGGCTATTGTGCTTATGAGAAATGTTATCTAGACAGCAGTGCACT 334
QY 1063 CCCCTAAGTCTGCTCAAAAAAACAATTTCTGGCCCCCAAGAAACAATCAGAAGAA 1122
DB 335 CCCCTAAGTCTGCTCAAAAAAACAATTTCTGGCCCCCAAGAAACAATCAGAAGAA 394
QY 1123 TTCACGTG 1129
DB 395 TTCACGTG 401

RESULT 42
CD630761 793 bp mRNA linear EST 12-JAN-2004
LOCUS 56071688J1 FLP Homo sapiens cDNA, mRNA sequence.
DEFINITION CD630761
ACCESSION CD630761.1 GI:40279027

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 793)
AUTHORS Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.

FEATURES
Source Location/Qualifiers
1..793
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"

ORIGIN
Query Match 13.3%; Score 360; DB 6; Length 793;
Best Local Similarity 99.2%; Pred. No. 1.1e-145;
Matches 730; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 782 TTGTTTCTGAAGAGAGAGACAGAGAGTACATTGAAGAGAGAGAGTGACAT 841
DB 50 TTGTTTCTGAAGAGAGAGACAGAGAGTACATTGAAGAGAGAGAGTGACAT 109
QY 842 TTGTCGGAAACTCCTAACATATGCCCATCTCTGGAGAGACAGAGTACGACACAAT 901
DB 110 TTGTCGGAAACTCCTAACATATGCCCATCTCTGGAGAGACAGAGTACGACACAAT 169
QY 902 CCCTCACACTAATAGAACATCCTAAAGAGATCCAGCAATACGTTTACTCCACTGT 961
DB 170 CCCTCACACTAATAGAACATCCTAAAGAGATCCAGCAATACGTTTACTCCACTGT 229
QY 962 GGAATACCGAAAAAGATGAAAAATCCCACTCACTGCTCAGATGCCAGACACACCAAG 1021
DB 230 GGAATACCGAAAAAGATGAAAAATCCCACTCACTGCTCAGATGCCAGACACCAAG 289
QY 1022 GCTATTGCTTATGAGAAATGTTATCTAGACAGCAGTGCACTCCCTTAACTCTGCTCAA 1081
DB 290 GCTATTGCTTATGAGAAATGTTATCTAGACAGCAGTGCACTCCCTTAACTCTGCTC-A 348
QY 1082 AAAAAAAAACAATTCTCGGCCCAAGAAAACAATCAGAAAGATTCAGATTGACTAGAA 1141
DB 349 AAAAAAAAACAATTCTCGGCCCAAGAAAACAATCAGAAAGATTCAGATTGACTAGAA 408
QY 1142 ACATCAAGGAAGATGAAGACGTTGCTTTTCCAGATAAATATCTCTGATGCTTC 1201
DB 409 ACATCAAGGAAGATGAAGACGTTGCTTTTCCAGATAAATATCTCTGATGCTTC 468
QY 1202 TTTAGATTAAAGCTTCGTAATTCATCCACTGCTGAGAAATTCCTCAAAACCAAGAGG 1261
DB 469 TTTAGATTAAAGCTTCATTAATTCATCCACTGCTGAGAAATTCCTCAAAACCAAGAGG 528
QY 1262 TTTAATCACTTCATCCCAAAAATGGGATTTGGAATGTCAGCAAAACCATAAAAAAGTGCT 1321
DB 529 TTTAATCACTTCATCCCAAAAATGGGATTTGGAATGTCAGCAAAACCATAAAAAAGTGCT 588
QY 1322 TAGAAGTATTCCTATAGAAATGTAAATGCAAGGTACACACATATTAATGACAGCCTGTTGT 1381
DB 589 TAGAAGTATTCCTATAGAAATGTAAATGCAAGGTACACACATATTAATGACAGCCTGTCGT 648
QY 1382 ATTAATGATGGCTCCAGGTCACTGCTGAGATTTCATTCATCCACGAGGCTTGATGTCA 1441
DB 649 ATTAATGATGGCTCCAGGTCACTGCTGAGATTTCATTCATCCACGAGGCTCGATGTCA 708
QY 1442 GGATTATACCAAGAGTCTTGCTACGAGAGGGCAAGAACCAAAACAGACAGACAAGTC 1501

Db 709 GGATATATACCAAGAGTCTTGCTACCAAGGAGGCAAGAACCAAAACAGACAGACAAGTC 768
OY 1502 CAGCAGAAGCAGATGC 1517
Db 769 CAGCAGAAGCAGATGC 784

RESULT 43
BE246373 442 bp mRNA linear EST 03-OCT-2001
LOCUS TCBAP1E2908 pediatric pre-B cell acute lymphoblastic leukemia
DEFINITION Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2908, mRNA
sequence.

ACCESSION BE246373
VERSION BE246373
KEYWORDS BE246373.1 GI:9098122
SOURCE EST.
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

TITLE Wei,Y., Tsang,Y.T.M., Mei,G., Ku,J.M., Ali-Osman Jr.,F.R.,
Muzny,D., Bouck,J., Gibbs,R.A. and Margolin,J.F.
JOURNAL Pediatric leukemia cDNA Sequencing Project
COMMENT Unpublished (2000)
Contact: Dr. Judith F. Margolin
Texas Children's Cancer Center and Human Genome Sequencing Center
at Baylor College of Medicine
1102 Bates, MC3-3320 Houston, TX 77030, USA
Tel: 832-824-4536
Fax: 832-825-4038

Email: clones@txccc.org
Citation: Carninci,P. and Hayashizaki,Y. High efficiency
full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Seq primer: M13 primer.

FEATURES
source location/Qualifiers
1. .442

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="TCBAP2908"
/sex="male"
/tissue_type="leukopheresis"
/cell_type="pre-B cell"
/dev_stage="pediatric 2 years"
/lab_host="DH10B"
/clone_lib="Pediatric pre-B cell acute lymphoblastic
leukemia Baylor-HGSC project=TCBA"
/note="Vector: lambda PSB; Site 1: BamHI; Site 2: EcoRI;
First strand cDNA was primed with an anchored
XhoI-oligo(dT) primer [5'GGAGACTCGAGCGCGCCGACGAGAG(7')VN
3'; V=A,C,G; N=A,C,G,T] and then dg tailed. Second strand
was primed with a BamHI-dC primer
[5'AGAGAGCTCGATCCGGCGCCGCAATATATATAT(C) 3'].
Double-stranded cDNA was then digested with BamHI and XhoI
and directionally cloned into the BamHI and SalI sites of
lambda PSB vector. Library was constructed by Wei Yu at RIKEN
of Japan (Carninci P, Westover A, Nishiyama Y, Ohsumi T,
Itoh M, Nagaoaka S, Sasaki N, Okazaki Y, Muramatsu M,
Schneider C, Hayashizaki Y, High efficiency selection of
full-length cDNA by improved biotinylated cap trapper.,
DNA Res 4: 1, 61-6, Feb 28, 1997)"

ORIGIN
Query Match 13.2%; Score 358; DB 2; Length 442;
Best Local Similarity 100.0%; Pred. No. 9.1e-145;
Matches 358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 418 AGCACTGTCAAAGCCTAAAGTCACCAATGGGTCTGCAGAGCAATTAAGATGGCACTGTG 477
Db 85 AGCACTGTCAAAGCCTAAAGTCACCAATGGGTCTGCAGAGCAATTAAGATGGCACTGTG 144

OY 478 TGACCAATCTGACATGCTGCATGGAACATGGGGAAGAGATGTGATTATACCTGGAAG 537
Db 145 TGACCAATCTGACATGCTGCATGGAACATGGGGAAGAGATGTGATTATACCTGGAAG 204
OY 538 CCCTGGGGCAAGCAGACGCCAATAGTCCCATATATGGGTCCATCCTCCCATCTCCTGAGAT 597
Db 205 CCCTGGGGCAAGCAGACGCCAATAGTCCCATATATGGGTCCATCCTCCCATCTCCTGAGAT 264
OY 598 GGGGAGAAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCCCTGTACAGAGAAACTTCT 657
Db 265 GGGGAGAAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCCCTGTACAGAGAAACTTCT 324
OY 658 CAAGCCCCATCCTTGGCCAGGAAGCTCTGTGAAGGTGCTGTGATGACCCAGATTCTTCCA 717
Db 325 CAAGCCCCATCCTTGGCCAGGAAGCTCTGTGAAGGTGCTGTGATGACCCAGATTCTTCCA 384
OY 718 TGGTCTCTCTGTGTCTCTGTGTGGTGCCCTCTCTGCTCAGTCTCTTTGTACTGGGCT 775
Db 385 TGGTCTCTCTGTGTCTCTGTGTGGTGCCCTCTCTGCTCAGTCTCTTTGTACTGGGCT 442

RESULT 44
AW197989/c 354 bp mRNA linear EST 29-NOV-1999
LOCUS x029a01.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2705352 3',
DEFINITION mRNA sequence.

ACCESSION AW197989
VERSION AW197989
KEYWORDS AW197989.1 GI:6477219
SOURCE EST.
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE 1 (bases 1 to 354)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.linl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco.

FEATURES
source location/Qualifiers
1. .354
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2705352"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Pan1"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.72 kb. Life Technologies catalog #:
11548-013"

ORIGIN
Query Match 13.1%; Score 354; DB 2; Length 354;
Best Local Similarity 100.0%; Pred. No. 5.2e-143;
Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1685 GGGCCAGGTGTGATCCACAGACTTGAAGGTCAAAGTTCAACAAGATGAAGAATCAGGG 1744
Db 354 GGGCCAGGTGTGATCCACAGACTTGAAGGTCAAAGTTCAACAAGATGAAGAATCAGGG 295

OY 1745 TAGCTGACCATGTTTGGCAGATACTATAATGAGACACAGAAGTGTGCATGGCCCAAGGA 1804
Db 294 TAGCTGACCATGTTTGGCAGATACTATAATGAGACACAGAAGTGTGCATGGCCCAAGGA 235

QY 1805 CAAGACCTCCAGCAGCTTCATTATGCACTTGTGCTGCAAAAGAAAGTTAGGTTT 1864
|||||
Db 234 CAAGACCTCCAGCAGCTTCATTATGCACTTGTGCTGCAAAAGAAAGTTAGGTTT 175
QY 1865 TAAGCTGTGCCAAGAACCCATCCCAATAAAGAGACCGGAGTCTGAAGTCACATTTGAATC 1924
|||||
Db 174 TAAGCTGTGCCAAGAACCCATCCCAATAAAGAGACCGGAGTCTGAAGTCACATTTGAATC 115
QY 1925 TAGGTAGAGACTTGGAGTCAGGCAGTGAAGTGTGGGCGACGGGGGCGAGTGGTAC 1984
|||||
Db 114 TAGGTAGAGACTTGGAGTCAGGCAGTGAAGTGTGGGCGACGGGGGCGAGTGGTAC 55
QY 1985 TTGTAACCTTTAAAGATGTTAATTCATTCAATGATATTATTAGAACCCTA 2038
|||||
Db 54 TTGTAACCTTTAAAGATGTTAATTCATTCAATGATATTATTAGAACCCTA 1

RESULT 45
AI989857/c 405 bp mRNA linear EST 08-MAR-2000
LOCUS w836c08.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2499278 3'
DEFINITION similar to contains Alu repetitive element;; mRNA sequence.
ACCESSION AI989857
VERSION AI989857.1 GI:5836738
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 405)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 473 Std Error: 0.00
Seq primer: -40UP from Gibco.
FEATURES
source
1. 405
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2499278"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/clone_lib="NCI_CGAP GC6"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA
from the normalized library NCI_CGAP GC4 was prepared, and
as circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
1257096-1258631, 1469064-1470983, and 1475592-1476743).
Subtraction by Bento Soares and M. Fatima Bonaldo."
ORIGIN
Query Match 13.1%; Score 354; DB 1; Length 405;
Best Local Similarity 99.8%; Pred. No. 5.1e-143;
Matches 404; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2288 CTCGGCCTAGCAAGAGCAAAACTCCAAATACAACAACAACCACTGTGCT 2347

Db 405 CTCCGGCCTAGCAAGAGCAAAACTCCAAATACAACAACAACCACTGTGCT 346
QY 2348 AGTCAGTCTGGCAGCTAAGATGAACATCCCTACCAACACAGAGCTCACCATCTTTATA 2407
|||||
Db 345 AGTCAGTCTGGCAGCTAAGATGAACATCCCTACCAACACAGAGCTCACCATCTTTATA 286
QY 2408 CTTAAGTGAACAAATGCGGAAGGGGAATGGCTGCTTTTGATATGTTCCCTGA 2467
|||||
Db 285 CTTAAGTGAACAAATGCGGAAGGGGAATGGCTGCTTTTGATATGTTCCCTGA 226
QY 2468 CGCATATCTTGAATGAGACCTCCCTACCAAGTGAAGAGTTGAAAACTTAATAAC 2527
|||||
Db 225 CACATATCTTGAATGAGACCTCCCTACCAAGTGAAGAGTTGAAAACTTAATAAC 166
QY 2528 AAATGCTTGTGGCAAGAATGGATGAGATTATCTTCTCAGAAAGCATTTGTGA 2587
|||||
Db 165 AAATGCTTGTGGCAAGAATGGATGAGATTATCTTCTCAGAAAGCATTTGTGA 106
QY 2588 GGAATTGAGCCAGATCTCTCTCCCTACTGCAAAACCCTATTGTAGTAAAAAGTCTTCT 2647
|||||
Db 105 GGAATTGAGCCAGATCTCTCTCCCTACTGCAAAACCCTATTGTAGTAAAAAGTCTTCT 46
QY 2648 TACTATCTTAATAAACAGATATTGTGAGATTCAATAAAAAAA 2692
|||||
Db 45 TACTATCTTAATAAACAGATATTGTGAGATTCAATAAAAAAA 1

RESULT 46
AA908670/c 396 bp mRNA linear EST 09-JUN-1998
LOCUS 0104d01.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1522465 3'
DEFINITION similar to contains element L1 repetitive element;; mRNA sequence.
ACCESSION AA908670
VERSION AA908670.1 GI:3048075
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 396)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 781 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 360.
FEATURES
source
1. 396
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1522465"
/tissue_type="carcinoid"
/lab_host="DH10B"
/clone_lib="NCI_CGAP Lu5"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
neuroendocrine lung carcinoid, and was then primed with a
Not I - oligo(dT) primer. Double-stranded cDNA was ligated
to Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified

PT73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "

Query Match 12.6%; Score 340; DB 1; Length 396;
Best Local Similarity 99.7%; Pred. No. 6.6e-137;
Matches 390; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

ORIGIN

QY 2295 CTAGGCAAGAGCAAACTCCAAATACAAACAACAACACCTGTGCTAGGTGAC 2354
|||||
DB 396 CTAGGCAAGAGCAAACTCCAAATACAAACAACAACACCTGTGCTAGGTGAC 337
QY 2355 TCTGGCAGCTAAGATGAACATCCCTACCAACACAGAGCTCACCATCTTATAGT 2414
|||||
DB 336 TCTGGCAGCTAAGATGAACATCCCTACCAACACAGAGCTCACCATCTTATAGT 277
QY 2415 GAAAAACATGGGGAAGGGGAATGGCTGCTTTGATATGTTCCCTGACGCATAT 2474
|||||
DB 276 GAAAAACATGGGGAAGGGGAATGGCTGCTTTGATATGTTCCCTGACGCATAT 217
QY 2475 CTTGAATGAGACCTCCCTACCAAGTGAAGTGTGAAAACTTAATACAAATGCT 2534
|||||
DB 216 CTTGAATGAGACCTCCCTACCAAGTGAAGTGTGAAAACTTAATACAAATGCT 157
QY 2535 TGTGGGCAAGATGGGATGAGATTACTTCTCTCAGAAAGCATGTGGAAGGAATTG 2594
|||||
DB 156 TGTGGGCAAGATGGGATGAGATTACTTCTCTCAGAAAGCATGTGGAAGGAATTG 97
QY 2595 AGCCAGATCTCTCTCCCTACTGCAAAACCTATTGTAGTAAAGTCTTCTTACTATC 2654
|||||
DB 96 AGCCAGATCTCTCTCCCTACTGCAAAACCTATTGTAGTAAAGTCTTCTTACTATC 37
QY 2655 TTAATAAACAAGATATTGTAGATTCAACATA 2685
|||||
DB 36 TTAATAAACAAGATATTGTAGATTCAACATA 6

RESULT 47
AM630293 426 bp mRNA linear EST 31-MAR-2000
LOCUS hh81a11.v1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2969180 5'
DEFINITION similar to TR:Q14775 Q14775 LY-9 PRECURSOR ; mRNA sequence.
ACCESSION AM630293
VERSION AM630293.1 GI:7377083
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 426)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Other_ESTs: hh81a11.x1
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov/image/html/iresources.shtml
Seq primer: -40RP from Gibco
High quality sequence stop: 424.

FEATURES
source 1..426
location/Qualifiers
1..426
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2969180"

/tissue_type="2 pooled high-grade transitional cell tumors"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_GU1"
/note="Organ: genitourinary tract; Vector: PCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies."

Query Match 12.6%; Score 340; DB 2; Length 426;
Best Local Similarity 100.0%; Pred. No. 6.5e-137;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN

QY 417 GAGCACCCTGCAAAAGCCTAAAGTCACCATGGTCTGCAGACCAATAGAATGGACCTGT 476
|||||
DB 87 GAGCACCCTGCAAAAGCCTAAAGTCACCATGGTCTGCAGACCAATAGAATGGACCTGT 146
QY 477 GTACCCAATCTGACATGCTTCATGGAACATGGGGAAGAGATGTGATTATACCTGGAAG 536
|||||
DB 147 GTACCCAATCTGACATGCTTCATGGAACATGGGGAAGAGATGTGATTATACCTGGAAG 206
QY 537 GCCCTGGGGCAAGCAGCCCAATGAGTCCCATATGGGTCCATCTCCCATCTCTGGAGA 596
|||||
DB 207 GCCCTGGGGCAAGCAGCCCAATGAGTCCCATATGGGTCCATCTCTCCCATCTCTGGAGA 266
QY 597 TGGGAGAAAGTATATGACTTCACTCTGCTGCGTCCAGAAACCTGTGAGCAGAAACTTC 656
|||||
DB 267 TGGGAGAAAGTATATGACTTCACTCTGCTGCGTCCAGAAACCTGTGAGCAGAAACTTC 326
QY 657 TCAAGCCCCATCTCTGCCAGGAAGCTCTGTGAAGTCTGTGATGACCCAGATTCCTCC 716
|||||
DB 327 TCAAGCCCCATCTCTGCCAGGAAGCTCTGTGAAGTCTGTGATGACCCAGATTCCTCC 386
QY 717 ATGCTCTCTCTGTGTCTCTCTGTGTTGGTGGCCCTCTGCTCA 756
|||||
DB 387 ATGCTCTCTCTGTGTCTCTCTGTGTTGGTGGCCCTCTGCTCA 426

RESULT 48
A1948861 372 bp mRNA linear EST 06-SEP-1999
LOCUS A1948861/c
DEFINITION wg37d09.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2473457 3', mRNA sequence.
ACCESSION A1948861
VERSION A1948861.1 GI:5741171
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 372)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 311.

FEATURES
source 1..372
location/Qualifiers
1..372
/organism="Homo sapiens"
/mol_type="mRNA"

/db_xref="taxon:9606"
/clone="IMAGE:2473457"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/clone_lib="NCI CGAP GC6"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA
from the normalized library NCI_CGAP_GC4 was prepared, and
as circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneids
1257096-1258631, 1469064-1470983, and 1475592-1476743).
Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 11.9%; Score 321; DB 1; Length 372;
Best Local Similarity 99.7%; Pred. No. 1.3e-128;
Matches 371; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2313 ACTCCATATACAAACAACAACAACACCTGTGCTAGCTCAGTCTGGACGTAAGTGA 2372
Db 372 ACTCCAATACAAACAACAACAACACCTGTGCTAGCTCAGTCTGGACGTAAGTGA 313
OY 2373 CATCCCTACCAACACAGAGCTCACCATCTCTTATACCTTAAGTGAACAAACATGGGGAAGG 2432
Db 312 CATCCCTACCAACACAGAGCTCACCATCTCTTATACCTTAAGTGAACAAACATGGGGAAGG 253
OY 2433 GAAAGGGGAATGGCTGCTTTTGATATGTTCCTGACGCATATCTGAATGAGACCTCCC 2492
Db 252 GAAAGGGGAATGGCTGCTTTTGATATGTTCCTGACGCATATCTGAATGAGACCTCCC 193
OY 2493 TACCAAGTGATGAAGTGTTGAAAAAAGTTAATAACAATGCTTGTGGGCAAGATGGGA 2552
Db 192 TACCAAGTGATGAAGTGTTGAAAAAAGTTAATAACAATGCTTGTGGGCAAGATGGGA 133
OY 2553 TTGAGGATTATCTTCTCAGAAAGGCATTGTGAAGATTGAGCCAGATCTCTCCCT 2612
Db 132 TTGAGGATTATCTTCTCAGAAAGGCATTGTGAAGATTGAGCCAGATCTCTCCCT 73
OY 2613 ACTGCAAAACCCCTATTGTAGTAAAGTCTTCTTACTATCTTAATAAAGATATTG 2672
Db 72 ACTGCAAAACCCCTATTGTAGTAAAGTCTTCTTACTATCTTAATAAAGATATTG 13
OY 2673 TGAGATTACAT 2684
Db 12 TGAGATTACAT 1

RESULT 49
H74227/c 451 bp mRNA linear EST 31-OCT-1995
LOCUS H74227
DEFINITION YU03f06.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone
IMAGE:232739 3', mRNA sequence.
ACCESSION H74227
VERSION H74227.1 GI:1047573
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chisoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W.,
Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,
Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
Rohlfing, T., Scheilenberg, K., Soares, M.B., Tan, F., Thierly-Meg, J.,
Trevaekis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
and Maira, M.
TITLE Generation and analysis of 280,000 human expressed sequence tags
JOURNAL Genome Res. 6 (9), 807-828 (1996)
MEDLINE 97044478
PUBMED 8889549

COMMENT

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1186
High quality sequence stops: 241
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert length: 1186 Std Error: 0.00
Seq primer: Promega -21ml3
High quality sequence stop: 241.
Location/Qualifiers

FEATURES

Source

1. 451
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3785916"
/db_xref="taxon:9606"
/clone="IMAGE:232739"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal liver spleen INFLS"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
1st strand cDNA was primed with a Pac I - oligo(dT) primer
[5' AACTGGAAGATTAAATTAAGATCTTTTCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 11.7%; Score 316; DB 7; Length 451;
Best Local Similarity 100.0%; Pred. No. 1.9e-126;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 761 CTTGTACTGGGCTATTCTTGTGTTCTGAAGAGAGAGACAGAGATGATGGA 820
Db 316 CTTGTACTGGGCTATTCTTGTGTTCTGAAGAGAGAGACAGAGATGATGGA 257
OY 821 AGAGAAAGAGAGAGTGAACATTTGTCGGGAAACTCCTAACATATGCCCCCATTTCTGGAGA 880
Db 256 AGAGAAAGAGAGTGAACATTTGTCGGGAAACTCCTAACATATGCCCCCATTTCTGGAGA 197
OY 881 GAACACAGAGTAGACACAATCCCTCAGACTAATAGAACAAATCTTAAAGGAAGATCCAGC 940
Db 196 GAACACAGAGTAGACACAATCCCTCAGACTAATAGAACAAATCTTAAAGGAAGATCCAGC 137
OY 941 AAATACGGTTTACTCCACTGTGAAATACGAAAAAGATGAAAAATCCCACTCACTGCT 1000
Db 136 AAATACGGTTTACTCCACTGTGAAATACGAAAAAGATGAAAAATCCCACTCACTGCT 77
OY 1001 CACGATGCCAGACACACCAAGGCTATTGCTTATGAGATGTTTCTAGACAGCAGTGA 1060
Db 76 CACGATGCCAGACACACCAAGGCTATTGCTTATGAGATGTTTCTAGACAGCAGTGA 17
OY 1061 CTCCCCTAAGTCTCTG 1076
Db 16 CTCCCCTAAGTCTCTG 1

RESULT 50
BF027036 935 bp mRNA linear EST 10-OCT-2000
LOCUS BF027036
DEFINITION 601671280F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954307 5',
mRNA sequence.
ACCESSION BF027036
VERSION BF027036.1 GI:10734748
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS 1 (bases 1 to 935)
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM826 row: p column: 20
High quality sequence start: 2
High quality sequence stop: 619.
Location/Qualifiers
1. 935
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3954307"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_20"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
ORIGIN
Query Match 11.6%; Score 314; DB 2; Length 935;
Best Local Similarity 99.7%; Pred. No. 1.3e-125;
Matches 364; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 21 GGCTGACTTCAGAGAGCAATATGGTGGTCCCAACATGCTCAACCTCATATATC 80
DB 1 GGCTGACTTCAGAGAGCAATATGGTGGTCCCAACATGCTCAACCTCATATATC 60
QY 81 CTTTGGCAGCTCACAGGGTCAGAGCCTCTGGAACCGTGAAGAAGCTGTCGGTCCGTT 140
DB 61 CTTTGGCAGCTCACAGAGTCAGAGCCTCTGGAACCGTGAAGAAGCTGTCGGTCCGTT 120
QY 141 GGTGGGCGGTGACTTTCCCGCTGAAGTCCAAGTAAGCAAGTGACTTATGTGTGG 200
DB 121 GGTGGGCGGTGACTTTCCCGCTGAAGTCCAAGTAAGCAAGTGACTTATGTGTGG 180
QY 201 ACCTTCAACACACCCCTCTGTGACCATACAGCCAGAGGGGGCACTATCATAGTGACC 260
DB 181 ACCTTCAACACACCCCTCTGTGACCATACAGCCAGAGGGGGCACTATCATAGTGACC 240
QY 261 CAAATCGTAATAGGGAGAGAGTAGACTTCCAGATGAGGCTACTCCCTGAAGCTCAGC 320
DB 241 CAAATCGTAATAGGGAGAGAGTAGACTTCCAGATGAGGCTACTCCCTGAAGCTCAGC 300
QY 321 AAAGTGAAGAAGTAGCTCAGGATCTATGTGGGATATACAGCTCATCACTCCAG 380
DB 301 AAAGTGAAGAAGTAGCTCAGGATCTATGTGGGATATACAGCTCATCACTCCAG 360
QY 381 CAGCC 385
DB 361 CAGCC 365

RESULT 51
AMS12079/c

LOCUS AW512079 369 bp mRNA linear EST 03-MAR-2000
DEFINITION xx70a08.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2848982 3', mRNA sequence.
ACCESSION AW512079
VERSION AW512079.1 GI:7150157
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS 1 (bases 1 to 369)
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11547-015
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov/image/html/lresources.shtml
Seq primer: -40UP from Gibco
High quality sequence stop: 340.
Location/Qualifiers
1. 369
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2848982"
/tissue_type="Lymphoma, follicular mixed small and large cell"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Lym12"
/note="Organ: lymph node; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.25 kb. Life Technologies catalog #: 11547-015"
ORIGIN
Query Match 11.5%; Score 311; DB 2; Length 369;
Best Local Similarity 99.7%; Pred. No. 3e-124;
Matches 361; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2326 CAAACAAACAAACACCTGCTAGTCACTGGCAGCTAAGTGAACATCCCTAACCAAC 2385
DB 362 CAAACAAACAAACACCTGCTAGTCACTGGCAGCTAAGTGAACATCCCTAACCAAC 303
QY 2386 ACAGAGCTCACCATCTCTTAATACTTAAGTGAAGAAACATGGGGAAGGGAATGG 2445
DB 302 ACAGAGCTCACCATCTCTTAATACTTAAGTGAAGAAACATGGGGAAGGGAATGG 243
QY 2446 CTGCTTTGATATGTTCCCTGACGCATATCTTGAATGGAGACCTCCCTACCAAGTATGA 2505
DB 242 CTGCTTTGATATGTTCCCTGACGCATATCTTGAATGGAGACCTCCCTACCAAGTATGA 183
QY 2506 AAGTGTGAAAACTTAATAACAATGCTTGTGGGCAAGAATGGATTGAGATTATCT 2565
DB 182 AAGTGTGAAAACTTAATAACAATGCTTGTGGGCAAGAATGGATTGAGATTATCT 123
QY 2566 TCTCTCAGAAAGGCATTTGAAGGAATTGAGCCAGATCTCTCCCTACTGCAAAACCTT 2625
DB 122 TCTCTCAGAAAGGCATTTGAAGGAATTGAGCCAGATCTCTCCCTACTGCAAAACCTT 63
QY 2626 ATTGTAGTAAAAAAGTCTTCTTACTATCTTAATATAAACAAGATATTGTGAGATTACATA 2685
DB 62 ATTGTAGTAAAAAAGTCTTCTTACTATCTTAATATAAACAAGATATTGTGAGATTACATA 3
QY 2686 AA 2687
DB 2 AA 1

```
RESULT 52
BG744563/c
LOCUS
DEFINITION BG744563 670 bp mRNA linear EST 15-MAY-2001
602722632T1 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:4849374 3',
mRNA sequence.
ACCESSION BG744563
VERSION BG744563.1 GI:14055216
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 670)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM168 row: o column: 07
High quality sequence stop: 670.
Location/Qualifiers
1. 670
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4849374"
/tissue_type="natural killer cells, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_106"
/note="Organ: blood; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
SuperScript II RT (Life Technologies). Note: this is a
NIH_MGC library."
```

ORIGIN

```
Query Match 11.4%; Score 309; DB 4; Length 670;
Best Local Similarity 99.7%; Pred. No. 2.1e-123;
Matches 359; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2255 GAGGTGAGTGAGCTGAGATGGCACCACCTGCACTCCGGCCTAGGCAACGAGCAAAAC 2314
|||||
DB 385 GAGGTGAGTGAGCTGAGATGGCACCACCTGCACTCCGGCCTAGGCAACGAGCAAAAC 326

OY 2315 TCCATATCAAAACAACAACAACACCTGTGTAGTCACTGTGACAGTAAGATGAACA 2374
|||||
DB 325 TCCATATCAAAACAACAACAACACCTGTGTAGTCACTGTGACAGTAAGATGAACA 266

OY 2375 TCCCTACCAACAGAGCTCAACCATCTTATATCTTAAGTAAAAACATGGGGAAGGGGA 2434
|||||
DB 265 TCCCTACCAACAGAGCTCAACCATCTTATATCTTAAGTAAAAACATGGGGAAGGGGA 206

OY 2435 AAGGGGAATGGCTGCTTTTGTATATGTTCCCTGACCGATATCTGAATGAGAGCTCCCTA 2494
|||||
DB 205 AAGGGGAATGGCTGCTTTTGTATATGTTCCCTGACCGATATCTGAATGAGAGCTCCCTA 146

OY 2495 CCAAGTGATGAAGTGTGAAAAAATTATTAACAAATGCTTGTGGCAAGATGGGATT 2554
|||||
DB 145 CCAAGTGATGAAGTGTGAAAAAATTATTAACAAATGCTTGTGGCAAGATGGGATT 86

OY 2555 GAGGATTATCTTCTCTCAGAAAGCATTTGGAAGGAATTGAGCCAGATCTCTCCCTAC 2614
|||||
DB 85 GAGGATTATCTTCTCTCAGAAAGCATTTGGAAGGAATTGAGCCAGATCTCTCCCTAC 26
```

```
RESULT 53
CD107362
LOCUS
DEFINITION CD107362 506 bp mRNA linear EST 15-MAY-2003
AGENCOURT 14016621 NIH_MGC_179 Homo sapiens cDNA clone
IMAGE:30368296 5', mRNA sequence.
ACCESSION CD107362
VERSION CD107362
KEYWORDS CD107362.1 GI:30760536
SOURCE EST.
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 506)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM430 row: n column: 17
High quality sequence stop: 427.
Location/Qualifiers
1. 506
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30368296"
/tissue_type="Pituitary"
/lab_host="DH10B-Ton A ( T1 and T5 phage resistances) "
/clone_lib="NIH_MGC_179"
/note="Organ: brain; Vector: pCMV-SPORT6.1; Site_1: EcoRV
(destroyed); Site_2: NotI; Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.1 kb. Library was
constructed by (Invitrogen). Note: this is a NIH_MGC
library."
```

FEATURES

Source

ORIGIN

```
Query Match 11.4%; Score 307; DB 6; Length 506;
Best Local Similarity 99.7%; Pred. No. 1.6e-122;
Matches 357; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 976 AGATGAAAAATCCCACTCACTGCTCAAGATGCCAGACACCAAGCTATTGGCTATG 1035
|||||
DB 110 AGATGAAAAATCCCACTCACTGCTCAAGATGCCAGACACCAAGCTATTGGCTATG 169

OY 1036 AGATGTTATCTAGACAGCAGTGCATCCCTTAAGTCTCTGCTCAAAAAACAATTC 1095
|||||
DB 170 AGATGTTATCTAGACAGCAGTGCATCCCTTAAGTCTCTGCTCAAAAAACAATTC 229

OY 1096 TCGGCCCAAGAAAAACAATCAGAAGATTCACTGATTGACTAGAAAAATCAAGGAAGA 1155
|||||
DB 230 TCGGCCCAAGAAAAACAATCAGAAGATTCACTGATTGACTAGAAAAATCAAGGAAGA 289

OY 1156 TGAAGAAGCTGACTTTTTCAGAGATAAATTATCTCTGATGCTTTAGATTAAAGAG 1215
|||||
DB 290 TGAAGAAGCTGACTTTTTCAGAGATAAATTATCTCTGATGCTTTAGATTAAAGAG 349

OY 1216 TTCGTAATTCATCCACTGCTGAGAAATCTCCTCAAAACCAGAAAGTTAATCACTCAT 1275
|||||
DB 350 TTCGTAATTCATCCACTGCTGAGAAATCTCCTCAAAACCAGAAAGTTAATCACTCAT 409

OY 1276 CCAAAAAATGGATTGTGAATGTCAAGAAACATAAAAAAGTGCTTAGAAGTATTC 1333
|||||
DB 410 CCAAAAAATGGATTGTGAATGTCAAGAAACATAAAAAAGTGCTTAGAAGTATTC 467
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RESULT 54
CD630758/c 280 bp mRNA linear EST 12-JAN-2004
LOCUS 56071680H1 FLP Homo sapiens cDNA, mRNA sequence.
DEFINITION CD630758
ACCESSION CD630758.1 GI:40279024
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 280)
AUTHORS Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Seuve,L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.

FEATURES
source 1..280
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"

ORIGIN
Query Match 10.3%; Score 278; DB 6; Length 280;
Best Local Similarity 100.0%; Pred. No. 7.6e-110;
Matches 278; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1762 CAGATACTATAATGAGACACAGAGTGTGATGGCCCAAGGACCAAGACCTCCAGCCAG 1821
DB 280 CAGATACTATAATGAGACACAGAGTGTGATGGCCCAAGGACCAAGACCTCCAGCCAG 221
QY 1822 GCTTCATTATGCACTGTGTCTGCAAAAAGTCTAGGTTTAAAGCTGTGCCAGAAC 1881
DB 220 GCTTCATTATGCACTGTGTCTGCAAAAAGTCTAGGTTTAAAGCTGTGCCAGAAC 161
QY 1882 CCATCCCAATAAAGAGACCGAGTCTGAAGTCACTTGTAAATCTAGTGAAGACTTGG 1941
DB 160 CCATCCCAATAAAGAGACCGAGTCTGAAGTCACTTGTAAATCTAGTGAAGACTTGG 101
QY 1942 AGTCAGGCGATGAGACTGTGGGGGCGACGGGGGCGAGTGGTACTGTAAACCTTAAAGA 2001
DB 100 AGTCAGGCGATGAGACTGTGGGGGCGACGGGGGCGAGTGGTACTGTAAACCTTAAAGA 41
QY 2002 TGGTTAATTCAATCAATAGATATTATTAAAGAACCTAC 2039
DB 40 TGGTTAATTCAATCAATAGATATTATTAAAGAACCTAC 3

RESULT 55
AW403028 282 bp mRNA linear EST 16-FEB-2000
LOCUS UI-HF-BK0-aa1-c-09-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
DEFINITION IMAGE:3053944 5', mRNA sequence.
ACCESSION AW403028
VERSION AW403028.1 GI:6921844
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 282)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrrp/image/image.html
Seq primer: M13 Forward.

FEATURES
source 1..282
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3053944"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/clone_lib="NIH MGC 36"
/note="Vector: pT7T3-Pac; Site 1: NotI; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN
Query Match 10.2%; Score 275; DB 2; Length 282;
Best Local Similarity 100.0%; Pred. No. 1.6e-108;
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 CAAATCGTATAGGAGAGAGTAGACTTCCAGATGAGGCTACTCCCTGAAGCTCAGC 320
DB 8 CAAATCGTATAGGAGAGAGTAGACTTCCAGATGAGGCTACTCCCTGAAGCTCAGC 67
QY 321 AAAGTGAAGAAGATGACTCAGGATCTACTATGTGGGATATACAGCTCATCTCAG 380
DB 68 AAAGTGAAGAAGATGACTCAGGATCTACTATGTGGGATATACAGCTCATCTCAG 127
QY 381 CAGCCCTCCACCCAGAGTACGTGCTGCATGTCTACAGCACCTGTCAAAGCCTAAAGTC 440
DB 128 CAGCCCTCCACCCAGAGTACGTGCTGCATGTCTACAGCACCTGTCAAAGCCTAAAGTC 187
QY 441 ACCATGGGTCTGCAGAGCAATAAGATGGCACCTGTGTGAACCAATCTGACATGCTGCATG 500
DB 188 ACCATGGGTCTGCAGAGCAATAAGATGGCACCTGTGTGAACCAATCTGACATGCTGCATG 247
QY 501 GAACATGGGGAAGAGATGATTATACCTGGAA 535
DB 248 GAACATGGGGAAGAGATGATTATACCTGGAA 282

RESULT 56
AI651934 431 bp mRNA linear EST 17-DEC-1999
LOCUS wbs1c08.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:2309198 3',
DEFINITION similar to contains_Alu repetitive element;contains element L1 L1
repetitive element ;, mRNA sequence.
ACCESSION AI651934
VERSION AI651934.1 GI:4735913
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 431)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 543 Std Error: 0.00
Seq primer: -40UP from Gibco.

FEATURES

Source

1. 431
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2309198"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/clone_lib="NCI CGAP GC6"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA from the normalized library NCI CGAP GC4 was prepared, and 88 circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneids 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 10.1%; Score 273; DB 1; Length 431;
Best Local Similarity 99.7%; Pred. No. 1.1e-107;
Matches 323; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2379 TACCAACACAGAGCTCACCATCTTATCTTAAGTGAATAAATCATGGGAGGGAAGG 2438
|||||
DB 328 TACCAACACAGAGCTCACCATCTTATCTTAAGTGAATAAATCATGGGAGGGAAGG 269
OY 2439 GGAATGGCTGCTTGTATGTTCCTGACGCATATCTTGAATGAGACCTCCCTAACCA 2498
|||||
DB 268 GGAATGGCTGCTTGTATGTTCCTGACGCATATCTTGAATGAGACCTCCCTAACCA 209
OY 2499 GTGATGAAAGTGTGAAAACTTAATAACAATGCTTGTGGGCAAGATGGGATTGAGG 2558
|||||
DB 208 GTGATGAAAGTGTGAAAACTTAATAACAATGCTTGTGGGCAAGATGGGATTGAGG 149
OY 2559 ATTATCTTCTCAGAAAGCATTTGTGAAGGAATTGAGCCAGATCTCTCCCTACTGCA 2618
|||||
DB 148 ATTATCTTCTCAGAAAGCATTTGTGAAGGAATTGAGCCAGATCTCTCCCTACTGCA 89
OY 2619 AAACCTATTTAGTAAAGTCTTCTTACTATCTTAATAAACAAGATATGTGAGAT 2678
|||||
DB 88 AAACCTATTTAGTAAAGTCTTCTTACTATCTTAATAAACAAGATATGTGAGAT 29
OY 2679 TCACATAAAAAA 2702
|||||
DB 28 TCACATAAAAAA 5

RESULT 57
AA604443/c 332 bp mRNA linear EST 08-OCT-1997
LOCUS np57g04.r1 NCI CGAP Br2 Homo sapiens CDNA clone IMAGE:1130454 5'
DEFINITION similar to contains Alu repetitive element;; mRNA sequence.
ACCESSION AA604443
VERSION AA604443.1 GI:2445352
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 332)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 492 Std Error: 0.00
Seq primer: -28m13 rev1 ET from Amersham.

FEATURES

Source

1. 332
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1130454"
/sex="female, pooled"
/tissue_type="breast"
/lab_host="DH10B"
/clone_lib="NCI CGAP Br2"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand CDNA was prepared from pooled bulk breast tumor tissue, and was then primed with a Not I - oligo(dT) primer. Double-stranded CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. This library is the normalized version of NCI CGAP Br1.1. Library was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 10.1%; Score 272; DB 1; Length 332;
Best Local Similarity 99.7%; Pred. No. 3.1e-107;
Matches 322; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2268 GCTGAGATGGCACCACTGCACCTCCGGCTTAGGCAACGAGCAAACTCCAATACAAACA 2327
|||||
DB 323 GCTGAGATGGCACCACTGCACCTCCGGCTTAGGCAACGAGCAAACTCCAATACAAACA 264
OY 2328 AACAAACAACACTGTGCTAGTGTGCGACGTAAGATGAACATCCCTAACCAAC 2387
|||||
DB 263 AACAAACAACACTGTGCTAGTGTGCGACGTAAGATGAACATCCCTAACCAAC 204
OY 2388 AGAGCTCACCACTCTTATCTTAAGTGAATAAATCATGGGAGGGAAGGGAATGGCT 2447
|||||
DB 203 AGAGCTCACCACTCTTATCTTAAGTGAATAAATCATGGGAGGGAAGGGAATGGCT 144
OY 2448 GCTTTGATATGCTCCCTGACGCATATCTTGAATGAGACCTCCCTACCAAGTGATGAAA 2507
|||||
DB 143 GCTTTGATATGCTCCCTGACGCATATCTTGAATGAGACCTCCCTACCAAGTGATGAAA 84
OY 2508 GTGTGAAAACTTAATAACAATGCTTGTGGGCAAGATGGGATTGAGATTATCTTC 2567
|||||
DB 83 GTGTGAAAACTTAATAACAATGCTTGTGGGCAAGATGGGATTGAGATTATCTTC 24
OY 2568 TCTCAGAAAGGCAATTGTGAAGGA 2590
|||||
DB 23 TCTCAGAAAGGCAATTGTGAAGGA 1

RESULT 58
AW138797/c 557 bp mRNA linear EST 29-OCT-1999
LOCUS AW138797
DEFINITION UI-H-B11-aep-d-12-0-UI.s1 NCI CGAP_Sub3 Homo sapiens CDNA clone
IMAGE:2719943 3', mRNA sequence.
ACCESSION AW138797

```

VERSION      AM138797.1  GI:6143115
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 557)
AUTHORS      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE        National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
              Tumor Gene Index
JOURNAL      Unpublished (1997)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-r@mail.nih.gov
              The sequence contained an oligo-dT track that was present in the
              oligonucleotide that was used to prime the synthesis of first
              strand cDNA and therefore this may represent a bonafide poly A
              tail. cDNA Library Preparation: M.B. Soares lab Clone distribution::
              NCI-CGAP clone distribution information can be found through the
              I.M.A.G.E. Consortium/LLNL at:
              www-bio.llnl.gov/bbrp/image/image.html The following repetitive
              elements were found in this cDNA sequence: 67-112,
              >MER31A#LTR/MER4-group
              Seq primer: M13 Forward
              POLYA=Yes.

FEATURES
  source
    1..557
      location/Qualifiers
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="IMAGE:2719943"
        /lab_host="DH10B (Life Technologies)"
        /clone_lib="NCI-CGAP Sub3"
        /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
        polylinker; Site 1: Not I; Site 2: Eco RI; The
        NCI-CGAP Sub3 library is a subtracted library derived from
        the NCI-CGAP Sub1 library, which is a subtracted library
        derived from B1. B1 constitutes a mixture of 21
        normalized or subtracted NCI-CGAP libraries:
        NCI-CGAP_Co4, NCI-CGAP_Pr22, NCI-CGAP_Pr28, NCI-CGAP_Co10,
        NCI-CGAP_Co16, NCI-CGAP_Kid5, NCI-CGAP_Kid12,
        NCI-CGAP_Kid3, NCI-CGAP_Kid11, NCI-CGAP_Lym2,
        NCI-CGAP_Br2, NCI-CGAP_Co8, NCI-CGAP_Cll1, NCI-CGAP_Le12,
        NCI-CGAP_Brn23, NCI-CGAP_Lu5, NCI-CGAP_Lu24,
        NCI-CGAP_Lu19, NCI-CGAP_GC4, NCI-CGAP_GC6,
        NCI-CGAP_Brn25. These 21 libraries were pooled and a
        single-stranded DNA preparation of the resulting mixture
        was used as a tracer in a subtractive hybridization with
        a driver whose composition is detailed below:
        NCI-CGAP_Kid3 pool 1 LLAM 3334-3337, 3682-3683,
        3798-3803 (IMAGE Clonoids 1322376-1323911,
        1456008-1456775, 1500552-1502855); NCI-CGAP_Kid5 pool 1
        LLAM 3338-3342, 3722-3725, 3776-3778 (IMAGE Clonoids
        1323912-1325831, 1471368-1472903, 1492104-1493255);
        NCI-CGAP_Lu5 pool 1 LLAM 3575-3582, 3851-3854 (IMAGE
        Clonoids 1414920-1417991, 1520904-1522439); NCI-CGAP_GC4
        pool 1 LLAM 3164-3167, 3716-3720, 3733-3735 (IMAGE
        Clonoids 1257096-1258631, 1469064-1470983,
        1475592-1476743); NCI-CGAP_Pr22 pool 1 LLAM 2457-2459,
        2758-2759, 3062-3068 (IMAGE Clonoids 985608-986759,
        1101192-1101959, 1217928-1220615); NCI-CGAP_Co10 pool 1
        LLAM 2644-2653, 2871-2872 (IMAGE Clonoids 1057416-1061255,
        1144584-1145351). Subtraction was performed as previously
        described (Bonaldo, Lennon & Soares (1996): Normalization
        and Subtraction: Two Approaches To Facilitate Gene
        Discovery. Genome Research 6, 791-806.
        TAG_TISSUE=leiomyosarcoma
        TAG_LIB=NCI-CGAP_Le12
        TAG_SEQ=AATCG"

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QY	2382	CAACACAGAGCTCACCACTCTTATCTTACTTAAGTGAATAAACATGGGGAAGGGGAAGGGGA	2441
Db	318	CAACACAGAGCTCACCACTCTTATCTTACTTAAGTGAATAAACATGGGGAAGGGGAAGGGGA	259
QY	2442	ATGGCTGCTTTGATATGTTTCCCTGACGCATATCTTGAATGGAGACCTCCCTACCAAGTG	2501
Db	258	ATGGCTGCTTTGATATGTTTCCCTGACGCATATCTTGAATGGAGACCTCCCTACCAAGTG	199
QY	2502	ATGAAAGTGTTGAAAAAAGCTTAATAACAAGTCTGTGGGCAAGAATGGATTGAGATT	2561
Db	198	ATGAAAGTGTTGAAAAAAGCTTAATAACAAGTCTGTGGGCAAGAATGGATTGAGATT	139
QY	2562	ATCTTCTCTCAGAAAGCATTTGTGAAGGAATTGAGCCAGATCTCTCCCTACTGCAAAA	2621
Db	138	ATCTTCTCTCAGAAAGCATTTGTGAAGGAATTGAGCCAGATCTCTCCCTACTGCAAAA	79
QY	2622	CCCTATTGTAGTAAAAAAGTCTTCTTTACTATCTTAATAAACAAGATATTGTGAGATTCA	2681
Db	78	CCCTATTGTAGTAAAAAAGTCTTCTTTACTATCTTAATAAACAAGATATTGTGAGATTCA	19
QY	2682	CATAAAAAAAAAAAAAAAAA	2699
Db	18	CATAAAAAAAAAAAAAAAAA	1

RESULT 59
 BQ440846
 LOCUS
 DEFINITION
 BQ440846 855 bp mRNA linear EST 24-MAY-2002
 AGENCOURT_7902875 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6158031
 5', mRNA sequence.
 ACCESSION
 BQ440846
 VERSION
 BQ440846.1 GI:21179922
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 855)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 COMMENT
 Contact: Robert Strausberg, Ph.D.

Tissue Procurement: ATCC/DCTD/DTP
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: L1AM13504 row: n column: 16
 High quality sequence stop: 277.

```

FEATURES
    source
        Location/Qualifiers
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                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:6158031"
                /tissue_type="melanotic melanoma"
                /lab_host="DH10B (phage-resistant)"
                /clone_lib="NIH_MGC_72"
                /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                Average insert size 2 kb. Library constructed by Life
                Technologies."

```

ORIGIN	no_duplicates
Query Match	9.9%; Score 267; DB 2; length 557;
Best Local Similarity	99.7%; Pred. No. 4.4e-105;
Matches 317; Conservative	0; Mismatches 1; Indels 0; Gaps 0;

ORIGIN	Query Match	Best Local Similarity	Score 261;	DB 5;	length 855;
	Matches 261;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	824	GAAGAGAGAGTGGACATTGTTCGGGAACCTCTAACATATATGCCCCCATTTGGAGAGAA			883

|||||
Db 1 GAAGAAGAGAGTGACATTTGTCCGGAACTCCCTAACATATGCCCCCATTTGGAGAGAA 60
QY 884 CACAGAGTACGACACAATCCCTCACAATAAGAACATCTTAAGGAAGATCCAGCAA 943
Db 61 CACAGAGTACGACACAATCCCTCACAATAAGAACATCTTAAGGAAGATCCAGCAA 120
QY 944 TACGGTTACTCCACTGTGGAAATACCGAAAAAGATGAAAAATCCCACTACTGCTCAC 1003
Db 121 TACGGTTACTCCACTGTGGAAATACCGAAAAAGATGAAAAATCCCACTACTGCTCAC 180
QY 1004 GATGCCAGACACACCAAGGCTATTGGCCTATGAGAAATGTTATCTAGACAGCAGTGCATC 1063
Db 181 GATGCCAGACACACCAAGGCTATTGGCCTATGAGAAATGTTATCTAGACAGCAGTGCATC 240
QY 1064 CCCTAAGTCTGCTCAAAA 1084
Db 241 CCCTAAGTCTGCTCAAAA 261
RESULT 60
H73135 436 bp mRNA linear EST 31-OCT-1995
LOCUS yu03f06.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone
DEFINITION IMAGE:232739 5', mRNA sequence.
ACCESSION H73135
VERSION H73135.1 GI:1046989
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 436)
AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chisoe,S., Dietrich,N., Dubuque,T., Pavello,A., Gish,W.,
Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
Rohlfing,T., Scheinberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J.,
Trevaskis,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R.
and Marra,M.
TITLE Generation and analysis of 280,000 human expressed sequence tags
JOURNAL Genome Res. 6 (9), 807-828 (1996)
MEDLINE 97044478
PUBMED 8889549
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1186
High quality sequence stops: 255
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 1186 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 255.
Location/Qualifiers
1. .436
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3785916"
/db_xref="taxon:9606"
/clone="IMAGE:232739"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal liver spleen INFLS"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;
1st strand cDNA was primed with a Pac I - oligo(dT) primer
[5', AACTGGAAGAAATTAATAAGATCTTTTTTTTTTTTTTTT 3'],

double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."
ORIGIN
Query Match 9.5%; Score 258; DB 7; Length 436;
Best Local Similarity 100.0%; Pred. No. 3.8e-101;
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 49 GTTCCCAACATGCTCACCCTCATCTATATCCTTTGGCAGCTCACAGGCTCAGCCT 108
Db 18 GTTCCCAACATGCTCACCCTCATCTATATCCTTTGGCAGCTCACAGGCTCAGCCT 77
QY 109 CTGACCCGTGAAGAGCTGTCGTTCCGTTGGTGGGGCCGTGACTTCCCCCTGAAGT 168
Db 78 CTGACCCGTGAAGAGCTGTCGTTCCGTTGGTGGGGCCGTGACTTCCCCCTGAAGT 137
QY 169 CCAAAGTAAAGCAAGTTGACTCTATTGCTGACCTTCAACACAAACCCCTTTGTACCA 228
Db 138 CCAAAGTAAAGCAAGTTGACTCTATTGCTGACCTTCAACACAAACCCCTTTGTACCA 197
QY 229 TACAGCCAGAAGGGGCATATCATAGTGACCCAAATCGTAATAGGAGAGTAGACT 288
Db 198 TACAGCCAGAAGGGGCATATCATAGTGACCCAAATCGTAATAGGAGAGTAGACT 257
QY 289 TCCAGATGAGGCTACT 306
Db 258 TCCAGATGAGGCTACT 275
RESULT 61
BU183701 774 bp mRNA linear EST 04-SEP-2002
LOCUS BU183701
DEFINITION AGENCOURT_7959586 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6165637
ACCESSION BU183701
VERSION BU183701.1 GI:22697685
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 774)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DRP
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: L1AM13524 row: k column: 14
High quality sequence stop: 561.
Location/Qualifiers
1. .774
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6165637"
/issue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."

ORIGIN

Query Match 9.2%; Score 250; DB 1; Length 354;
Best Local Similarity 99.7%; Pred. No. 1.2e-97;
Matches 300; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2381 CCAACACAGAGCTCACCATCTCTTATACCTTAAGTGAACAAACATGGGAGGGAAGGGG 2440
|||||
Db 313 CCAACACAGAGCTCACCATCTCTTATACCTTAAGTGAACAAACATGGGAGGGAAGGGG 254
|||||

OY 2441 AATGGCTGCTTTGATATGTTCCCTGACGCATATCTTGAATGAGAGACTCCCTACCAAGT 2500
|||||
Db 253 AATGGCTGCTTTGATATGTTCCCTGACACATATCTTGAATGAGAGACTCCCTACCAAGT 194
|||||

OY 2501 GATGAAAGTGTGAAAACTTAATAACAATGCTTGTGGGCAAGAATGGGATTGAGGAT 2560
|||||
Db 193 GATGAAAGTGTGAAAACTTAATAACAATGCTTGTGGGCAAGAATGGGATTGAGGAT 134
|||||

OY 2561 TATCTTCTCTCAGAAAGGCAATTGTGAAGGAATTGAGCCAGATCTCTCCCTACTGCAAA 2620
|||||
Db 133 TATCTTCTCTCAGAAAGGCAATTGTGAAGGAATTGAGCCAGATCTCTCCCTACTGCAAA 74
|||||

OY 2621 ACCCTATTGTAGTAAAAAGCTCTCTTACTATCTTAATAAACAAGATATTGTGAGATTG 2680
|||||
Db 73 ACCCTATTGTAGTAAAAAGCTCTCTTACTATCTTAATAAACAAGATATTGTGAGATTG 14
|||||

OY 2681 A 2681
|
Db 13 A 13

RESULT 64
AI521522/c 321 bp mRNA linear EST 12-MAY-1999
LOCUS to64b07.x1 NCI_CGAP Gas4 Homo sapiens cDNA clone IMAGE:2183029 3'
DEFINITION similar to contains element MER6 MER6 repetitive element ;, mRNA
sequence.

ACCESSION AI521522 GI:4435657
VERSION AI521522.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 321)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 728 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 295
POLYA=No.

FEATURES
source 1. .321
Location/Qualifiers
1. .321
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2183029"
/tissue_type="poorly differentiated adenocarcinoma with
signed ring cell features"
/lab_host="DH10B"
/clone_lib="NCI_CGAP Gas4"
/note="Organ: stomach; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.

ORIGIN
Average insert size 1.69 kb. Life Technologies catalog #: 11549-011"

Query Match 9.2%; Score 249; DB 1; Length 321;
Best Local Similarity 99.7%; Pred. No. 3.4e-97;
Matches 299; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2381 CCAACACAGAGCTCACCATCTCTTATACCTTAAGTGAACAAACATGGGAGGGAAGGGG 2440
|||||
Db 321 CCAACACAGAGCTCACCATCTCTTATACCTTAAGTGAACAAACATGGGAGGGAAGGGG 262
|||||

OY 2441 AATGGCTGCTTTGATATGTTCCCTGACGCATATCTTGAATGAGAGACTCCCTACCAAGT 2500
|||||
Db 261 AATGGCTGCTTTGATATGTTCCCTGACACATATCTTGAATGAGAGACTCCCTACCAAGT 202
|||||

OY 2501 GATGAAAGTGTGAAAACTTAATAACAATGCTTGTGGGCAAGAATGGGATTGAGGAT 2560
|||||
Db 201 GATGAAAGTGTGAAAACTTAATAACAATGCTTGTGGGCAAGAATGGGATTGAGGAT 142
|||||

OY 2561 TATCTTCTCTCAGAAAGGCAATTGTGAAGGAATTGAGCCAGATCTCTCCCTACTGCAAA 2620
|||||
Db 141 TATCTTCTCTCAGAAAGGCAATTGTGAAGGAATTGAGCCAGATCTCTCCCTACTGCAAA 82
|||||

OY 2621 ACCCTATTGTAGTAAAAAGCTCTCTTACTATCTTAATAAACAAGATATTGTGAGATTG 2680
|||||
Db 81 ACCCTATTGTAGTAAAAAGCTCTCTTACTATCTTAATAAACAAGATATTGTGAGATTG 22
|||||

RESULT 65
AW080386/c 315 bp mRNA linear EST 14-OCT-1999
LOCUS xe41e10.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2610474 3',
DEFINITION mRNA sequence.

ACCESSION AW080386 GI:6035538
VERSION AW080386
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 315)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Nan Hu, M.D., Ph.D., Mark Roth, M.D., Phillip
Taylor, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 309.

FEATURES
source 1. .315
Location/Qualifiers
1. .315
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2610474"
/tissue_type="squamous cell carcinoma"
/lab_host="DH10B"
/clone_lib="NCI_CGAP Eso2"
/note="Organ: esophagus; Vector: pCMV-SPORT6; Site 1:
SalI; Site 2: NotI; Cloned unidirectionally. Primer:
Oligo dT. Average insert size 1.1 kb. Life Technologies
catalog #: 11502-010"

ORIGIN

Query Match 9.1%; Score 247; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 2.5e-96;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1610 CCTCATGAATTTGGCTCCAAATGAATGAATCTTTCATGAGCAGTTGTAGCAGGCTGA 1669
DB 315 CCTCATGAATTTGGCTCCAAATGAATGAATCTTTCATGAGCAGTTGTAGCAGGCTGA 256
QY 1670 CCACAGATTTCCAGAGGGCCAGGTGTGATCCACAGACTTGAAGTCAAAAGTTCACAAA 1729
DB 255 CCACAGATTTCCAGAGGGCCAGGTGTGATCCACAGACTTGAAGTCAAAAGTTCACAAA 196
QY 1730 GATGAAGAATCAGGGTAGCTGACCATGTTTGGCAGATCTATTAATGAGACACAGAAGTG 1789
DB 195 GATGAAGAATCAGGGTAGCTGACCATGTTTGGCAGATCTATTAATGAGACACAGAAGTG 136
QY 1790 TGCATGGCCCAAGACAGACCTCCAGCCAGCTTCATTATGCACTTGTGCTGCAAAA 1849
DB 135 TGCATGGCCCAAGACAGACCTCCAGCCAGCTTCATTATGCACTTGTGCTGCAAAA 76
QY 1850 GAAAAGT 1856
DB 75 GAAAAGT 69

RESULT 66
AM379005/c 493 bp mRNA linear EST 04-FEB-2000
LOCUS AM379005 RC3-HT0230-241099-012-b08 HT0230 Homo sapiens cDNA, mRNA sequence.
DEFINITION AM379005
ACCESSION AM379005.1 GI:6883664
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 493)
AUTHORS HCGP <http://www.ludwig.org.br/ORESTES>.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC3<2=RC3-HT0230-241099-012-b08<3=1999-10-24<4=1>)
Seq primer: puc 18 forward
High quality sequence start: 14
High quality sequence stop: 492.

FEATURES
source 1. 493
location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="HT0230"
/note="Organ: head neck; Vector: puc18; Site 1: Sma1; Site 2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 9.1%; Score 245; DB 2; Length 493;
Best Local Similarity 99.4%; Pred. No. 1.8e-95;

Matches 465; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 1314 AAAGTCTTAGAAGTATTCCTATAGAAATGTAAATGCAAGCTCACACATATTATGACAG 1373
DB 472 AAAGTCTTAGAAGTATTCCTATAGAAATGTAAATGCAAGCTCACACATATTATGACAG 413
QY 1374 CCTGTTGATTAAATGATGGCTCCAGGTCAAGTGTCTGAGTTTCATTCCATCCAGGGCTT 1433
DB 412 CCTGTTGATTAAATGATGGCTCCAGGTCAAGTGTCTGAGTTTCATTCCATCCAGGGCTT 353
QY 1434 GGAATGTCAGGATTATACCAAGAGTCTTGTCTACACAGAGGGCAAGAAGACCAAAACAGACA 1493
DB 352 GGAATGTCAGGATTATACCAAGAGTCTTGTCTACACAGAGGGCAAGAAGACCAAAACAGACA 293
QY 1494 GACAAGTCCAG-CAGAAGCAGATGCACCTGACAAAATGATGTATTATTGGCTCTATA 1552
DB 292 GACAAGTCCAGCAGAAGCAGATGCACCTGACAAAATGATGTATTATTGGCTCTATA 233
QY 1553 AACTATGTGCCCAAGCAGCTATGCTGAGCTTACACTAATTGGTCAGACGTGCTGTGCCCT 1612
DB 232 AACTATGTGCCCAAGCAGCTATGCTGAGCTTACACTAATTGGTCAGACGTGCTGTGCCCT 173
QY 1613 CATGAATTTGGCTCCAAATGAATGAATGAATCTTTCATGAGCAGTGTAGCAGGCTGACCA 1672
DB 172 CATGAATTTGGCTCCAAATGAATGAATGAATCTTTCATGAGCAGTGTAGCAGGCTGACCA 113
QY 1673 CAGATTCCAGAGGGCCAGGTGTGATCCACAGAGCTTGAAGGTCAAAAGTTCACAAAAGAT 1732
DB 112 CAGATTCCAGAGGGCCAGGTGTGATCCACAGAGCTTGAAGGTCAAAAGTTCACAAAAGAT 53
QY 1733 GAAGAATCAGGGTAGCTGACCATGTTTGGCAGATCTATAATGAGAC 1780
DB 52 GAAGAATCAGGGTAGCTGACCATGTTTGGCAGATCTATAATGAGAC 5

RESULT 67
AA554342/c 411 bp mRNA linear EST 09-SEP-1997
LOCUS AA554342 n103e08.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:1029254 3', mRNA sequence.
DEFINITION AA554342
ACCESSION AA554342.1 GI:2324881
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 411)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arraying: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
www.bio.lnl.gov/bbrp/image/image.html
Insert length: 579 Std Error: 0.00
Seq primer: -40m13 fwd..ET from Amersham
High quality sequence stop: 388.
location/Qualifiers
1. 411
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1029254"
/sex="pooled"
/tissue_type="colon"

FEATURES
source 1. 411
location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1029254"
/sex="pooled"
/tissue_type="colon"

/lab_host="DH10B"
/clone_lib="NCI_CGAP_C03"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from 12 pooled bulk tumor samples and primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT7T3 vector. Library went through one round of
normalization."

ORIGIN

Query Match 8.9%; Score 240; DB 1; Length 411;
Best Local Similarity 99.7%; Pred. No. 2.7e-93;
Matches 290; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2394 CACCATCTCTTATCTTAAGTGAACAAACATGGGAGGGAAGGGAATGGCTGCTTTT 2453
|||||
Db 291 CACCATCTCTTATCTTAAGTGAACAAACATGGGAGGGAAGGGAATGGCTGCTTTT 232
|||||

QY 2454 GATATGTTCCCTGACGCATCTTGAATGAGACCTCCCTACCAAGTGAAGTGTG 2513
|||||
Db 231 GATATGTTCCCTGACACATATCTTGAATGAGACCTCCCTACCAAGTGAAGTGTG 172
|||||

QY 2514 AAAAAGCTTAATACAAATGCTTGTGGCAAGATGGGATGAGATATCTCTCTCAG 2573
|||||
Db 171 AAAAAGCTTAATACAAATGCTTGTGGCAAGATGGGATGAGATATCTCTCTCAG 112
|||||

QY 2574 AAAGGCATGTGAAGAAATTGAGCCAGATCTCTCTCCCTACTGCACAAACCTTATTGTA 2633
|||||
Db 111 AAAGGCATGTGAAGAAATTGAGCCAGATCTCTCTCCCTACTGCACAAACCTTATTGTA 52
|||||

QY 2634 AAAAAAGCTTCTTACTATCTTAATAAACAGATATTGTGAGATTACAT 2684
|||||
Db 51 AAAAAAGCTTCTTACTATCTTAATAAACAGATATTGTGAGATTACAT 1
|||||

RESULT 68
AI366936/c 343 bp mRNA linear EST 15-FEB-1999
LOCUS AI366936/c
DEFINITION qw18b04.x1 NCI_CGAP_Ut3 Homo sapiens cDNA clone IMAGE:1991407 3',
mRNA sequence.
ACCESSION AI366936
VERSION AI366936.1 GI:4136681
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 343)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1130 Std Error: 0.00
Seq primer: -40UP from G1bco
High quality sequence stop: 341.
Location/Qualifiers

FEATURES

Source
1..343
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1991407"

/tissue_type="poorly-differentiated endometrial
adenocarcinoma, 2 pooled tumors"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Ut3"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.45 kb. Life Technologies catalog #:
11541-018"

ORIGIN

Query Match 8.6%; Score 233; DB 1; Length 343;
Best Local Similarity 99.6%; Pred. No. 3.2e-90;
Matches 283; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2401 TCTTATCTTAAGTGAACAAACATGGGAGGGAAGGGAATGGCTGCTTTGATATGT 2460
|||||
Db 284 TCTTATCTTAAGTGAACAAACATGGGAGGGAAGGGAATGGCTGCTTTGATATGT 225
|||||

QY 2461 TCCCTGACCATATCTTGAATGAGACCTCCCTACCAAGTGAAGTGTGAAAACT 2520
|||||
Db 224 TCCCTGACACATATCTTGAATGAGACCTCCCTACCAAGTGAAGTGTGAAAACT 165
|||||

QY 2521 TAATAACAATGCTTGTGGCAAGATGGGATGAGATATCTCTCTCAGAAAGCA 2580
|||||
Db 164 TAATAACAATGCTTGTGGCAAGATGGGATGAGATATCTCTCTCAGAAAGCA 105
|||||

QY 2581 TTGTGAAGAAATTGAGCCAGATCTCTCTCCCTACTGCACAAACCTTATTGTA 2640
|||||
Db 104 TTGTGAAGAAATTGAGCCAGATCTCTCTCCCTACTGCACAAACCTTATTGTA 45
|||||

QY 2641 TCTTCTTACTTCTTAATAAACAGATATTGTGAGATTACAT 2684
|||||
Db 44 TCTTCTTACTTCTTAATAAACAGATATTGTGAGATTACAT 1
|||||

RESULT 69
CA432799/c 245 bp mRNA linear EST 08-NOV-2002
LOCUS CA432799/c
DEFINITION UI-H-CO0-aqc-g-08-0-UI.s1 NCI CGAP_Sub9 Homo sapiens cDNA clone
UI-H-CO0-aqc-g-08-0-UI 3', mRNA sequence.
ACCESSION CA432799
VERSION CA432799.1 GI:24797217
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 245)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
Seq primer: M13 FORWARD
POLYA=Yes.
Location/Qualifiers

FEATURES

Source
1..245
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-CO0-aqc-g-08-0-UI"
/tissue_type="mixed"
/dev_stage="mixed"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_Sub9"
/note="Vector: pT7T3-Pac (Pharmacia) with a modified

polylinker; Site_1: EcoR I; Site_2: Not I; tissues: Cholonic mucosa with Crohns disease, Cholonic mucosa with ulcerative colitis, Fetal thymus, Cervix, Cervical adenosquamous carcinoma, Ligament cells, Prostate carcinoma, Bladder carcinoma, Brain oligodendroga; NCI_CGAP_Sub9 is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are CGTC, AACG, GGGCC, GGAGG, TAGC, TAAGC, ATGG, AGACA, ATCAC. For additional information, contact: Bento Soares, bento-soares@uiowa.edu TAG_TISSUE=Cervical Adenosquamous Carcinoma TAG_LIB=UI-H-COO TAG_SEQ=CGAAG"

ORIGIN

Query Match 8.2%; Score 223; DB 6; Length 245; Best Local Similarity 100.0%; Pred. No. 7.6e-86; Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1686 GGCCAGGTGTGGATCCACAGACTTGAAGTCAAAAGTTCACAAAGATGAAGATCAGGGT 1745
DB 245 GGCCAGGTGTGGATCCACAGACTTGAAGTCAAAAGTTCACAAAGATGAAGATCAGGGT 186
OY 1746 AGCTGACCATGTTTGGCAGATACTATAATGAGACACAGAAGTGTGCATGGCCCCAAGGAC 1805
DB 185 AGCTGACCATGTTTGGCAGATACTATAATGAGACACAGAAGTGTGCATGGCCCCAAGGAC 126
OY 1806 AAGGACCTCCAGCCAGGCTTCATTATGCACTTGTGTCGCAAAAGAAAGTCTAGGTTT 1865
DB 125 AAGGACCTCCAGCCAGGCTTCATTATGCACTTGTGTCGCAAAAGAAAGTCTAGGTTT 66
OY 1866 AAGGCTGTGCCAGAACCCATCCCAATTAAGAGACCGAGTCTGA 1908
DB 65 AAGGCTGTGCCAGAACCCATCCCAATTAAGAGACCGAGTCTGA 23

RESULT 70
AV713600 789 bp mRNA linear EST 11-OCT-2000

LOCUS AV713600 DCB Homo sapiens cDNA clone DCBAVH04 5', mRNA sequence.
DEFINITION AV713600
ACCESSION AV713600
VERSION AV713600.1 GI:10795117

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 789)
AUTHORS Xu,X., Gu,J., Liu,F., Qu,J., Zhao,M., Li,Y., Huang,Q., Zhou,J., Song,H., Gu,Y., Yang,Y., Gao,G., Xiao,H., Li,N., Qian,B., Gao,X., Cheng,Z., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Cheng,Z. and Han,Z.
Homo sapiens cDNA DCB clones

TITLE Unpublished (2000)
JOURNAL Contact: Zeguang Han
COMMENT Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn

FEATURES
source 1. .789
This clone is available at CHGC in Shanghai.
location/Qualifiers

1. .789
/organism="Homo sapiens"
/mol_type="mRNA"

/db_xref="taxon:9606"
/clone="DCBAVH04"
/cell_type="dendritic cells"
/dev_stage="mature"
/lab_host="BM25.8"
/clone_lib="DCB"
/note="Vector: pTriplex2; Site_1: sfiIA; Site_2: sfiIB"

ORIGIN

Query Match 7.9%; Score 214; DB 1; Length 789; Best Local Similarity 100.0%; Pred. No. 5.5e-82; Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2255 GAGGTTGCACTGAGCTGAGATGGCACCACTGCACCTCCGGCCTTAGGCAACGAGAGCAAAAC 2314
DB 347 GAGGTTGCACTGAGCTGAGATGGCACCACTGCACCTCCGGCCTTAGGCAACGAGAGCAAAAC 406
OY 2315 TCCAATACAACAACAACAACAACAACACCTGTGCTAGGTCAGTCTGGCACGTAAGATGAACA 2374
DB 407 TCCAATACAACAACAACAACAACAACACCTGTGCTAGGTCAGTCTGGCACGTAAGATGAACA 466
OY 2375 TCCCTACCAACACAGAGCTCACCATCTCTTATACTTAAGTGAATAACATGGGAGGGGA 2434
DB 467 TCCCTACCAACACAGAGCTCACCATCTCTTATACTTAAGTGAATAACATGGGAGGGGA 526
OY 2435 AAGGGAATGGCTGCTTTGATATATGTTCCCTGAC 2468
DB 527 AAGGGAATGGCTGCTTTGATATATGTTCCCTGAC 560

RESULT 71

BX279875 466 bp mRNA linear EST 04-MAR-2003
LOCUS BX279875 NIH_MGC_72 Homo sapiens cDNA clone IMAGE998J1212256 ;
DEFINITION IMAGE:5548139, mRNA sequence.
ACCESSION BX279875
VERSION BX279875.1 GI:28613477

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 466)
AUTHORS Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M., Radejof,U., Schneider,D. and Korn,B.
Human Unigeneset - RZPD3

TITLE Unpublished (2003)
JOURNAL Contact: Ina Rolfs
COMMENT RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGE998J1212256.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human Unigeneset - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/cgi-bin/showlib.pl.cgi?response?libNo=972 Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13u, Primer sequence: CGTGTAAACGACGCCAGT.
location/Qualifiers

FEATURES

source 1. .466
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE998J1212256 ; IMAGE:5548139"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;

Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life Technologies."

ORIGIN

Query Match 7.5%; Score 204; DB 5; Length 466;
Best Local Similarity 99.6%; Pred. No. 1.4e-77;
Matches 254; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1784 GAAGTGTGCATGGCCCAAGACAAGACCTCCAGCCAGCTTCATTATGCACTGTGCT 1843
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Db 1 GAAGTGTGCATGGCCCAAGACAAGACCTCCAGCCAGCTTCATTATGCACTGTGCT 60
|||||

QY 1844 GCAAAAGAAAAGTCTAGCTTTTAAAGCTGTGCCAGAACCCATCCCAATAAAGAGACCGAG 1903
|||||
Db 61 GCAAAAGAAAAGTCTAGCTTTTAAAGCTGTGCCAGAACCCATCCCAACAAGAGACCGAG 120
|||||

QY 1904 TCTGAAGTCACATGTGTAATCTAGTGTAGAGACTTGAGTCAAGCAGTGAAGTGTGG 1963
|||||
Db 121 TCTGAAGTCACATGTGTAATCTAGTGTAGAGACTTGAGTCAAGCAGTGAAGTGTGG 180
|||||

QY 1964 GGCACGGGGGCGAGTGGTACTTGTAAACCTTTAAAGATGTTAATTCATTCAATAGATA 2023
|||||
Db 181 GGCACGGGGGCGAGTGGTACTTGTAAACCTTTAAAGATGTTAATTCATTCAATAGATA 240
|||||

QY 2024 TTTATTAGAACCCTA 2038
|||||
Db 241 TTTATTAGAACCCTA 255
|||||

RESULT 72

BM551726 1026 bp mRNA linear EST 20-FEB-2002
LOCUS BM551726
DEFINITION AGENCOURT_6544759 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5548139
5', mRNA sequence.

ACCESSION BM551726
VERSION BM551726.1 GI:18788997

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1026)

REFERENCE NIH-MGC <http://mgs.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rt@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
<http://image.llnl.gov>
Plate: LLM12256 row: j column: 12
High quality sequence stop: 552.

FEATURES
SOURCE 1. 1026
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5548139"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."

ORIGIN

Query Match

7.5%; Score 202; DB 4; Length 1026;

Best Local Similarity 99.6%; Pred. No. 9.2e-77;
Matches 252; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1786 AGTGTGCATGGCCCAAGACAAGACCTCCAGCCAGCTTCATTATGCACTGTGCTGC 1845
|||||
Db 1 AGTGTGCATGGCCCAAGACAAGACCTCCAGCCAGCTTCATTATGCACTGTGCTGC 60
|||||

QY 1846 AAAAGAAAAGTCTAGCTTTTAAAGGCTGTGCCAGAACCCATCCCAATAAAGAGACCGAGTC 1905
|||||
Db 61 AAAAGAAAAGTCTAGCTTTTAAAGGCTGTGCCAGAACCCATCCCAACAAGAGACCGAGTC 120
|||||

QY 1906 TGAAGTCACATGTGTAATCTAGTGTAGAGACTTGAGTCAAGCAGTGAAGTGTGGG 1965
|||||
Db 121 TGAAGTCACATGTGTAATCTAGTGTAGAGACTTGAGTCAAGCAGTGAAGTGTGGG 180
|||||

QY 1966 CACGGGGGCGAGTGGTACTTGTAAACCTTTAAAGATGTTAATTCATTCAATAGATATT 2025
|||||
Db 181 CACGGGGGCGAGTGGTACTTGTAAACCTTTAAAGATGTTAATTCATTCAATAGATATT 240
|||||

QY 2026 TATTAGAACCCTA 2038
|||||
Db 241 TATTAGAACCCTA 253
|||||

RESULT 73

AA381714 321 bp mRNA linear EST 21-APR-1997
LOCUS AA381714
DEFINITION EST94847 Activated T-cells 1 Homo sapiens cDNA 5' end, mRNA
sequence.

ACCESSION AA381714
VERSION AA381714.1 GI:2034053

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 321)

REFERENCE Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-wai,C.,
Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palanges,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Saudke,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dimke,D., Feng,D.-F., Ferris,A., Fischer,C., Hastings,G.A.,
He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weisner,P.S., Olsen,H.,
Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
Fraser,C.M. and Venter,J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence

JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)
MEDLINE 96026280
PUBMED 7566098
COMMENT Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/cdb/hgi/hgi.html>)
Seq primer: M13 Reverse.

FEATURES
SOURCE 1. 321
Location/Qualifiers
/organism="Homo sapiens"

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/mol_type="mRNA"
/db_xref="ATCC (inhost):186105"
/db_xref="taxon:9606"
/cell_type="T-lymphocyte"
/dev_stage="adult"
/clone_lib="Activated T-cells I"
/notes="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI"

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ORIGIN

Query Match	7.4%	Score 200	DB 1	Length 321
Best Local Similarity	99.3%	Pred. No. 7.9e-76		
Matches 300	Conservative 0	Mismatches 2	Indels 0	Gaps 0
QY	20	TGGCTGACTTCCAGAGAGCAATATGGCTGTTCCCCCAACATGCTCACCCTCATCTATAT	79	
Db	20	TGGCTGACTTCCAGAGAGCAATATGGCTGTTCCCCCAACATGCTCACCCTCATCTATAT	79	
QY	80	CCTTTGGAGCTCACAGGCTCAGCAGCTCTGAGCCCGTGAAAGAGCTGTGGTTCCGT	139	
Db	80	CCTTTGGAGCTCACAGGCTCAGCAGCTCTGAGCCCGTGAAAGAGCTGTGGTTCCGT	139	
QY	140	TGGTGGGGCGTGACTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTTATTTGCTG	199	
Db	140	TGGTGGGGCGTGACTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTTATTTGTTG	199	
QY	200	GACCTTCAACACAAACCCCTTGTCAACCATACAGCCAGAGGGGGCACTATCATAGTAC	259	
Db	200	GACCTTCAACACAAACCCCTTGTCAACCATACAGCCAGAGGGGGCACTATCATAGTAC	259	
QY	260	CCAAATCGTAATAGGAGAGAGTAGACTTCCCAAGATGAGGCTACTCCCTGAAGCTCAG	319	
Db	260	CCAAATCGTAATAGGAGAGAGTAGACTTCCCAAGATGAGGCTACTCCCTGAAGCTCAG	319	
QY	320	CA 321		
Db	320	CA 321		

RESULT 74					
LOCUS	AW515147/c				
DEFINITION	xu92b03.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2809133',	201 bp	mRNA	linear	EST 03-MAR-2000
ACCESSION	AW515147				
VERSION	AW515147.1	GI:7153229			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 201)				
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .				
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index				
COMMENT	Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ lntl.nlh.nih.gov/image/ image.lnl.gov/image/htcml/iresources.shtm Seq primer: -40UP from Gibco.				

FEATURES

source

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/organism="Homo sapiens"  
/mol_type="mRNA"  
/db_xref="taxon:9606"  
/clone="IMAGE:2809133"
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/tissue_type="moderately-differentiated endometrial
adenocarcinoma, 3 pooled tumors"
/lab_host="DH10B"
/clone_1ib="NCI CGAP Ut2"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.85 kb. Life Technologies catalog #:
11539-012"

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ORIGIN

Query Match	7.4%;	Score 199;	DB 2;	Length 201;
Best Local Similarity	100.0%;	Pred. No. 2.3e-75;		
Matches 199;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	2487	CCTCCCTACCAAGTGATGAAAGTGTGAAAACTTAATACAAATGCTTGTGGGCAAGA	2546	
Db	201	CCTCCCTACCAAGTGATGAAAGTGTGAAAACTTAATACAAATGCTTGTGGGCAAGA	142	
Qy	2547	ATGGGATTGAGATTATCTTCTCTCAGAAAGCATTGTGAAGGAATTGAGCCAGATCTCT	2606	
Db	141	ATGGGATTGAGATTATCTTCTCTCAGAAAGCATTGTGAAGGAATTGAGCCAGATCTCT	82	
Qy	2607	CTCCCTACTGCAAAACCCTATTGTAGTAATAAAGTCTTCTTACTATCTTAATAAACAG	2666	
Db	81	CTCCCTACTGCAAAACCCTATTGTAGTAATAAAGTCTTCTTACTATCTTAATAAACAG	22	
Qy	2667	ATATTGTGAGATTCACATA	2685	
Db	21	ATATTGTGAGATTCACATA	3	

RESULT 75	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
AI917364/c	AI917364	ts83f07.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2237893 3', mRNA sequence.	AI917364	AI917364	EST.	Homo sapiens (human)	Homo sapiens	1 (bases 1 to 294)	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	Unpublished (1997)	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
		294 bp mRNA linear EST 28-JUL-1999										cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
												cDNA Library Arrayed by: Greg Lennon, Ph.D.
												DNA Sequencing by: Washington University Genome Sequencing Center
												Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
												www-bio.lnl.gov/bbrp/image/image.html
												Seq primer: -40UP from Gibco
												High quality sequence stop: 281.

FEATURES

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1. . 294
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:2237893"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/clone_lib="NCI CGAP GC6"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; plasmid DNA
from the normalized library NCI_CGAP_GC4 was prepared, and

```

as circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 7.2%; Score 194; DB 1; Length 294;
Best Local Similarity 100.0%; Pred. No. 3.3e-73;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2487 CCTCCCTACCAAGTGAAGTGTGAAAACTTAATAACAATGCTTGTGGCAAGA 2546
|||
Db 223 CCTCCCTACCAAGTGAAGTGTGAAAACTTAATAACAATGCTTGTGGCAAGA 164

QY 2547 ATGGATTGAGATTATCTTCTCTCAGAAAGCAATTGGAAGATTGAGCCAGATCTCT 2606
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Db 163 ATGGATTGAGATTATCTTCTCTCAGAAAGCAATTGGAAGATTGAGCCAGATCTCT 104

QY 2607 CTCCCTACTGCAAAACCTTATTGTAGTAAAAAGTCTTCTTACTATCTAATAAAACAG 2666
|||
Db 103 CTCCCTACTGCAAAACCTTATTGTAGTAAAAAGTCTTCTTACTATCTAATAAAACAG 44

QY 2667 ATATTGTGAGATTTC 2680
|||
Db 43 ATATTGTGAGATTTC 30

Search completed: October 28, 2004, 19:18:41
Job time : 8276 secs

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ALIGNMENTS

RESULT 1

US-09-023-655-401

; Sequence 401, Application US/09023655
; Patent No. 6607879

; GENERAL INFORMATION:

; APPLICANT: Cocks, Benjamin G.

; APPLICANT: Susan G. Stuart

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE

; NUMBER OF SEQUENCES: 1508

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/023,655

; FILING DATE: HERewith

; CLASSIFICATION:

; PRIORITY APPLICATION DATA:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Zeller, Karen J.

; REGISTRATION NUMBER: 37,071

; REFERENCE/DOCKET NUMBER: PA-0001 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (650) 855-0555

; TELEFAX: (650) 845-4166

; INFORMATION FOR SEQ ID NO: 401:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 921 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: THPLPLB02

; CLONE: 156352

US-09-023-655-401

Query Match 24.0%; Score 649; DB 4; Length 921;

Best Local Similarity 99.8%; Pred. No. 2.4e-269;

Matches 819; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 1220 TAAATTCATCCACTGCTGAGAAATCTCTCAAAACCCAGAAAGTTTAATCACTTCATCCCA 1279

DB 99 TAAATTCATCCACTGCTGAGAAATCTCTCAAAACCCAGAAAGTTTAATCACTTCATCCCA 158

OY 1280 AAAATGGATTGTGAATGTACAGCAAAACCATAAAAAGTGTGAAGTATTCCTATAGA 1339

DB 159 AAAATGGATTGTGAATGTACAGCAAAACCATAAAAAGTGTGAAGTATTCCTATAGA 218

OY 1340 AATGTAATGCAAGTCAACATATTAATGACAGCCTGTGTATTAATGATGGTCCAGG 1399

DB 219 AATGTAATGCAAGTCAACATATTAATGACAGCCTGTGTATTAATGATGGTCCAGG 278

OY 1400 TCAGTGTGAGATTTCATTCATCCCAAGGGCTTGATGTACAGATTATACCAAGAGTCT 1459

DB 279 TCAGTGTGAGATTTCATTCATCCCAAGGGCTTGATGTACAGATTATACCAAGAGTCT 338

OY 1460 TGCTACCAGAGGGCAAGAGACCAAAACAGACAGAGTCCAGAGAGCAGATGCAC 1519

DB 339 TGCTACCAGAGGGCAAGAGACCAAAACAGACAGAGTCCAGAGAGCAGATGCAC 398

OY 1520 CTGACAAAATGATGTATTAATTGGCTCTATAAATATGTGCCAGCAGCTATGCTGAC 1579

DB 399 CTGACAAAATGATGTATTAATTGGCTCTATAAATATGTGCCAGCAGCTATGCTGAC 458

OY 1580 TTACACTAATTGGTCAGACGCTGTCTGCCCTCATGAATTTGGCTCCAAATGAATGAAC 1639

DB 459 TTACACTAATTGGTCAGACGCTGTCTGCCCTCATGAATTTGGCTCCAAATGAATGAAC 518

OY 1640 TAC-TTTCATGAGCAGTTGTAGCAGGCTGACCACAGATTCCAGAGGCCAGGTGGA 1698

DB 519 TACTTTTCATGAGCAGTTGTAGCAGGCTGACCACAGATTCCAGAGGCCAGGTGGA 578

OY 1699 TCCACAGACTTGAAGTCAAGTTCCAAAGATGAAGATCAGGGTAGCTGACCATGTT 1758

DB 579 TCCACAGACTTGAAGTCAAGTTCCAAAGATGAAGATCAGGGTAGCTGACCATGTT 638

OY 1759 TGGCAGATCTATATGAGACACAGAAGTGTGCATGGCCCAAGACAAAGACCTCCAGC 1818

DB 639 TGGCAGATCTATATGAGACACAGAAGTGTGCATGGCCCAAGACAAAGACCTCCAGC 698

OY 1819 CAGGCTTCATTATGACCTTGTCTGCACAAAAGAAAGTCTAGGTTTAAAGCTGTGCCAG 1878

DB 699 CAGGCTTCATTATGACCTTGTCTGCACAAAAGAAAGTCTAGGTTTAAAGCTGTGCCAG 758

OY 1879 AACCCATCCCAATTAAGAGACCGAGTCTGAAGTCAATTGTAATCTAGTGTAGAGACT 1938

DB 759 AACCCATCCCAATTAAGAGACCGAGTCTGAAGTCAATTGTAATCTAGTGTAGAGACT 818

OY 1939 TGGAGTCAGGAGTGAGACTGTGGGCGACGGGGGCACTGGTACTTGTAAACCTTTAA 1998

DB 819 TGGAGTCAGGAGTGAGACTGTGGGCGACGGGGGCACTGGTACTTGTAAACCTTTAA 878

OY 1999 AGATGTTAATTCATTCATTAATAGATATTATTAAAGAACTTAC 2039

DB 879 AGATGTTAATTCATTCATTAATAGATATTATTAAAGAACTTAC 919

RESULT 2

US-09-513-999C-395

; Sequence 395, Application US/09513999C

; Patent No. 6783961

; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.

; APPLICANT: Duclet, A.

; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

; Patent No. 6783961

; FILE REFERENCE: 59.US2.REG

; CURRENT APPLICATION NUMBER: US/09/513,999C

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/122,487

; NUMBER OF SEQ ID NOS: 36681

; SOFTWARE: Patent.pm

; SEQ ID NO 395

; LENGTH: 344

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 54..344

; FEATURE:

; NAME/KEY: sig_peptide

; LOCATION: 54..119

; OTHER INFORMATION: score 5..9

; OTHER INFORMATION: seq LYLILWQLTGSAA/SG

; FEATURE:

; NAME/KEY: misc_feature

! LOCATION: 197
! OTHER INFORMATION: k=g or t
US-09-513-999C-395

Query Match	10.4%	Score 281;	DB 4;	Length 344;
Best Local Similarity	99.7%	Pred. No. 3.3e-111;		
Matches 331; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

OY	1	GGAAGTGGCTTCATTTCAAGTGCGTACCTTCCAGAGAACAATATGCGTGTGCCCAACAT	60
Dd	13	GGAAGTGGCTTCATTCAAGTGCGTACTTCCAGAGAACAAATATGCGTGTGCCCAACAT	72
OY	61	GCCTCACCCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGCACCCTGA	120
Dd	73	GCCTCACCCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGCACCCTGA	132
OY	121	AAGAGCTGGTCGGTTCGGTTGGTGGGGCCGTGACTTCCCCCTGAAGTCCAAGTAAGC	180
Dd	133	AAGAGCTGGTCGGTTCGGTTGGTGGGGCCGTGACTTCCCCCTGAAGTCCAAGTAAGC	192
OY	181	AAGTTGACTCTATTGTCTGACCTTCAACACACCCTCTTGTCACCATAACAGCCAGAAG	240
Dd	193	AAGTKGACTCTATTGTCTGACCTTCAACACACCCTCTTGTCACCATAACAGCCAGAAG	252
OY	241	GGGGCACTATCATAGTAGACCCCAAATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAG	300
Dd	253	GGGGCACTATCATAGTAGACCCCAAATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAG	312
OY	301	GCTA CTCCCTGAAGCTCAGCAAACTGAAGAAG	332
Dd	313	GCTA CTCCCTGAAGCTCAGCAAACTGAAGAAG	344

```

RESULT 3
US-09-513-999C-21312
; Sequence 21312, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 21312
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-21312

```

	Query Match	6.7%;	Score 182;	DB 4;	Length 435;
	Best Local Similarity	100.0%;	Pred. No. 1.1e-68;		
	Matches 182;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1857 CTAGGTTTAAAGCGCTGTGCCAGAACCCATCCCATAAAGAGACCGAGTCTGAAGTCACAT				1916
Db	1 CTAGGTTTAAAGCGCTGTGCCAGAACCCATCCCATAAAGAGACCGAGTCTGAAGTCACAT				60
QY	1917 TGTAAATCTAGTGTAGGAGACTTGGAGTCAGGCAGTGAGACTGCTGGGGCACGGGGGGCA				1976
Db	61 TGTAAATCTAGTGTAGGAGACTTGGAGTCAGGCAGTGAGACTGCTGGGGCACGGGGGGCA				120
QY	1977 GTGGGCTACTGTAAACCCTTTAAAGATGGTTAATTCAATCATTCAATAGATATTTATTTAAGAACC				2036
Db	121 GTGGGCTACTGTAAACCCTTTAAAGATGGTTAATTCAATCATTCAATAGATATTTATTTAAGAACC				180
QY	2037 TA 2038				

Db 181 TA 182

RESULT 4
US-08-618-100B-3
; Sequence 3, Application US/08618100B
; Patent No. 6068976

```

; GENERAL INFORMATION:
; APPLICANT: Briggs, Michael R.
; APPLICANT: Auwerx, Johan
; APPLICANT: de Vos, Piet
; APPLICANT: Staels, Bart
; APPLICANT: Croston, Glenn E.
; APPLICANT: Miller, Stephen G.
; TITLE OF INVENTION: MODULATORS OF cb GENE AND
; TITLE OF INVENTION: SCREENING METHODS THEREFOR
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/618,100B
; FILING DATE: March 19, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/558,588
; FILING DATE: October 30, 1995
; APPLICATION NUMBER: 08/510,584
; FILING DATE: August 2, 1995
; APPLICATION NUMBER: 08/418,096
; FILING DATE: April 5, 1995
; APPLICATION NUMBER: 08/408,584
; FILING DATE: March 20, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 219/075
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10684 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: Sequence between exon 1 and exon 2
; Patent No. 6068976
; US-08-618-100B-3

Query Match      2.3%; Score 61; DB 3; Length 10684;
Best Local Similarity 100.0%; Pred. No. 9.5e-17;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2107 ATCTGAGTCAAGAGTTCAAGACCAGCCTGGCCACATGTGAACCCCATCTACTAA 2166
        |||||||
Db       6766 ATCTGAGTCAAGAGTTCAAGACCAGCCTGGCCACATGTGAACCCCATCTACTAA 6825

```



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/ APPLICATION NUMBER: US/08/531,927B
/ FILING DATE: 21-SEP-1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: JP H6-251600
/ FILING DATE: 21-SEP-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Granahan, Patricia
/ REGISTRATION NUMBER: 32,227
/ REFERENCE/DOCKET NUMBER: ATH95-01A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617-861-6240
/ TELEFAX: 617-861-9540
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1776 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 36..1115
/ US-08-531-927B-1

Query Match      2.2%; Score 59; DB 2; Length 1776;
Best Local Similarity 100.0%; Pred. No. 7.5e-16;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2109 CTGAGGTCAAGAGTTCAAGACCAGCCTGGCCCAACATGTTGAAACCCCATCTCTACTAAA 2167
Db      1535 CTGAGGTCAAGAGTTCAAGACCAGCCTGGCCCAACATGTTGAAACCCCATCTCTACTAAA 1593

RESULT 9
US-09-041-886-12
/ Sequence 12, Application US/09041886
/ Patent No. 6235872
/ GENERAL INFORMATION:
/ APPLICANT: Bredesen, Dale E.
/ APPLICANT: Rabizadeh, Sharrooz
/ TITLE OF INVENTION: Proapoptotic Peptides, Dependence
/ TITLE OF INVENTION: Polypeptides and Methods of Use
/ NUMBER OF SEQUENCES: 72
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Campbell & Flores LLP
/ STREET: 4370 La Jolla Village Drive, Suite 700
/ CITY: San Diego
/ STATE: California
/ COUNTRY: United States
/ ZIP: 92122
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/041,886
/ FILING DATE:
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Campbell, Cathryn A.
/ REGISTRATION NUMBER: 31,815
/ REFERENCE/DOCKET NUMBER: P-LJ 2626
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (619) 535-9001
/ TELEFAX: (619) 535-8949
/ INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1776 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
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/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 36..1116
/ US-09-041-886-12

Query Match      2.2%; Score 59; DB 3; Length 1776;
Best Local Similarity 100.0%; Pred. No. 7.5e-16;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2109 CTGAGGTCAAGAGTTCAAGACCAGCCTGGCCCAACATGTTGAAACCCCATCTCTACTAAA 2167
Db      1535 CTGAGGTCAAGAGTTCAAGACCAGCCTGGCCCAACATGTTGAAACCCCATCTCTACTAAA 1593

RESULT 10
US-09-526-193A-20/c
/ Sequence 20, Application US/09526193A
/ Patent No. 6617122
/ GENERAL INFORMATION:
/ APPLICANT: Hayden, Michael R.
/ APPLICANT: Brooks-Wilson, Angela R.
/ APPLICANT: Pimstone, Simon N.
/ TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING
/ TITLE OF INVENTION: CHOLESTEROL LEVELS
/ FILE REFERENCE: 50110/002005
/ CURRENT APPLICATION NUMBER: US/09/526,193A
/ CURRENT FILING DATE: 2000-03-15
/ PRIOR APPLICATION NUMBER: 60/124,702
/ PRIOR FILING DATE: 1999-03-15
/ PRIOR APPLICATION NUMBER: 60/138,048
/ PRIOR FILING DATE: 1999-06-08
/ PRIOR APPLICATION NUMBER: 60/139,600
/ PRIOR FILING DATE: 1999-06-17
/ PRIOR APPLICATION NUMBER: 60/151,977
/ PRIOR FILING DATE: 1999-09-01
/ NUMBER OF SEQ ID NOS: 287
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 20
/ LENGTH: 8981
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-09-526-193A-20

Query Match      2.2%; Score 59; DB 4; Length 8981;
Best Local Similarity 100.0%; Pred. No. 7e-16;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2109 CTGAGGTCAAGAGTTCAAGACCAGCCTGGCCCAACATGTTGAAACCCCATCTCTACTAAA 2167
Db      6592 CTGAGGTCAAGAGTTCAAGACCAGCCTGGCCCAACATGTTGAAACCCCATCTCTACTAAA 6534

RESULT 11
US-09-780-172-18/c
/ Sequence 18, Application US/09780172
/ Patent No. 6607916
/ GENERAL INFORMATION:
/ APPLICANT: Robert McKay
/ APPLICANT: Susan M. Freier
/ APPLICANT: Jacqueline Wyatc
/ TITLE OF INVENTION: ANTISENSE MODULATION OF CASEIN KINASE 2-ALPHA EXPRESSION
/ FILE REFERENCE: RTS-0159
/ CURRENT APPLICATION NUMBER: US/09/780,172
/ CURRENT FILING DATE: 2001-02-08
/ NUMBER OF SEQ ID NOS: 96
/ SEQ ID NO 18
/ LENGTH: 63000
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ US-09-780-172-18

Query Match      2.2%; Score 59; DB 4; Length 63000;
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Best Local Similarity 100.0%; Pred. No. 6.3e-16;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2109 CTGAGTCAGAGGTTCAAGACCAGCCTGGCCACATGTGAACCCCATCTCTACTAA 2167
|||||
DB 60071 CTGAGTCAGAGGTTCAAGACCAGCCTGGCCACATGTGAACCCCATCTCTACTAA 60013

RESULT 12
US-09-078-294-24

; Sequence 24, Application US/09078294

; Patent No. 6265211

; GENERAL INFORMATION:

; APPLICANT: Choo, Kong-Hong Andy

; APPLICANT: Du Sart, Desiree

; APPLICANT: Cancilla, Michael R.

; TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE

; FILE REFERENCE: Davies Col

; CURRENT APPLICATION NUMBER: US/09/078,294

; CURRENT FILING DATE: 1998-05-13

; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 24

; LENGTH: 330

; TYPE: DNA

; ORGANISM: BAC-F2 contig 47 fragment 4

US-09-078-294-24

Query Match 2.1%; Score 58; DB 3; Length 330;
Best Local Similarity 100.0%; Pred. No. 2.2e-15;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2110 TGAGTCAGAGGTTCAAGACCAGCCTGGCCACATGTGAACCCCATCTCTACTAA 2167
|||||
DB 91 TGAGTCAGAGGTTCAAGACCAGCCTGGCCACATGTGAACCCCATCTCTACTAA 148

RESULT 13

US-10-140-002-385/C

; Sequence 385, Application US/10140002

; Patent No. 6725730

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3330R1C59

; CURRENT APPLICATION NUMBER: US/10/140,002

; CURRENT FILING DATE: 2002-05-06

; Prior Application removed - See Palm or File Wrapper

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 385

; LENGTH: 2749

; TYPE: DNA

; ORGANISM: Homo Sapien

; NAME/KEY: unsure

; LOCATION: 1869, 1887

; OTHER INFORMATION: unknown base
US-10-140-002-385

Query Match 2.1%; Score 58; DB 4; Length 2749;
Best Local Similarity 100.0%; Pred. No. 2e-15;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2110 TGAGTCAGAGGTTCAAGACCAGCCTGGCCACATGTGAACCCCATCTCTACTAA 2167
|||||
DB 2360 TGAGTCAGAGGTTCAAGACCAGCCTGGCCACATGTGAACCCCATCTCTACTAA 2303

RESULT 14

US-09-078-294-7

; Sequence 7, Application US/09078294

; Patent No. 6265211

; GENERAL INFORMATION:

; APPLICANT: Choo, Kong-Hong Andy

; APPLICANT: Du Sart, Desiree

; APPLICANT: Cancilla, Michael R.

; TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE

; FILE REFERENCE: Davies Col

; CURRENT APPLICATION NUMBER: US/09/078,294

; CURRENT FILING DATE: 1998-05-13

; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 7

; LENGTH: 11811

; TYPE: DNA

; ORGANISM: BAC-F2 contig 3

US-09-078-294-7

Query Match 2.1%; Score 58; DB 3; Length 11811;
Best Local Similarity 100.0%; Pred. No. 1.8e-15;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2110 TGAGTCAGAGGTTCAAGACCAGCCTGGCCACATGTGAACCCCATCTCTACTAA 2167
|||||
DB 10756 TGAGTCAGAGGTTCAAGACCAGCCTGGCCACATGTGAACCCCATCTCTACTAA 10813

RESULT 15

US-09-009-217-11

; Sequence 11, Application US/09009217

; Patent No. 6132729

; GENERAL INFORMATION:

; APPLICANT: Thorpe, Philip E.

; APPLICANT: King, Steven W.

; TITLE OF INVENTION: COMBINED TISSUE FACTOR AND

; TITLE OF INVENTION: CHEMOTHERAPEUTIC METHODS AND COMPOSITIONS FOR COAGULATION

; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee

; STREET: P. O. Box 4433

; CITY: Houston

; STATE: Texas

; COUNTRY: USA

; ZIP: 77210

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/009,217

; FILING DATE: Concurrently Herewith

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/042,427

; FILING DATE: 27-MAR-1997

; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/036,205
FILING DATE: 27-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,920
FILING DATE: 22-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: UTSD:536
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1385 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-009-217-11

Query Match 2.1%; Score 58; DB 3; Length 13865;
Best Local Similarity 100.0%; Pred. No. 1.8e-15;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2110 TGAGTCAGAGTTCAGACCAAGCCCTGGCCACATGTGAAACCCCATCTCTACTAA 2167
DB 8456 TGAGTCAGAGTTCAGACCAAGCCCTGGCCACATGTGAAACCCCATCTCTACTAA 8513

RESULT 16

US-09-009-656-11

Sequence 11, Application US/09009656

Patent No. 6132730

GENERAL INFORMATION:

APPLICANT: Thorpe, Philip E.

APPLICANT: King, Steven W.

APPLICANT: Gao, Boning

TITLE OF INVENTION: COMBINED TISSUE FACTOR AND FACTOR VIIA

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR COAGULATION AND TUMOR

TITLE OF INVENTION: TREATMENT

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: USA

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/009,656

FILING DATE: Concurrently Herewith

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/042,427

FILING DATE: 27-MAR-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/036,205

FILING DATE: 27-JAN-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/035,920

FILING DATE: 22-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Hibler, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: UTSD:537

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512/418-3000

TELEFAX: 512/474-7577

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1385 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-009-656-11

Query Match 2.1%; Score 58; DB 3; Length 13865;
Best Local Similarity 100.0%; Pred. No. 1.8e-15;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2110 TGAGTCAGAGTTCAGACCAAGCCCTGGCCACATGTGAAACCCCATCTCTACTAA 2167
DB 8456 TGAGTCAGAGTTCAGACCAAGCCCTGGCCACATGTGAAACCCCATCTCTACTAA 8513

RESULT 17

US-09-054-272-11

Sequence 11, Application US/09054272

Patent No. 6692909

GENERAL INFORMATION:

APPLICANT: Lander, Eric S.

APPLICANT: Daley, George O.

APPLICANT: Cargill, Michele

APPLICANT: Ireland, James S.

APPLICANT: Rozen, Steven G.

TITLE OF INVENTION: CODING SEQUENCE POLYMORPHISMS

TITLE OF INVENTION: IN VASCULAR PATHOLOGY GENES

NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:

ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.

STREET: Two Militia Drive

CITY: Lexington

STATE: MA

COUNTRY: USA

ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: FastSeq for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/054,272

FILING DATE: 01-APR-1998

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Granahan, Patricia

REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: WHI98-05

TELECOMMUNICATION INFORMATION:

TELEPHONE: 781-861-6240

TELEFAX: 781-861-9540

TELEX:

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 1385 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Genomic DNA

FEATURE:

US-09-054-272-11

Query Match 2.1%; Score 58; DB 4; Length 13865;
Best Local Similarity 100.0%; Pred. No. 1.8e-15;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2110 TGAGTCAGAGTTCAGACCAAGCCCTGGCCACATGTGAAACCCCATCTCTACTAA 2167
DB 8456 TGAGTCAGAGTTCAGACCAAGCCCTGGCCACATGTGAAACCCCATCTCTACTAA 8513

Db 8456 TGAGGTCAGAGTTCAAGACCAGCCTGGCCCAACATGGTGAAACCCCATCTCTACTAAA 8513

RESULT 18

US-09-759-359A-3/c
; Sequence 3, Application US/09759359A
; Patent No. 6492153
; GENERAL INFORMATION:
; APPLICANT: ABU-THREIDEH, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001043
; CURRENT APPLICATION NUMBER: US/09/759,359A
; CURRENT FILING DATE: 2001-01-16
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 90541
; TYPE: DNA
; ORGANISM: Human
US-09-759-359A-3

Query Match 2.1%; Score 58; DB 4; Length 90541;
Best Local Similarity 100.0%; Pred. No. 1.7e-15;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2110 TGAGGTCAGAGTTCAAGACCAGCCTGGCCCAACATGGTGAAACCCCATCTCTACTAAA 2167
Db 5701 TGAGGTCAGAGTTCAAGACCAGCCTGGCCCAACATGGTGAAACCCCATCTCTACTAAA 5644

RESULT 19

US-10-207-973-3/c
; Sequence 3, Application US/10207973
; Patent No. 6753175
; GENERAL INFORMATION:
; APPLICANT: ABU-THREIDEH, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001043
; CURRENT APPLICATION NUMBER: US/10/207,973
; CURRENT FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 90541
; TYPE: DNA
; ORGANISM: Human
US-10-207-973-3

Query Match 2.1%; Score 58; DB 4; Length 90541;
Best Local Similarity 100.0%; Pred. No. 1.7e-15;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2110 TGAGGTCAGAGTTCAAGACCAGCCTGGCCCAACATGGTGAAACCCCATCTCTACTAAA 2167
Db 5701 TGAGGTCAGAGTTCAAGACCAGCCTGGCCCAACATGGTGAAACCCCATCTCTACTAAA 5644

RESULT 20

US-09-754-250-3/c
; Sequence 3, Application US/09754250
; Patent No. 6376225
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHODIESTERASE
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
; TITLE OF INVENTION: PHOSPHODIESTERASE PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL001063
; CURRENT APPLICATION NUMBER: US/09/754,250
; CURRENT FILING DATE: 2001-01-05

; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 111282
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(111282)
; OTHER INFORMATION: n = A,T,C or G
US-09-754-250-3

Query Match 2.1%; Score 58; DB 3; Length 111282;
Best Local Similarity 100.0%; Pred. No. 1.6e-15;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2110 TGAGGTCAGAGTTCAAGACCAGCCTGGCCCAACATGGTGAAACCCCATCTCTACTAAA 2167
Db 14711 TGAGGTCAGAGTTCAAGACCAGCCTGGCCCAACATGGTGAAACCCCATCTCTACTAAA 14654

RESULT 21

US-08-599-252-94
; Sequence 94, Application US/08599252
; Patent No. 5705343
; GENERAL INFORMATION:
; APPLICANT: DRAVNA, DENNIS T.
; APPLICANT: FEDER, JOHN N.
; APPLICANT: GNIRKE, ANDREAS
; APPLICANT: KIMMEL, BRUCE E.
; APPLICANT: THOMAS, WINSTON J.
; APPLICANT: WOLFF, ROGER K.
; TITLE OF INVENTION: METHOD TO DIAGNOSE HEREDITARY
; TITLE OF INVENTION: HEMOCHROMATOSIS
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,252
; FILING DATE: 09-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 9053-0001.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 688 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-599-252-94

Query Match 2.1%; Score 57; DB 1; Length 688;
Best Local Similarity 100.0%; Pred. No. 5.7e-15;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2109 CTGAGGTCAGAGTTCAAGACCAGCCTGGCCCAACATGGTGAAACCCCATCTCTACTA 2165

Db 7 CTGAGGTCAGAGTTCAAGACCAGCCTGGCCCAACATGTTGAACCCTCTCTACTA 63

RESULT 22

PCT-US96-06352-94

; Sequence 94, Application PC/TUS9606352

; GENERAL INFORMATION:

; APPLICANT: DRAYNA, DENNIS T.

; APPLICANT: FEDER, JOHN N.

; APPLICANT: GNIKE, ANDREAS

; APPLICANT: KIMMEL, BRUCE E.

; APPLICANT: THOMAS, WINSTON J.

; APPLICANT: WOLFF, ROGER K.

; TITLE OF INVENTION: METHOD TO DIAGNOSE HEREDITARY

; TITLE OF INVENTION: HEMOCHROMATOSIS

; NUMBER OF SEQUENCES: 124

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORRISON & FOERSTER

; STREET: 2000 Pennsylvania Ave. N.W., Suite 5500

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20006-1888

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US96/06352

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/599,252

; FILING DATE: 09-FEB-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: MURASHIGE, KATE H.

; REGISTRATION NUMBER: 29,959

; REFERENCE/DOCKET NUMBER: 9053-0001.21

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 887-1500

; TELEFAX: (202) 887-0763

; TELEX: 90-4030

; INFORMATION FOR SEQ ID NO: 94:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 688 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

PCT-US96-06352-94

Query Match 2.1%; Score 57; DB 5; Length 688;

Best Local Similarity 100.0%; Pred. No. 5.7e-15;

Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2109 CTGAGTCAGAGTTCAAGACCAGCCTGGCCCAACATGTTGAACCCTCTCTACTA 2165

Db 7 CTGAGGTCAGAGTTCAAGACCAGCCTGGCCCAACATGTTGAACCCTCTCTACTA 63

RESULT 23

PCT-US96-06583-94

; Sequence 94, Application PC/TUS9606583

; GENERAL INFORMATION:

; APPLICANT: DRAYNA, DENNIS T.

; APPLICANT: FEDER, JOHN N.

; APPLICANT: GNIKE, ANDREAS

; APPLICANT: KIMMEL, BRUCE E.

; APPLICANT: THOMAS, WINSTON J.

; APPLICANT: WOLFF, ROGER K.

; TITLE OF INVENTION: METHOD TO DIAGNOSE HEREDITARY

; TITLE OF INVENTION: HEMOCHROMATOSIS

; NUMBER OF SEQUENCES: 124

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORRISON & FOERSTER

; STREET: 2000 Pennsylvania Ave. N.W., Suite 5500

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20006-1888

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US96/06583

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/599,252

; FILING DATE: 09-FEB-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: MURASHIGE, KATE H.

; REGISTRATION NUMBER: 29,959

; REFERENCE/DOCKET NUMBER: 9053-0001.21

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 887-1500

; TELEFAX: (202) 887-0763

; TELEX: 90-4030

; INFORMATION FOR SEQ ID NO: 94:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 688 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

PCT-US96-06583-94

Query Match 2.1%; Score 57; DB 5; Length 688;

Best Local Similarity 100.0%; Pred. No. 5.7e-15;

Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2109 CTGAGTCAGAGTTCAAGACCAGCCTGGCCCAACATGTTGAACCCTCTCTACTA 2165

Db 7 CTGAGGTCAGAGTTCAAGACCAGCCTGGCCCAACATGTTGAACCCTCTCTACTA 63

RESULT 24

US-09-544-398B-11

; Sequence 11, Application US/09544398B

; Patent No. 6770461

; GENERAL INFORMATION:

; APPLICANT: CARULLI, John P.

; APPLICANT: LITTLE, Randall D.

; APPLICANT: RECKER, Robert R.

; APPLICANT: JOHNSON, Mark L.

; TITLE OF INVENTION: High bone mass gene of 11q13.3

; FILE REFERENCE: 032796-013

; CURRENT APPLICATION NUMBER: US/09/544,398B

; CURRENT FILING DATE: 2002-06-10

; PRIOR APPLICATION NUMBER: US 09/229,319

; PRIOR FILING DATE: 1999-01-13

; PRIOR APPLICATION NUMBER: US 60/071,449

; PRIOR FILING DATE: 1998-01-13

; PRIOR APPLICATION NUMBER: US 60/105,511

; PRIOR FILING DATE: 1998-10-23

; NUMBER OF SEQ ID NOS: 641

; SOFTWARE: FastSeq for windows Version 4.0

; SEQ ID NO 11

; LENGTH: 66933

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-544-398B-11

Query Match 2.1%; Score 57; DB 4; Length 66933;

Best Local Similarity 100.0%; Pred. No. 4.5e-15;

Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2111 GAGTCAGAGTTCAAGACCAGCCTGGCCAAACATGTTGAAACCCCATCTCTACTAA 2167
|||||
Db 35735 GAGTCAGAGTTCAAGACCAGCCTGGCCAAACATGTTGAAACCCCATCTCTACTAA 35791

RESULT 25

US-09-543-771-11

; Sequence 11, Application US/09543771

; Patent No. 6780609

; GENERAL INFORMATION:

; APPLICANT: John P. Carulli et al.

; TITLE OF INVENTION: THE HIGH BONE MASS GENE OF 11q13.3

; FILE REFERENCE: 032796-013

; CURRENT APPLICATION NUMBER: US/09/543,771

; EARLIER FILING DATE: 2000-04-05

; EARLIER APPLICATION NUMBER: US 09/229,319

; EARLIER FILING DATE: 1999-01-13

; EARLIER APPLICATION NUMBER: US 60/071,449

; EARLIER FILING DATE: 1998-01-13

; EARLIER APPLICATION NUMBER: US 60/105,511

; EARLIER FILING DATE: 1998-10-23

; NUMBER OF SEQ ID NOS: 62

; SEQ ID NO 11

; LENGTH: 66933

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-543-771-11

Query Match

2.1%; Score 57; DB 4; Length 66933;

Best Local Similarity 100.0%; Pred. No. 4.5e-15;

Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2111 GAGTCAGAGTTCAAGACCAGCCTGGCCAAACATGTTGAAACCCCATCTCTACTAA 2167
|||||

Db 35735 GAGTCAGAGTTCAAGACCAGCCTGGCCAAACATGTTGAAACCCCATCTCTACTAA 35791

RESULT 26

US-09-544-398B-9

; Sequence 9, Application US/09544398B

; Patent No. 6770461

; GENERAL INFORMATION:

; APPLICANT: Carulli, John P.

; APPLICANT: Little, Randall D.

; APPLICANT: Recker, Robert R.

; APPLICANT: Johnson, Mark L.

; TITLE OF INVENTION: High bone mass gene of 11q13.3

; FILE REFERENCE: 032796-013

; CURRENT APPLICATION NUMBER: US/09/544,398B

; CURRENT FILING DATE: 2002-06-10

; PRIOR APPLICATION NUMBER: US 09/229,319

; PRIOR FILING DATE: 1999-01-13

; PRIOR APPLICATION NUMBER: US 60/071,449

; PRIOR FILING DATE: 1998-01-13

; PRIOR APPLICATION NUMBER: US 60/105,511

; PRIOR FILING DATE: 1998-10-23

; NUMBER OF SEQ ID NOS: 641

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 9

; LENGTH: 72049

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (8356), (8385), (38585)

; OTHER INFORMATION: Identity of nucleotide sequences at the above locations are unkno

Query Match

2.1%; Score 57; DB 4; Length 72049;

Best Local Similarity 100.0%; Pred. No. 4.5e-15;

Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2111 GAGTCAGAGTTCAAGACCAGCCTGGCCAAACATGTTGAAACCCCATCTCTACTAA 2167
|||||
Db 39324 GAGTCAGAGTTCAAGACCAGCCTGGCCAAACATGTTGAAACCCCATCTCTACTAA 39380

RESULT 27

US-09-543-771-9

; Sequence 9, Application US/09543771

; Patent No. 6780609

; GENERAL INFORMATION:

; APPLICANT: John P. Carulli et al.

; TITLE OF INVENTION: THE HIGH BONE MASS GENE OF 11q13.3

; FILE REFERENCE: 032796-013

; CURRENT APPLICATION NUMBER: US/09/543,771

; EARLIER FILING DATE: 2000-04-05

; EARLIER APPLICATION NUMBER: US 09/229,319

; EARLIER FILING DATE: 1999-01-13

; EARLIER APPLICATION NUMBER: US 60/071,449

; EARLIER FILING DATE: 1998-01-13

; EARLIER APPLICATION NUMBER: US 60/105,511

; EARLIER FILING DATE: 1998-10-23

; NUMBER OF SEQ ID NOS: 62

; SEQ ID NO 9

; LENGTH: 72049

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (8356), (8385), (38585)

; OTHER INFORMATION: Identity of nucleotide sequences at the above locations are unkno

Query Match

2.1%; Score 57; DB 4; Length 72049;

Best Local Similarity 100.0%; Pred. No. 4.5e-15;

Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2111 GAGTCAGAGTTCAAGACCAGCCTGGCCAAACATGTTGAAACCCCATCTCTACTAA 2167
|||||

Db 39324 GAGTCAGAGTTCAAGACCAGCCTGGCCAAACATGTTGAAACCCCATCTCTACTAA 39380

RESULT 28

US-09-513-999C-35299/C

; Sequence 35299, Application US/09513999C

; Patent No. 6783961

; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.

; APPLICANT: Duclet, A.

; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

; Patent No. 6783961

; FILE REFERENCE: 59.US2.REG

; CURRENT APPLICATION NUMBER: US/09/513,999C

; CURRENT FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/122,487

; PRIOR FILING DATE: 1999-02-26

; NUMBER OF SEQ ID NOS: 36681

; SOFTWARE: Patent.pm

; SEQ ID NO 35299

; LENGTH: 153

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-513-999C-35299

Query Match

2.1%; Score 56; DB 4; Length 153;

Best Local Similarity 100.0%; Pred. No. 1.7e-14;

Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2111 GAGTCAGAGTTCAAGACCAGCCTGGCCAAACATGTTGAAACCCCATCTCTACTAA 2166
|||||

Db 56 GAGTCAGAGTTCAAGACCAGCCTGGCCAAACATGTTGAAACCCCATCTCTACTAA 1

RESULT 29
US-09-534-638-3
; Sequence 3, Application US/09534638
; Patent No. 6320038
; GENERAL INFORMATION:
; APPLICANT: Panula, Pertti A.J.
; APPLICANT: Brandt, Annika
; APPLICANT: Westerlund, Johanna
; TITLE OF INVENTION: Promoter for Neuropeptide FF Promoter and use thereof
; FILE REFERENCE: 2530-104
; CURRENT APPLICATION NUMBER: US/09/534,638
; CURRENT FILING DATE: 2000-03-27
; EARLIER APPLICATION NUMBER: 09/365755
; EARLIER FILING DATE: 1999-08-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2480
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-534-638-3

Query Match 2.0%; Score 55; DB 3; Length 2480;
Best Local Similarity 100.0%; Pred. No. 3.9e-14;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2110 TGAGGTCAAGAGTTCAAGACCAAGCCTGGCCCAACATGTTGTAACCCCATCTTACT 2164
DB 216 TGAGGTCAAGAGTTCAAGACCAAGCCTGGCCCAACATGTTGTAACCCCATCTTACT 270

RESULT 30
US-09-621-976-691
; Sequence 691, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 691
; LENGTH: 473
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 263..472
US-09-621-976-691

Query Match 2.0%; Score 54; DB 4; Length 473;
Best Local Similarity 100.0%; Pred. No. 1.1e-13;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2110 TGAGGTCAAGAGTTCAAGACCAAGCCTGGCCCAACATGTTGTAACCCCATCTTACT 2163
DB 333 TGAGGTCAAGAGTTCAAGACCAAGCCTGGCCCAACATGTTGTAACCCCATCTTACT 386

RESULT 31
US-09-435-739-42
; Sequence 42, Application US/09435739
; Patent No. 6664105
; GENERAL INFORMATION:
; APPLICANT: Pecker, Iris
; APPLICANT: Vlodayvsky, Israel
; APPLICANT: Feinstein, Elena
US-09-435-739-42

; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY
; FILE REFERENCE: 00/20454
; CURRENT APPLICATION NUMBER: US/09/435,739
; CURRENT FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 42
; LENGTH: 44848
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-435-739-42

Query Match 2.0%; Score 54; DB 4; Length 44848;
Best Local Similarity 100.0%; Pred. No. 9e-14;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2109 CTGAGTCAAGAGTTCAAGACCAAGCCTGGCCCAACATGTTGTAACCCCATCTCTA 2162
DB 12111 CTGAGTCAAGAGTTCAAGACCAAGCCTGGCCCAACATGTTGTAACCCCATCTCTA 12164

RESULT 32
US-09-988-113-42
; Sequence 42, Application US/09988113
; Patent No. 6790658
; GENERAL INFORMATION:
; APPLICANT: Pecker, Iris
; APPLICANT: Vlodayvsky, Israel
; APPLICANT: Feinstein, Elena
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY
; FILE REFERENCE: 01/22781
; CURRENT APPLICATION NUMBER: US/09/988,113
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 09/776,874
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US09/258,892
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: PCT/US98/17954
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: US 09/109,386
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 08/922,170
; PRIOR FILING DATE: 1997-09-02
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 42
; LENGTH: 44848
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-988-113-42

Query Match 2.0%; Score 54; DB 4; Length 44848;
Best Local Similarity 100.0%; Pred. No. 9e-14;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2109 CTGAGTCAAGAGTTCAAGACCAAGCCTGGCCCAACATGTTGTAACCCCATCTCTA 2162
DB 12111 CTGAGTCAAGAGTTCAAGACCAAGCCTGGCCCAACATGTTGTAACCCCATCTCTA 12164

RESULT 33
US-09-751-389-3/c
; Sequence 3, Application US/09751389
; Patent No. 6630334
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001067
; CURRENT APPLICATION NUMBER: US/09/751,389


```
; CURRENT FILING DATE: 2001-01-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 786431
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(786431)
; OTHER INFORMATION: n = A,T,C or G
US-09-751-389-3

Query Match      2.0%; Score 54; DB 4; Length 786431;
Best Local Similarity 100.0%; Pred. No. 7.8e-14;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2050 GGCATGGTGCACACCTGTATCCAGCACTTGGAGGCCAAGTGGGTGG 2103
          |||||||||||||||||||||||||||||||||||||||||||
Db      251148 GGCATGGTGCCTCACACCTGTATCCAGCACTTGGAGGCCAAGTGGGTGG 251095

RESULT 34
US-08-611-587-1
; Sequence 1, Application US/08611587
; Patent No. 6150091
; GENERAL INFORMATION:
; APPLICANT: PANDOLFO, MASSIMO
; APPLICANT: MONTERMINI, LAURA
; APPLICANT: MOLTO, MARIA D.
; APPLICANT: Koenig, Michael
; APPLICANT: Campuzano, Victoria
; APPLICANT: Cossee, Mireille
; TITLE OF INVENTION: Direct Diagnosis of Friedreich Ataxia
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P. Patent Dept.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/611,587
; FILING DATE: 03-MAR-1996
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Brashers-Macatee, Sarah J.
; REGISTRATION NUMBER: 38,087
; REFERENCE/DOCKET NUMBER: D-5901
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-651-5620
; TELEFAX: 713-651-5246
; TELEX: 76-2829
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8353 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapien
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 9q13
; UNITS: bp
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US-08-611-587-1

Query Match      2.0%; Score 53; DB 3; Length 8353;
Best Local Similarity 100.0%; Pred. No. 2.6e-13;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2115 TCAGAGTTCAGACCGCTGGCCCAACATGTGAACCCCATCTCTACTAAA 2167
          |||||||||||||||||||||||||||||||||||||||||||
Db      5792 TCAGAGTTCAGACCGCTGGCCCAACATGTGAACCCCATCTCTACTAAA 5844

RESULT 35
US-09-818-512-3
; Sequence 3, Application US/09818512
; Patent No. 6537780
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, Ellen et al.
; TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001192
; CURRENT APPLICATION NUMBER: US/09/818,512
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 116592
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(116592)
; OTHER INFORMATION: n = A,T,C or G
US-09-818-512-3

Query Match      2.0%; Score 53; DB 4; Length 116592;
Best Local Similarity 100.0%; Pred. No. 2.3e-13;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2109 CTGAGTTCAGAGTTCAGACCGCTGGCCCAACATGTGAACCCCATCTCT 2161
          |||||||||||||||||||||||||||||||||||||||||||
Db      24563 CTGAGTTCAGAGTTCAGACCGCTGGCCCAACATGTGAACCCCATCTCT 24615

RESULT 36
US-09-671-317-485
; Sequence 485, Application US/09671317
; Patent No. 6528260
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
; FILE REFERENCE: 62.US3.CIP
; CURRENT APPLICATION NUMBER: US/09/671,317
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 09/536,178
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT/IB00/00403
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: US 60/126,269
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 60/131,961
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 977
; SOFTWARE: Patent.pm
; SEQ ID NO 485
; LENGTH: 49312
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
```

LOCATION: 5466..7466
OTHER INFORMATION: 5'regulatory region
NAME/KEY: exon
LOCATION: 7467..7725
OTHER INFORMATION: exon 1
NAME/KEY: exon
LOCATION: 20256..20355
OTHER INFORMATION: exon 2
NAME/KEY: exon
LOCATION: 36905..36975
OTHER INFORMATION: exon 3
NAME/KEY: exon
LOCATION: 45167..45248
OTHER INFORMATION: exon 4
NAME/KEY: exon
LOCATION: 45728..45965
OTHER INFORMATION: exon 5
NAME/KEY: misc_feature
LOCATION: 45966..49312
OTHER INFORMATION: 3'regulatory region
NAME/KEY: allele
LOCATION: 7564
OTHER INFORMATION: 10-286-289 : polymorphic base G or C
NAME/KEY: allele
LOCATION: 7619
OTHER INFORMATION: 10-286-345 : polymorphic base A or T
NAME/KEY: allele
LOCATION: 7649
OTHER INFORMATION: 10-286-375 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 17258
OTHER INFORMATION: 12-425-57 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 21590
OTHER INFORMATION: 12-421-135 : insertion of T
NAME/KEY: allele
LOCATION: 21595
OTHER INFORMATION: 12-421-140 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 36971
OTHER INFORMATION: 10-523-232 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 45214
OTHER INFORMATION: 10-289-201 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 45741
OTHER INFORMATION: 10-290-37 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 46029
OTHER INFORMATION: 10-290-326 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 46032
OTHER INFORMATION: 10-290-328 : deletion of G
NAME/KEY: primer_bind
LOCATION: 7276..7294
OTHER INFORMATION: 10-286.pu
NAME/KEY: primer_bind
LOCATION: 7676..7694
OTHER INFORMATION: 10-286.rp complement
NAME/KEY: primer_bind
LOCATION: 16839..16856
OTHER INFORMATION: 12-425.rp
NAME/KEY: primer_bind
LOCATION: 17297..17314
OTHER INFORMATION: 12-425.pu complement
NAME/KEY: primer_bind
LOCATION: 21456..21474
OTHER INFORMATION: 12-421.pu
NAME/KEY: primer_bind
LOCATION: 21886..21906
OTHER INFORMATION: 12-421.rp complement
NAME/KEY: primer_bind
LOCATION: 36740..36758

OTHER INFORMATION: 10-523.pu
NAME/KEY: primer_bind
LOCATION: 36997..37015
OTHER INFORMATION: 10-523.rp complement
NAME/KEY: primer_bind
LOCATION: 45020..45037
OTHER INFORMATION: 10-289.pu
NAME/KEY: primer_bind
LOCATION: 45413..45432
OTHER INFORMATION: 10-289.rp complement
NAME/KEY: primer_bind
LOCATION: 45705..45724
OTHER INFORMATION: 10-290.pu
NAME/KEY: primer_bind
LOCATION: 46104..46123
OTHER INFORMATION: 10-290.rp complement
NAME/KEY: primer_bind
LOCATION: 7545..7563
OTHER INFORMATION: 10-286-289.mis
NAME/KEY: primer_bind
LOCATION: 7565..7583
OTHER INFORMATION: 10-286-289.mis complement
NAME/KEY: primer_bind
LOCATION: 7600..7618
OTHER INFORMATION: 10-286-345.mis
NAME/KEY: primer_bind
LOCATION: 7620..7638
OTHER INFORMATION: 10-286-345.mis complement
NAME/KEY: primer_bind
LOCATION: 7630..7648
OTHER INFORMATION: 10-286-375.mis
NAME/KEY: primer_bind
LOCATION: 7650..7668
OTHER INFORMATION: 10-286-375.mis complement
NAME/KEY: primer_bind
LOCATION: 17239..17257
OTHER INFORMATION: 12-425-57.mis
NAME/KEY: primer_bind
LOCATION: 17259..17277
OTHER INFORMATION: 12-425-57.mis complement
NAME/KEY: primer_bind
LOCATION: 21576..21594
OTHER INFORMATION: 12-421-140.mis
NAME/KEY: primer_bind
LOCATION: 21596..21614
OTHER INFORMATION: 12-421-140.mis complement
NAME/KEY: primer_bind
LOCATION: 36952..36970
OTHER INFORMATION: 10-523-232.mis
NAME/KEY: primer_bind
LOCATION: 36972..36990
OTHER INFORMATION: 10-523-232.mis complement
NAME/KEY: primer_bind
LOCATION: 45195..45213
OTHER INFORMATION: 10-289-201.mis
NAME/KEY: primer_bind
LOCATION: 45215..45233
OTHER INFORMATION: 10-289-201.mis complement
NAME/KEY: primer_bind
LOCATION: 45722..45740
OTHER INFORMATION: 10-290-37.mis
NAME/KEY: primer_bind
LOCATION: 45742..45760
OTHER INFORMATION: 10-290-37.mis complement
NAME/KEY: primer_bind
LOCATION: 46010..46028
OTHER INFORMATION: 10-290-326.mis
NAME/KEY: primer_bind
LOCATION: 46030..46048
OTHER INFORMATION: 10-290-326.mis complement
NAME/KEY: misc_binding
LOCATION: 7552..7576
OTHER INFORMATION: 10-286-289.probe

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; NAME/KEY: misc_binding
; LOCATION: 7607..7631
; OTHER INFORMATION: 10-286-345.probe
; NAME/KEY: misc_binding
; LOCATION: 7637..7661
; OTHER INFORMATION: 10-286-375.probe
; NAME/KEY: misc_binding
; LOCATION: 17246..17270
; OTHER INFORMATION: 12-425-57.probe
; NAME/KEY: misc_binding
; LOCATION: 21583..21607
; OTHER INFORMATION: 12-421-140.probe
; NAME/KEY: misc_binding
; LOCATION: 36959..36983
; OTHER INFORMATION: 10-523-232.probe
; NAME/KEY: misc_binding
; LOCATION: 45202..45226
; OTHER INFORMATION: 10-289-201.probe
; NAME/KEY: misc_binding
; LOCATION: 45729..45753
; OTHER INFORMATION: 10-290-37.probe
; NAME/KEY: misc_binding
; LOCATION: 46017..46041
; OTHER INFORMATION: 10-290-326.probe
; US-09-671-317-485
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Query Match          1.9%; Score 52; DB 4; Length 49312;
Best Local Similarity 100.0%; Pred. No. 6.5e-13;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy      2110 TCAGGTCAGAGTTCAGACCAAGCCCTGGCCCAACATGTTGAACCCCATCTCT 2161
          |||
Db      16276 TGAGGTCAAGAGTTCAGACCAAGCCCTGGCCCAACATGTTGAACCCCATCTCT 16327
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RESULT 37
US-09-497-855A-32
; Sequence 32, Application US/09497855A
; Patent No. 6605432
; GENERAL INFORMATION:
; APPLICANT: Huang, Tim
; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION
; FILE REFERENCE: UMO1523
; CURRENT APPLICATION NUMBER: US/09/497,855A
; CURRENT FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/120,592
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: 60/118,760
; PRIOR FILING DATE: 1999-02-05
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
; LENGTH: 118067
; TYPE: DNA
; ORGANISM: Homo sapiens;
US-09-497-855A-32
```

```
Query Match          1.9%; Score 51; DB 4; Length 118067;
Best Local Similarity 100.0%; Pred. No. 1.7e-12;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy      2116 CAGAGTTCAGACCAAGCCCTGGCCCAACATGTTGAACCCCATCTCTACTAA 2166
          |||
Db      14295 CAGAGTTCAGACCAAGCCCTGGCCCAACATGTTGAACCCCATCTCTACTAA 14345
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RESULT 38
US-09-621-976-12888
; Sequence 12888, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
```

```
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 12888
; LENGTH: 297
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-12888
```

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Query Match          1.8%; Score 50; DB 4; Length 297;
Best Local Similarity 100.0%; Pred. No. 6.1e-12;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy      2115 TCAGAGTTCAGACCAAGCCCTGGCCCAACATGTTGAACCCCATCTCTACT 2164
          |||
Db      89 TCAGAGTTCAGACCAAGCCCTGGCCCAACATGTTGAACCCCATCTCTACT 138
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```
RESULT 39
US-09-621-976-12887
; Sequence 12887, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 12887
; LENGTH: 307
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 305
; OTHER INFORMATION: n=a, g, c or t
US-09-621-976-12887
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```
Query Match          1.8%; Score 50; DB 4; Length 307;
Best Local Similarity 100.0%; Pred. No. 6.1e-12;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Oy      2115 TCAGAGTTCAGACCAAGCCCTGGCCCAACATGTTGAACCCCATCTCTACT 2164
          |||
Db      89 TCAGAGTTCAGACCAAGCCCTGGCCCAACATGTTGAACCCCATCTCTACT 138
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RESULT 40
US-09-621-976-9714/C
; Sequence 9714, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 9714
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Homo sapiens
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US-09-621-976-9714

Query Match 1.8%; Score 50; DB 4; Length 369;
Best Local Similarity 100.0%; Pred. No. 6e-12;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2118 GGAGTCAAGACCAGCCTGGCCAACATGTGAAACCCCATCTCTACTAA 2167
DB 369 GGAGTCAAGACCAGCCTGGCCAACATGTGAAACCCCATCTCTACTAA 320

RESULT 41

US-09-783-203-1
; Sequence 1, Application US/09783203
; Patent No. 6576464
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Gold, Joseph
; APPLICANT: Lebkowski, Jane
; TITLE OF INVENTION: Tpacked stem cells
; FILE REFERENCE: 096/003
; CURRENT APPLICATION NUMBER: US/09/783,203
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/253,443
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/253,357
; PRIOR FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; LENGTH: 15418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-783-203-1

Query Match 1.8%; Score 50; DB 4; Length 15418;
Best Local Similarity 100.0%; Pred. No. 5e-12;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2054 TGGTGCTCACACCTGTATCCAGCACTTTGGAGGCCCAAGTGGTGG 2103
DB 580 TGGTGCTCACACCTGTATCCAGCACTTTGGAGGCCCAAGTGGTGG 629

RESULT 42

US-09-994-427A-1
; Sequence 1, Application US/09994427A
; Patent No. 6713055
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Schif, J. Michael
; TITLE OF INVENTION: GLYCOSYLTRANSFERASE VECTORS FOR TREATING CANCER
; FILE REFERENCE: 083,002
; CURRENT APPLICATION NUMBER: US/09/994,427A
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 60/253,395
; PRIOR FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 15418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-994-427A-1

Query Match 1.8%; Score 50; DB 4; Length 15418;
Best Local Similarity 100.0%; Pred. No. 5e-12;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2054 TGGTGCTCACACCTGTATCCAGCACTTTGGAGGCCCAAGTGGTGG 2103
DB 580 TGGTGCTCACACCTGTATCCAGCACTTTGGAGGCCCAAGTGGTGG 629

RESULT 43

US-09-244-438-1
; Sequence 1, Application US/09244438
; Patent No. 6777203
; GENERAL INFORMATION:
; APPLICANT: Morin, Gregg B.
; APPLICANT: Lichtsteiner, Serge
; APPLICANT: Vassero, Alain
; APPLICANT: Adams, Robert R.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Telomerase Reverse Transcriptase Transcriptional
; TITLE OF INVENTION: Regulatory Sequences and Methods of Using
; FILE REFERENCE: 019/246P
; CURRENT APPLICATION NUMBER: US/09/244,438
; CURRENT FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 15418
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human TERT promoter
US-09-244-438-1

Query Match 1.8%; Score 50; DB 4; Length 15418;
Best Local Similarity 100.0%; Pred. No. 5e-12;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2054 TGGTGCTCACACCTGTATCCAGCACTTTGGAGGCCCAAGTGGTGG 2103
DB 580 TGGTGCTCACACCTGTATCCAGCACTTTGGAGGCCCAAGTGGTGG 629

RESULT 44

US-09-785-381-6/c
; Sequence 6, Application US/09785381
; Patent No. 6602992
; GENERAL INFORMATION:
; APPLICANT: DALLOS, Peter
; APPLICANT: ZHENG, Jing
; APPLICANT: MADISON, Laird
; TITLE OF INVENTION: A MAMMALIAN PRESTIN
; FILE REFERENCE: 0290-37U1
; CURRENT APPLICATION NUMBER: US/09/785,381
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 60/183,461
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 6
; LENGTH: 29485
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-785-381-6

Query Match 1.8%; Score 50; DB 4; Length 29485;
Best Local Similarity 100.0%; Pred. No. 4.8e-12;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2109 CTGAGTCAAGAGTTCAAGACCAGCCTGGCCAACATGTGAAACCCATC 2158
DB 2858 CTGAGTCAAGAGTTCAAGACCAGCCTGGCCAACATGTGAAACCCATC 28539

RESULT 45

US-09-513-999C-30096
; Sequence 30096, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclerc, A.

```
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 30096
; LENGTH: 191
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-30096

Query Match          1.8%; Score 49; DB 4; Length 191;
Best Local Similarity 100.0%; Pred. No. 1.7e-11;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2055 GGTGGCTCACACCTGTAATCCAGACACTTTGGAGGCCCAAGGTGGTGG 2103
Db      59 GGTGGCTCACACCTGTAATCCAGACACTTTGGAGGCCCAAGGTGGTGG 107

RESULT 46
US-09-513-999C-29901/C
; Sequence 29901, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 29901
; LENGTH: 256
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-29901

Query Match          1.8%; Score 49; DB 4; Length 256;
Best Local Similarity 100.0%; Pred. No. 1.6e-11;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2109 CTGAGGTCAGAGTTCAGAGCCAGCCTGGCCACATGTGAACCCCAT 2157
Db      232 CTGAGGTCAGAGTTCAGAGCCAGCCTGGCCACATGTGAACCCCAT 184

RESULT 47
US-09-621-976-1354/C
; Sequence 1354, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 1354
; LENGTH: 511
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 183..398
; NAME/KEY: sig_peptide
; LOCATION: 183..251
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 11.1000003814697
; OTHER INFORMATION: seq LFLLLFLRLSLT/LS
US-09-621-976-1354

Query Match          1.8%; Score 49; DB 4; Length 511;
Best Local Similarity 100.0%; Pred. No. 1.6e-11;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2109 CTGAGGTCAGAGTTCAGAGCCAGCCTGGCCACATGTGAACCCCAT 2157
Db      452 CTGAGGTCAGAGTTCAGAGCCAGCCTGGCCACATGTGAACCCCAT 404

RESULT 48
US-08-480-784-20/C
; Sequence 20, Application US/08480784
; Patent No. 5693473
; GENERAL INFORMATION:
; APPLICANT: Skolnick, Mark H.
; APPLICANT: Goldgar, David E.
; APPLICANT: Miki, Yoshio
; APPLICANT: Swenson, Jeff
; APPLICANT: Kamb, Alexander
; APPLICANT: Harshman, Keith D.
; APPLICANT: Shattuck-Eidens, Donna M.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Wiseman, Roger W.
; APPLICANT: Futreal, P. Andrew
; TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
; TITLE OF INVENTION: Susceptibility Gene
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, N.W., Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,784
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/409,305
; FILING DATE: 24-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/348,824
; FILING DATE: 29-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/308,104
; FILING DATE: 16-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/300,266
; FILING DATE: 02-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/289,221
; FILING DATE: 12-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
```

```
; REFERENCE/DOCKET NUMBER: 24884-109347
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6769 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-08-480-784-20

Query Match      1.8%; Score 49; DB 1; Length 6769;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2119 GAGTCAAGACCAAGCCTGGCCACATGCTGAACCCCATCTCTACTAA 2167
DB      5670 GAGTCAAGACCAAGCCTGGCCACATGCTGAACCCCATCTCTACTAA 5622

RESULT 49
US-08-483-553-20/c
; Sequence 20, Application US/08483553
; Patent No. 5709999
; GENERAL INFORMATION:
; APPLICANT: Skolnick, Mark H.
; APPLICANT: Goldgar, David E.
; APPLICANT: Miki, Yoshio
; APPLICANT: Swenson, Jeff
; APPLICANT: Kamb, Alexander
; APPLICANT: Harshman, Keith D.
; APPLICANT: Shattuck-Eidens, Donna M.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Wiseman, Roger W.
; APPLICANT: Futreal, P. Andrew
; TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
; TITLE OF INVENTION: Susceptibility Gene
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, N.W., Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,553
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/409,305
; FILING DATE: 24-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/348,824
; FILING DATE: 29-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/308,104
; FILING DATE: 16-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/300,266
; FILING DATE: 02-SEP-1994
; PRIOR APPLICATION DATA:
```

```
; APPLICATION NUMBER: US 08/289,221
; FILING DATE: 12-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihmen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109347
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6769 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-08-483-553-20

Query Match      1.8%; Score 49; DB 1; Length 6769;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2119 GAGTCAAGACCAAGCCTGGCCACATGCTGAACCCCATCTCTACTAA 2167
DB      5670 GAGTCAAGACCAAGCCTGGCCACATGCTGAACCCCATCTCTACTAA 5622

RESULT 50
US-08-487-002-20/c
; Sequence 20, Application US/08487002
; Patent No. 5710001
; GENERAL INFORMATION:
; APPLICANT: Shattuck-Eidens, Donna M.
; APPLICANT: Simard, Jacques
; APPLICANT: Eml, Mitsuru
; APPLICANT: Nakamura, Yusuke
; APPLICANT: Durocher, Francine
; TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
; TITLE OF INVENTION: Susceptibility Gene
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, N.W., Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,002
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/409,305
; FILING DATE: 24-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/348,824
; FILING DATE: 29-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/308,104
; FILING DATE: 16-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/300,266
; FILING DATE: 02-SEP-1994
; PRIOR APPLICATION DATA:
```


APPLICATION NUMBER: US 08/289,221
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109347
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 6769 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-487-002-20

Query Match 1.8%; Score 49; DB 1; Length 6769;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2119 GAGTTCAGACGACGCTGGCCAACATGTTGAACCCCATCTCTACTAA 2167
|||||
Db 5670 GAGTTCAGACGACGCTGGCCAACATGTTGAACCCCATCTCTACTAA 5622

RESULT 51

US-08-483-554B-20/c
Sequence 20, Application US/08483554B

Patent No. 5747282

GENERAL INFORMATION:

APPLICANT: Skolnick, Mark H.
APPLICANT: Goldgar, David E.
APPLICANT: Miki, Yoshio
APPLICANT: Swenson, Jeff
APPLICANT: Kamb, Alexander
APPLICANT: Harshman, Keith D.
APPLICANT: Shattuck-Eidens, Donna M.
APPLICANT: Tavitigian, Sean V.
APPLICANT: Wiseman, Roger W.
APPLICANT: Futreal, P. Andrew
TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:

ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/483,554B

FILING DATE: 07-JUN-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/409,305

FILING DATE: 24-MAR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/348,824

FILING DATE: 29-NOV-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/308,104

FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,221
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109347
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 6769 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-483-554B-20

Query Match 1.8%; Score 49; DB 1; Length 6769;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2119 GAGTTCAGACGACGCTGGCCAACATGTTGAACCCCATCTCTACTAA 2167
|||||
Db 5670 GAGTTCAGACGACGCTGGCCAACATGTTGAACCCCATCTCTACTAA 5622

RESULT 52

US-08-488-011B-20/c

Sequence 20, Application US/08488011B

Patent No. 5753441

GENERAL INFORMATION:

APPLICANT: Skolnick, Mark H.
APPLICANT: Goldgar, David E.
APPLICANT: Miki, Yoshio
APPLICANT: Swenson, Jeff
APPLICANT: Kamb, Alexander
APPLICANT: Harshman, Keith D.
APPLICANT: Shattuck-Eidens, Donna M.
APPLICANT: Tavitigian, Sean V.
APPLICANT: Wiseman, Roger W.
APPLICANT: Futreal, P. Andrew
TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:

ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/488,011B

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/409,305

FILING DATE: 24-MAR-1995

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/348,824
; FILING DATE: 29-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/308,104
; FILING DATE: 16-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/300,266
; FILING DATE: 02-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/289,221
; FILING DATE: 12-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109347-09
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6769 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
;
US-08-488-011B-20
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Query Match 1.8%; Score 49; DB 1; Length 6769;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 2119 GAGTCAAGACGAGCCTGGCCACATGTGAAACCCCATCTCTACTAA 2167
Db 5670 GAGTCAAGACGAGCCTGGCCACATGTGAAACCCCATCTCTACTAA 5622
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```

RESULT 53
US-08-850-727-20/c
; Sequence 20, Application US/08850727
; Patent No. 6162897
; GENERAL INFORMATION:
; APPLICANT: Skolnick, Mark H.
; APPLICANT: Goldgar, David E.
; APPLICANT: Miki, Yoshio
; APPLICANT: Swenson, Jeff
; APPLICANT: Kamb, Alexander
; APPLICANT: Harshman, Keith D.
; APPLICANT: Shattuck-Eidens, Donna M.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Wiseman, Roger W.
; APPLICANT: Futreal, P. Andrew
; TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
; TITLE OF INVENTION: Susceptibility Gene
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, N.W., Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/850,727
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; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/483,554
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/348,824
; FILING DATE: 29-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/308,104
; FILING DATE: 16-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/300,266
; FILING DATE: 02-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/289,221
; FILING DATE: 12-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109347
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6769 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
;
US-08-850-727-20
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Query Match 1.8%; Score 49; DB 3; Length 6769;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 2119 GAGTCAAGACGAGCCTGGCCACATGTGAAACCCCATCTCTACTAA 2167
Db 5670 GAGTCAAGACGAGCCTGGCCACATGTGAAACCCCATCTCTACTAA 5622
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```

RESULT 54
PCT-US95-10202-20/c
; Sequence 20, Application PC/TUS9510202
; GENERAL INFORMATION:
; APPLICANT: Shattuck-Eidens, Donna M.
; APPLICANT: Simard, Jacques
; APPLICANT: Eml, Mitsuru
; APPLICANT: Nakamura, Yusuke
; APPLICANT: Durocher, Francine
; TITLE OF INVENTION: In Vivo Mutations and Polymorphisms
; TITLE OF INVENTION: In the 17q-Linked Breast and Ovarian Cancer
; TITLE OF INVENTION: Susceptibility Gene
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, N.W., Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/10202
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; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/409,305
; FILING DATE: 24-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/348,824
; FILING DATE: 29-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08-308,104
; FILING DATE: 16-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/300,266
; FILING DATE: 02-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/289,221
; FILING DATE: 12-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109347
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6769 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
;
PCT-US95-10202-20

Query Match          1.8%; Score 49; DB 5; Length 6769;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2119 GAGTCAAGACGAGCCTGGCCACATGTGTAACCCCATCTCTACTAA 2167
        |||||||
Db       5670 GAGTCAAGACGAGCCTGGCCACATGTGTAACCCCATCTCTACTAA 5622

RESULT 55
; Sequence 20, Application PC/TUS9510203
; GENERAL INFORMATION:
; APPLICANT: Skolnick, Mark H.
; APPLICANT: Goldgar, David E.
; APPLICANT: Miki, Yoshio
; APPLICANT: Swenson, Jeff
; APPLICANT: Kamb, Alexander
; APPLICANT: Harshman, Keith D.
; APPLICANT: Shattuck-Eidens, Donna M.
; APPLICANT: Tavligian, Sean V.
; APPLICANT: Wiseman, Roger W.
; APPLICANT: Futreal, P. Andrew
; TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, N.W., Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
```

```
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/10203
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/409,305
; FILING DATE: 24-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/348,824
; FILING DATE: 29-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08-308,104
; FILING DATE: 16-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/300,266
; FILING DATE: 02-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/289,221
; FILING DATE: 12-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109347
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6769 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
;
PCT-US95-10203-20

Query Match          1.8%; Score 49; DB 5; Length 6769;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2119 GAGTCAAGACGAGCCTGGCCACATGTGAACCCCATCTCTACTAA 2167
        |||||||
Db       5670 GAGTCAAGACGAGCCTGGCCACATGTGAACCCCATCTCTACTAA 5622

RESULT 56
; Sequence 20, Application PC/TUS9510220
; GENERAL INFORMATION:
; APPLICANT: Skolnick, Mark H.
; APPLICANT: Goldgar, David E.
; APPLICANT: Miki, Yoshio
; APPLICANT: Swenson, Jeff
; APPLICANT: Kamb, Alexander
; APPLICANT: Harshman, Keith D.
; APPLICANT: Shattuck-Eidens, Donna M.
; APPLICANT: Tavligian, Sean V.
; APPLICANT: Wiseman, Roger W.
; APPLICANT: Futreal, P. Andrew
; TITLE OF INVENTION: Method for Diagnosing a
; NUMBER OF SEQUENCES: 85
; Predisposition for Breast and Ovarian Cancer
```

```

;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, N.W., Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/10220
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/409,305
; FILING DATE: 24-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/348,824
; FILING DATE: 29-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08-308,104
; FILING DATE: 16-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/300,266
; FILING DATE: 02-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/289,221
; FILING DATE: 12-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109347.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6769 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; PCT-US95-10220-20

Query Match 1.8%; Score 49; DB 5; length 6769;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2119 GAGTCAAGACCGCTGGCCACATGTGTAACCCCATCTCTACTAA 2167
      |||||||
Db 5670 GAGTCAAGACCGACCTGGCCACATGTGTAACCCCATCTCTACTAA 5622

RESULT 57
US-07-914-281-5/c
; Sequence 5, Application US/07914281
; Patent No. 5324663
; GENERAL INFORMATION:
; APPLICANT: LOWE, JOHN B.
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
; TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
; TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
; TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
```

```

;
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/914,281
; FILING DATE: 19920720
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Lavelleye, Jean-Paul M. P.
; REGISTRATION NUMBER: 31,451
; REFERENCE/DOCKET NUMBER: 2363-060-55
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8174 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: NO
; US-07-914-281-5

Query Match 1.8%; Score 49; DB 1; length 8174;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2055 GGTGGCTACACCTGTATCCAGCACTTTGGAGGCCAAGTGGTG 2103
      |||||||
Db 4287 GGTGGCTACACCTGTATCCAGCACTTTGGAGGCCAAGTGGTG 4239

RESULT 58
US-08-393-246-5/c
; Sequence 5, Application US/08393246
; Patent No. 5595900
; GENERAL INFORMATION:
; APPLICANT: LOWE, JOHN B.
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
; TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
; TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
; TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/393,246
; FILING DATE:
; CLASSIFICATION: 530
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PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/220,433
; FILING DATE: 30-MAR-1994
; APPLICATION NUMBER: US 07/914,281
; FILING DATE: 20-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Lavallee, Jean-Paul M. P.
; REGISTRATION NUMBER: 31,451
; REFERENCE/DOCKET NUMBER: 2363-060-55
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8174 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: NO
; US-08-393-246-5

Query Match 1.8%; Score 49; DB 1; Length 8174;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2055 GGTGGCTCACACCTGTATCCAGCACTTTGGAGGCCAAGTGGTGG 2103
|||
Db 4287 GGTGGCTCACACCTGTATCCAGCACTTTGGAGGCCAAGTGGTGG 4239

RESULT 59
US-08-525-058A-5/c
; Sequence 5, Application US/08525058A
; Patent No. 5770420
; GENERAL INFORMATION:
; APPLICANT: LOWE, JOHN B.
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
; TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
; TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
; TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTURES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,058A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lavallee, Jean-Paul M. P.
; REGISTRATION NUMBER: 31,451
; REFERENCE/DOCKET NUMBER: 2363-060-55
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8174 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: NO
; US-08-525-058A-5

Query Match 1.8%; Score 49; DB 1; Length 8174;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2055 GGTGGCTCACACCTGTATCCAGCACTTTGGAGGCCAAGTGGTGG 2103
|||
Db 4287 GGTGGCTCACACCTGTATCCAGCACTTTGGAGGCCAAGTGGTGG 4239

RESULT 60
US-08-696-731-5/c
; Sequence 5, Application US/08696731
; Patent No. 5955347
; GENERAL INFORMATION:
; APPLICANT: LOWE, JOHN B.
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
; TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
; TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
; TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/696,731
; FILING DATE: 14-AUG-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/393,246
; FILING DATE:
; APPLICATION NUMBER: US 08/220,433
; FILING DATE: 30-MAR-1994
; APPLICATION NUMBER: US 07/914,281
; FILING DATE: 20-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Lavallee, Jean-Paul M. P.
; REGISTRATION NUMBER: 31,451
; REFERENCE/DOCKET NUMBER: 2363-060-55
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8174 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: NO
; US-08-696-731-5

Query Match 1.8%; Score 49; DB 2; Length 8174;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2055 GGTGGCTCACACCTGTATCCAGCACTTTGGAGGCCAAGTGGTGG 2103
|||
Db 4287 GGTGGCTCACACCTGTATCCAGCACTTTGGAGGCCAAGTGGTGG 4239

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RESULT 61
US-09-042-531-5/c
; Sequence 5, Application US/09042531
; Patent No. 6268193
; GENERAL INFORMATION:
; APPLICANT: LOWE, JOHN B.
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
; OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
; TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
; TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,531
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/393,246
; FILING DATE:
; APPLICATION NUMBER: US 08/220,433
; FILING DATE: 30-MAR-1994
; APPLICATION NUMBER: US 07/914,281
; FILING DATE: 20-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Lavalleye, Jean-Paul M. P.
; REGISTRATION NUMBER: 31,451
; REFERENCE/DOCKET NUMBER: 2363-060-55
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8174 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: NO
; US-09-042-531-5

Query Match      1.8%; Score 49; DB 3; Length 8174;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      2055 GGTGGCTCACACCTGTAATCCAGCACTTTGGAGGCCCAAGGTGGTGG 2103
      |||||||
Db      4287 GGTGGCTCACACCTGTAATCCAGCACTTTGGAGGCCCAAGGTGGTGG 4239

RESULT 62
PCT-US91-00899-3/c
; Sequence 3, Application PC/TUS9100899
; GENERAL INFORMATION:
; APPLICANT: Lowe, John B.
; TITLE OF INVENTION: Method and Products For the Synthesis of
; OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS, GLYCOLIPIDS,
; TITLE OF INVENTION: OR AS FREE MOLECULES, AND FOR THE ISOLATION OF CLONED
; TITLE OF INVENTION: Genetic Sequences That Determine These Structur
```

```
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/00899
; FILING DATE: 19910214
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lavalleye Ph.D., Jean-Paul
; REGISTRATION NUMBER: 31,451
; REFERENCE/DOCKET NUMBER: 2363-021-55 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-5940
; TELEFAX: (703)486-2347
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8174 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: Blood
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 4686..5780
; OTHER INFORMATION: /label= mat_peptide
; PCT-US91-00899-3

Query Match      1.8%; Score 49; DB 5; Length 8174;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      2055 GGTGGCTCACACCTGTAATCCAGCACTTTGGAGGCCCAAGGTGGTGG 2103
      |||||||
Db      4287 GGTGGCTCACACCTGTAATCCAGCACTTTGGAGGCCCAAGGTGGTGG 4239

RESULT 63
US-09-345-882-1/c
; Sequence 1, Application US/09345882
; Patent No. 6399373
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)
; FILE REFERENCE: GENSET.031A
; CURRENT APPLICATION NUMBER: US/09/345,882
; CURRENT FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: US 60/091,315
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/111,909
; PRIOR FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: Patent.pm
; SEQ ID NO 1
; LENGTH: 162450
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
```

NAME/KEY: allele
LOCATION: 72794
OTHER INFORMATION: 5-124-273 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 88073
OTHER INFORMATION: 5-127-261 : polymorphic base A or C
FEATURE:
NAME/KEY: allele
LOCATION: 90842
OTHER INFORMATION: 99-1437-325 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 93714
OTHER INFORMATION: 5-128-60 : polymorphic base deletion of GT
FEATURE:
NAME/KEY: allele
LOCATION: 97122
OTHER INFORMATION: 99-1442-224 : polymorphic base G or T
FEATURE:
NAME/KEY: allele
LOCATION: 97152
OTHER INFORMATION: 5-129-144 : polymorphic base deletion of T
FEATURE:
NAME/KEY: allele
LOCATION: 99098
OTHER INFORMATION: 5-130-257 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 99117
OTHER INFORMATION: 5-130-276 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 103806
OTHER INFORMATION: 5-131-395 : polymorphic base A or T
FEATURE:
NAME/KEY: allele
LOCATION: 106940
OTHER INFORMATION: 5-133-375 : polymorphic base insertion of A
FEATURE:
NAME/KEY: allele
LOCATION: 108106
OTHER INFORMATION: 5-135-155 : polymorphic base insertion of A
FEATURE:
NAME/KEY: allele
LOCATION: 108149
OTHER INFORMATION: 5-135-198 : polymorphic base insertion of GTTT
FEATURE:
NAME/KEY: allele
LOCATION: 108308
OTHER INFORMATION: 5-135-357 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 108471
OTHER INFORMATION: 5-136-174 : polymorphic base C or T
FEATURE:
NAME/KEY: allele
LOCATION: 134134
OTHER INFORMATION: 5-140-120 : polymorphic base C or T
FEATURE:
NAME/KEY: allele
LOCATION: 134362
OTHER INFORMATION: 5-140-348 : polymorphic base insertion of A
FEATURE:
NAME/KEY: allele
LOCATION: 134374
OTHER INFORMATION: 5-140-361 : polymorphic base insertion of CA
FEATURE:
NAME/KEY: allele
LOCATION: 146328
OTHER INFORMATION: 5-143-84 : polymorphic base A or G
FEATURE:
NAME/KEY: allele

LOCATION: 146345
OTHER INFORMATION: 5-143-101 : polymorphic base A or C
FEATURE:
NAME/KEY: allele
LOCATION: 150329
OTHER INFORMATION: 5-145-24 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 160031
OTHER INFORMATION: 5-148-352 : polymorphic base G or T
FEATURE:
NAME/KEY: allele
LOCATION: 72771..72817
OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID30
FEATURE:
NAME/KEY: allele
LOCATION: 72771..72817
OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID51
FEATURE:
NAME/KEY: allele
LOCATION: 88050..88096
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID31
FEATURE:
NAME/KEY: allele
LOCATION: 88050..88096
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID52
FEATURE:
NAME/KEY: allele
LOCATION: 90819..90865
OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID49
FEATURE:
NAME/KEY: allele
LOCATION: 90819..90865
OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID70
FEATURE:
NAME/KEY: allele
LOCATION: 93690..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID32
FEATURE:
NAME/KEY: allele
LOCATION: 93690..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID53
FEATURE:
NAME/KEY: allele
LOCATION: 97099..97145
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID50
FEATURE:
NAME/KEY: allele
LOCATION: 97099..97145
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID71
FEATURE:
NAME/KEY: allele
LOCATION: 97130..97177
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID33
FEATURE:
NAME/KEY: allele
LOCATION: 97130..97177
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID54
FEATURE:
NAME/KEY: allele
LOCATION: 99075..99121
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID34
FEATURE:
NAME/KEY: allele
LOCATION: 99075..99121
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID55
FEATURE:
NAME/KEY: allele
LOCATION: 99094..99140
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID35
FEATURE:
NAME/KEY: allele
LOCATION: 99094..99140

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; OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID56
; FEATURE:
; NAME/KEY: allele
; LOCATION: 103783..103828
; OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID36
; FEATURE:
; NAME/KEY: allele
; LOCATION: 103783..103828
; OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID57
; FEATURE:
; NAME/KEY: allele
; LOCATION: 106918..106966
; OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID37
; FEATURE:
; NAME/KEY: allele
; LOCATION: 106918..106966
; OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID58
; FEATURE:
; NAME/KEY: allele
; LOCATION: 108084..108130
; OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID38
; FEATURE:
; NAME/KEY: allele
; LOCATION: 108084..108130
; OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID59
; FEATURE:
; NAME/KEY: allele
; LOCATION: 108127..108177
; OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID39
; FEATURE:
; NAME/KEY: allele
; LOCATION: 108127..108177
; OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID60
; FEATURE:
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```
Query Match 1.8%; Score 49; DB 3; Length 162450;
Best Local Similarity 100.0%; Pred. No. 1.2e-11;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2109 CTGAGGTCAGAGTTCAGAGCCAGCCTGGCCACATGTGTGAACCCCA 2157
Db 153776 CTGAGGTCAGAGTTCAGAGCCAGCCTGGCCACATGTGTGAACCCCA 153728
```

RESULT 64

```
US-09-513-999C-20281
; Sequence 20281, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclet, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 20281
; LENGTH: 141
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-513-999C-20281
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Query Match 1.8%; Score 48; DB 4; Length 141;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 2109 CTGAGGTCAGAGTTCAGAGCCAGCCTGGCCACATGTGTGAACCCCA 2156
|||||
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```
Db 92 CTGAGGTCAGAGTTCAGAGCCAGCCTGGCCACATGTGTGAACCCCA 139
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RESULT 65

```
US-08-916-901-6
; Sequence 6, Application US/08916901
; Patent No. 5892012
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: RAB PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/916,901
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0367 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2713 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-916-901-6
```

```
Query Match 1.8%; Score 48; DB 2; Length 2713;
Best Local Similarity 100.0%; Pred. No. 3.9e-11;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 2109 CTGAGGTCAGAGTTCAGAGCCAGCCTGGCCACATGTGTGAACCCCA 2156
Db 1901 CTGAGGTCAGAGTTCAGAGCCAGCCTGGCCACATGTGTGAACCCCA 1948
```

RESULT 66

```
US-09-154-602-6
; Sequence 6, Application US/09154602
; Patent No. 6300472
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: RAB PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
```


ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/154,602
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/916,901
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0367 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-845-4166
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2713 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-154-602-6

Query Match 1.8%; Score 48; DB 3; Length 2713;
Best Local Similarity 100.0%; Pred. No. 3.9e-11;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2109 CTGAGTCAGAGTTCAGAGCCAGCCTGGCCACATGTGAACCCCA 2156
|||
DB 1901 CTGAGTCAGAGTTCAGAGCCAGCCTGGCCACATGTGAACCCCA 1948

RESULT 67

US-09-054-272-41/c

; Sequence 41, Application US/09054272

; Patent No. 6692909

; GENERAL INFORMATION:

; APPLICANT: Lander, Eric S.

; APPLICANT: Daley, George Q.

; APPLICANT: Cargill, Michele

; APPLICANT: Ireland, James S.

; APPLICANT: Rozen, Steven G.

; TITLE OF INVENTION: CODING SEQUENCE POLYMORPHISMS

; TITLE OF INVENTION: IN VASCULAR PATHOLOGY GENES

; NUMBER OF SEQUENCES: 59

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.

; STREET: Two Militia Drive

; CITY: Lexington

; STATE: MA

; COUNTRY: USA

; ZIP: 02173

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows 95

; SOFTWARE: FastSEQ for Windows Version 2.0b

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/054,272

; FILING DATE: 01-APR-1998

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Granahan, Patricia

; REGISTRATION NUMBER: 32,227

; REFERENCE/DOCKET NUMBER: WHI98-05

; TELECOMMUNICATION INFORMATION:

; TELECOMMUNICATION INFORMATION:

TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
TELEX:
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 26928 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
US-09-054-272-41

Query Match 1.8%; Score 48; DB 4; Length 26928;
Best Local Similarity 100.0%; Pred. No. 3.5e-11;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2111 GAGTCAGAGTTCAGAGCCAGCCTGGCCACATGTGAACCCCATC 2158
|||
DB 18730 GAGTCAGAGTTCAGAGCCAGCCTGGCCACATGTGAACCCCATC 18683

RESULT 68

US-09-009-913-1/c

; Sequence 1, Application US/09009913

; Patent No. 6087485

; GENERAL INFORMATION:

; APPLICANT: Axy's Pharmaceuticals, Inc.

; TITLE OF INVENTION: Asthma Related Genes

; NUMBER OF SEQUENCES: 339

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Bozicevic & Reed, LLP

; STREET: 285 Hamilton Ave, Suite 200

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94301

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/009,913

; FILING DATE: 21-JAN-1998

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Sherwood, Pamela J

; REGISTRATION NUMBER: 36,677

; REFERENCE/DOCKET NUMBER: SEQ-4P

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-327-3231

; TELEFAX: 650-327-3231

; TELEX:

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 72928 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: Genomic DNA

; US-09-009-913-1

Query Match 1.8%; Score 48; DB 3; Length 72928;
Best Local Similarity 100.0%; Pred. No. 3.3e-11;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2120 AGTCAAGACAGCCTGGCCACATGTGAACCCCATCTACTAA 2167
|||
DB 55445 AGTCAAGACAGCCTGGCCACATGTGAACCCCATCTACTAA 55398

```
RESULT 69
US-09-792-616-1
; Sequence 1, Application US/09792616
; Patent No. 6780587
; GENERAL INFORMATION:
; APPLICANT: PXE International, Inc.
; APPLICANT: University of Hawaii
; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing
; TITLE OF INVENTION: Pseudoxanthoma Elasticum
; FILE REFERENCE: PXE-001
; CURRENT APPLICATION NUMBER: US/09/792,616
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; LENGTH: 107820
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "n" can be an A or a T or a G or a C
US-09-792-616-1
```

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Query Match      1.8%; Score 48; DB 4; Length 107820;
Best Local Similarity 100.0%; Pred. No. 3.3e-11;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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QY      2120 AGTCAAGACCAAGCCTGGCCCAACATGTGAACCCCACTCTACTAA 2167
          |||
Db       60456 AGTCAAGACCAAGCCTGGCCCAACATGTGAACCCCACTCTACTAA 60503
```

```
RESULT 70
US-10-148-806-3
; Sequence 3, Application US/10148806
; Patent No. 6762042
; GENERAL INFORMATION:
; APPLICANT: Bai, Chang
; APPLICANT: Metzger, Michael
; APPLICANT: Liu, Xiaomel
; TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN NHL, A DNA
; TITLE OF INVENTION: HELICASE
; FILE REFERENCE: 20585P
; CURRENT APPLICATION NUMBER: US/10/148,806
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: US00/33065
; PRIOR FILING DATE: 2000-12-09
; PRIOR APPLICATION NUMBER: 60/169,970
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 114793
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-148-806-3
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Query Match      1.8%; Score 48; DB 4; Length 114793;
Best Local Similarity 100.0%; Pred. No. 3.3e-11;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      2056 GTGGCTACACCTGTATCCCAAGCACTTTGGAGGCCCAAGTGGTGG 2103
          |||
Db       106838 GTGGCTACACCTGTATCCCAAGCACTTTGGAGGCCCAAGTGGTGG 106885
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RESULT 71
US-09-513-999C-17885/C
; Sequence 17885, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
```

```
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 17885
; LENGTH: 274
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 146
; OTHER INFORMATION: w=a or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 215
; OTHER INFORMATION: s=g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 222
; OTHER INFORMATION: y=c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 224
; OTHER INFORMATION: m=a or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 240
; OTHER INFORMATION: k=g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 248
; OTHER INFORMATION: m=a or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 254
; OTHER INFORMATION: k=g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 259
; OTHER INFORMATION: m=a or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 261
; OTHER INFORMATION: s=g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 264
; OTHER INFORMATION: m=a or c
US-09-513-999C-17885
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Query Match      1.7%; Score 47; DB 4; Length 274;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      2109 CTGAGTCAGAGTTCAGACCAAGCCTGGCCCAACATGTGAACCCC 2155
          |||
Db       208 CTGAGTCAGAGTTCAGACCAAGCCTGGCCCAACATGTGAACCCC 162
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RESULT 72
US-08-849-701-7
; Sequence 7, Application US/08849701
; Patent No. 5922544
; GENERAL INFORMATION:
; APPLICANT: Miyai, Kiyoshi
; APPLICANT: Naitoh, Tsutomu
```

```
; APPLICANT: Yonekawa, Toshihiro
; TITLE OF INVENTION: Method of Cell Detection
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/849,701
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP95/02734
; FILING DATE: 27-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: EIKEN1.001APC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-760-0404
; TELEFAX: 714-760-9502
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 280 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: Alu sequence BLUR11
; US-08-849-701-7

Query Match          1.7%; Score 47; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2109 CTGAGGTCAAGAGTTCAGACCAGCCTGGCCACATGTGAAACCCC 2155
         |||||||
Db       44  CTGAGGTCAAGAGTTCAGACCAGCCTGGCCACATGTGAAACCCC 90

RESULT 73
US-08-133-629-8
; Sequence 8, Application US/08133629
; Patent No. 5597694
; GENERAL INFORMATION:
; APPLICANT: Munroe, David J.
; APPLICANT: Housman, David E.
; TITLE OF INVENTION: AMPLIFICATION OF NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: United States of America
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/133,629
; FILING DATE: 07-OCT-1993
```

```
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Greer, Helen
; REGISTRATION NUMBER: 36,816
; REFERENCE/DOCKET NUMBER: M0828/7001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; TELEX: 92-1742 EZEKIEL
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 282 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-133-629-8

Query Match          1.7%; Score 47; DB 1; Length 282;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2109 CTGAGGTCAAGAGTTCAGACCAGCCTGGCCACATGTGAAACCCC 2155
         |||||||
Db       65  CTGAGGTCAAGAGTTCAGACCAGCCTGGCCACATGTGAAACCCC 111

RESULT 74
US-08-579-445-26
; Sequence 26, Application US/08579445
; Patent No. 6566053
; GENERAL INFORMATION:
; APPLICANT: Perucho, Manuel
; APPLICANT: Pelnado, Miguel A.
; APPLICANT: Ionov, Yuri
; APPLICANT: Malkhosyan, Sergei
; TITLE OF INVENTION: Identification of Neoplasms by Detection
; TITLE OF INVENTION: of Genetic Deletions
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/579,445
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/152,484
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kirkpatrick, Anita M.
; REGISTRATION NUMBER: 32,617
; REFERENCE/DOCKET NUMBER: STRATAG.009A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 283 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
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US-08-579-445-26

Query Match 1.7%; Score 47; DB 4; Length 283;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2109 CTGAGGTCAAGAGTTCAAGACCAAGCTGGCCCAACATGTTGAACCCC 2155
|||||
Db 65 CTGAGGTCAAGAGTTCAAGACCAAGCTGGCCCAACATGTTGAACCCC 111

RESULT 75

US-09-513-999C-27220/C

; Sequence 27220, Application US/09513999C

; Patent No. 6783961

; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.

; APPLICANT: Duclert, A.

; APPLICANT: Giordano, J.Y.

; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

; Patent No. 6783961

; FILE REFERENCE: 59.US2.REG

; CURRENT APPLICATION NUMBER: US/09/513, 999C

; CURRENT FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/122, 487

; PRIOR FILING DATE: 1999-02-26

; NUMBER OF SEQ ID NOS: 36681

; SOFTWARE: Patent.pm

; SEQ ID NO 27220

; LENGTH: 330

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 128

; OTHER INFORMATION: r=a or g

US-09-513-999C-27220

Query Match 1.7%; Score 47; DB 4; Length 330;

Best Local Similarity 100.0%; Pred. No. 1.2e-10;

Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2109 CTGAGGTCAAGAGTTCAAGACCAAGCTGGCCCAACATGTTGAACCCC 2155
|||||
Db 262 CTGAGGTCAAGAGTTCAAGACCAAGCTGGCCCAACATGTTGAACCCC 216

Search completed: October 28, 2004, 19:22:26

Job time : 238 secs

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